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Description	P0AEI6
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Protein structure analysis of the N-terminal region (residues 1-120) of the protein. The analysis includes the amino acid sequence, predicted secondary structure, and confidence scores for the structure and disorder.

**Sequence:** MF KPHVTTVACVVHAEGKFLVVEETI NGKALWNQPAAGHL EADETLVEAAARELWEETGI SA


**Secondary structure:** The structure is primarily composed of alpha-helices (represented by blue arrows) and beta-strands (represented by green zig-zags). The first segment (residues 1-60) contains several alpha-helices and a beta-strand. The second segment (residues 61-120) contains a large alpha-helix and a beta-strand.

**SS confidence:** The confidence scores for the secondary structure are generally high, with some lower confidence regions (indicated by yellow and orange) around residues 10-20 and 40-50.


**Disorder:** The protein is predicted to be disordered in several regions, indicated by question marks (???) above the sequence.


**Disorder confidence:** The confidence scores for the disorder prediction are generally low, with some higher confidence regions (indicated by red) around residues 10-20 and 40-50.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand