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Protein structure prediction results for the protein sequence MERVSI TERP DWREKAHEYGFNFHTMYGEPYWCEDAYYKLT LAQVEKLEEVTAELHQMCL. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-600 residues).

Sequence: MERVSI TERP DWREKAHEYGFNFHTMYGEPYWCEDAYYKLT LAQVEKLEEVTAELHQMCL

Secondary structure: The structure is primarily composed of alpha-helices (green) and loops (blue). Key features include a long alpha-helix from residue 10 to 20, a loop from 25 to 35, and a long alpha-helix from 40 to 60. The structure continues with a series of alpha-helices and loops, ending with a long alpha-helix from 580 to 600.

SS confidence: The confidence is generally high, with some lower confidence regions (yellow/green) around residues 25-35 and 40-60.

Disorder: The protein is mostly ordered, with some disordered regions (red) indicated by question marks (e.g., residues 10-20, 25-35, 40-60).

Disorder confidence: The confidence is generally high, with some lower confidence regions (yellow/green) indicated by question marks (e.g., residues 10-20, 25-35, 40-60).

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