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Description	P0AGG2
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This section provides a detailed view of the protein structure prediction results for the full-length protein, showing sequence, secondary structure, and disorder predictions across the entire length (1-280 residues).

Sequence: MSQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHSYFLRPGDSKKPIIYDVELRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGFEHQKTMPSAPAPDGLPSETQIAQSLAHLPPVCLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQVWIRANGSVPPDDL RVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWLLYSVESTSASSARGFVRGEFYTQDGVLVASTVQEGVMRNHN


Secondary structure: The diagram shows alpha-helices (green cylinders) and beta-strands (blue arrows) predicted for the full-length protein. Key features include a large alpha-helical region at the N-terminus (residues 1-60), a beta-strand region (residues 70-110), and a large alpha-helical region at the C-terminus (residues 120-180).

SS confidence: A bar chart showing the confidence of the secondary structure predictions, with colors indicating different confidence levels (red for high, yellow for medium, green for low).


Disorder: A bar chart showing the predicted disorder of the protein, with colors indicating different disorder levels (red for high, yellow for medium, green for low).


Disorder confidence: A bar chart showing the confidence of the disorder predictions, with colors indicating different confidence levels (red for high, yellow for medium, green for low).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand