


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Description	P0ADP7
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Unique Job ID	f0ef3621f3d13d28

The image displays a protein structure prediction for a 200-amino acid protein. The visualization is organized into four segments, each corresponding to a different region of the protein. Each segment includes the following information:


- Sequence:** The amino acid sequence for that segment, with residues numbered at the top.
- Secondary structure:** A representation of the protein's fold, showing alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS (Solvent Accessibility):** A bar chart showing the relative solvent accessibility of each residue.
- confidence:** A bar chart showing the confidence score for each residue, with colors indicating different levels of confidence.
- Disorder:** A bar chart showing the predicted disorder of each residue, with colors indicating different levels of disorder.
- Disorder confidence:** A bar chart showing the confidence score for the disorder prediction.


The protein structure is characterized by several alpha-helices and beta-strands, with some regions of high confidence and others of lower confidence or disorder. The overall structure is a complex fold, typical of a protein of this size.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand