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Protein structure prediction results for the protein sequence: MKFI GKLLLY I L I A L L V A I A G L Y F L L Q T R W G A E H I S A W V S E N S D Y H L A F G A M D H R F S A P S.

The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-600).

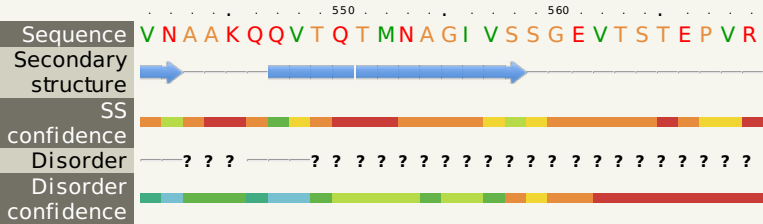
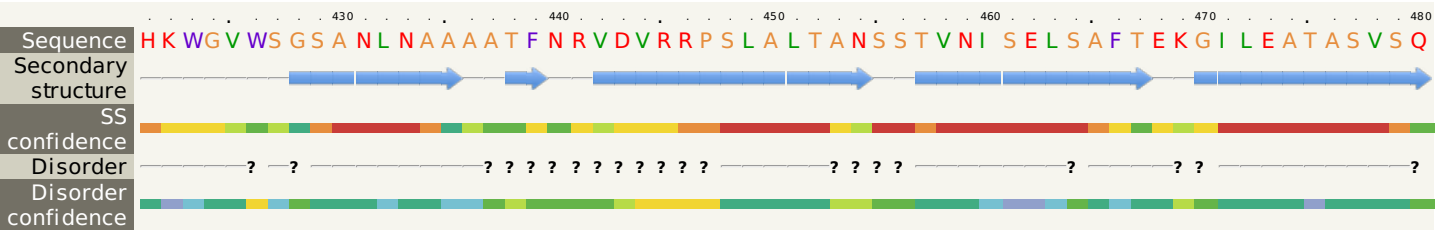
Sequence: MKFI GKLLLY I L I A L L V A I A G L Y F L L Q T R W G A E H I S A W V S E N S D Y H L A F G A M D H R F S A P S

Secondary structure: The structure is primarily composed of alpha-helices (represented by blue arrows) and beta-strands (represented by green cylinders). Notable features include a long alpha-helix from residue 1 to 30, a beta-strand at residue 31, and a long alpha-helix from residue 32 to 45. There are also several shorter alpha-helices and beta-strands scattered throughout the sequence.

SS confidence: The confidence is generally high, with many segments reaching a confidence of 1.0 (represented by green bars).

Disorder: The protein is mostly ordered, with some regions marked as disordered (represented by red bars). These regions are primarily located at the N-terminus (residues 1-10) and in the middle of the protein (residues 110-120).

Disorder confidence: The confidence in the disorder prediction is generally low, with many segments marked as '?' (represented by grey bars).



Confidence Key
High(9) Low (0)
? Disordered
Alpha helix
Beta strand