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Protein structure and disorder analysis of the full-length protein (1-380 aa). The figure displays the amino acid sequence, secondary structure, and disorder predictions across the entire protein. The sequence is color-coded by physicochemical properties. The secondary structure is shown as a green ribbon model. The disorder predictions are shown as horizontal bars with color-coded confidence levels. The protein is composed of several alpha-helices and beta-strands, with a central region (residues 100-150) showing a high degree of disorder.

Residue Range	Sequence	Secondary Structure	Disorder
1 - 60	MI YLVI SVFLITAFICLYLK KDI FYPAVCVNIIFALVLLGYEITSDIYAFQLNDATLIFL	Alpha-helices	Disordered
60 - 120	LCNVLTFTLSCLLTESVLDLNI RKVNNAIYSIPSKKVHNVGLLVI SFSMIYICMRLSNYQ	Alpha-helices	Disordered
120 - 180	FGTSLLSYMNLI RDADV E DTSRNFSAYMQPIILTTFALFI WSKKFTNTKVSKTFTLLVFI	Alpha-helices	Disordered
180 - 240	VFI FAIILNT GKQIVFMV I SYAFI VGVNRVKHYVYLITAVGVLFSLYMLFLRGLPGGMA	Alpha-helices	Disordered
240 - 300	YYLSMYLVSP I I AFQEFYFQQVSN SASSHVFWF FERLMGLLTGGVSM SLHKEFVWVGLPT	Alpha-helices	Disordered
300 - 360	NVYTAFSDYVYI SAE LSYLMMVI HGCISGV LWRLSRNYI SVKIFYSYFIYTF SFI FYHES	Alpha-helices	Disordered
360 - 380	FMTNI SSWI QITLCIIVFSQFLKAQKI K	Alpha-helices	Disordered

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