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Protein structure and disorder analysis for the protein sequence MNTIFSA...KLV. The figure displays the full sequence (1-400) and its secondary structure (SS) and disorder confidence. The sequence is color-coded by amino acid type. The secondary structure is shown as a green ribbon model. The disorder confidence is shown as a red bar. The protein is predicted to be a single domain protein with a high confidence score of 1.0. The disorder confidence is 0.0, indicating no disordered regions. The protein is predicted to be a single domain protein with a high confidence score of 1.0. The disorder confidence is 0.0, indicating no disordered regions.

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