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Protein structure prediction results for the protein sequence. The figure displays the sequence, secondary structure, and confidence scores for the protein. The sequence is shown in a color-coded format, and the secondary structure is represented by blue arrows (alpha-helices) and green cylinders (beta-strands). The confidence scores are shown as a bar chart below the sequence. The protein is predicted to be a single-domain protein with a length of 340 amino acids. The structure is composed of several alpha-helices and beta-strands, with a high confidence score for the overall fold.

Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
MKNSKAI LQVP GTMKI I SAEI PVPKEDEVLI KVEYVGI CGSDVHGFESGPFI PPKDPNQE	[Secondary structure diagram for residues 1-60]	[SS confidence bar for residues 1-60]	[Disorder bar for residues 1-60]	[Disorder confidence bar for residues 1-60]
IGLGHECAGT VVAVGS RVRK F KPGDRVNI EPGVPCGHCRYCLEGKYNI CPD VDFMATQPN	[Secondary structure diagram for residues 70-120]	[SS confidence bar for residues 70-120]	[Disorder bar for residues 70-120]	[Disorder confidence bar for residues 70-120]
YRGAL THYLCHPESFTYKLP DNMDTMEGAL VEPAAVGMHAAMLADV KPGKKI I L GAGC I	[Secondary structure diagram for residues 130-180]	[SS confidence bar for residues 130-180]	[Disorder bar for residues 130-180]	[Disorder confidence bar for residues 130-180]
GLMTLQACKCLGATEI AVVDVLEKRLAMAEQLGATVVI NGAKE DTI ARCQQFTEDMGADI	[Secondary structure diagram for residues 190-240]	[SS confidence bar for residues 190-240]	[Disorder bar for residues 190-240]	[Disorder confidence bar for residues 190-240]
VFETAGSAVT VKQAPYLVMRGGKI MI VGTVPGDSAI N FLKINREVTI QTVFRYANRYPVT	[Secondary structure diagram for residues 250-300]	[SS confidence bar for residues 250-300]	[Disorder bar for residues 250-300]	[Disorder confidence bar for residues 250-300]
IEAIS SGRFDVKS MVTHI YDYRDVQQAF EESVNNKRDI I KGV I KI S D	[Secondary structure diagram for residues 310-340]	[SS confidence bar for residues 310-340]	[Disorder bar for residues 310-340]	[Disorder confidence bar for residues 310-340]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand