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Protein structure and disorder analysis of the first 110 amino acids of the protein. The top panel shows the full sequence with secondary structure elements (alpha helices and beta strands) and disorder predictions. The bottom panel shows a zoomed-in view of residues 70-110.

Sequence: QLLPS A Y S C S R V D L Y K P P L R R E D C R D S L N L F P V P N G D N V I Y L G S G N W R G C G S C K V T I Y N R

Secondary structure: The structure shows several alpha helices (green cylinders) and beta strands (blue arrows). The first alpha helix is located between residues 10 and 20. The second alpha helix is located between residues 20 and 30. The third alpha helix is located between residues 30 and 40. The fourth alpha helix is located between residues 40 and 50. The fifth alpha helix is located between residues 50 and 60. The sixth alpha helix is located between residues 60 and 70. The seventh alpha helix is located between residues 70 and 80. The eighth alpha helix is located between residues 80 and 90. The ninth alpha helix is located between residues 90 and 100. The tenth alpha helix is located between residues 100 and 110.

SS confidence: The confidence scores for the secondary structure elements are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the alpha helices and lower for the beta strands.

Disorder: The disorder predictions are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the regions between the alpha helices and lower for the alpha helices themselves.

Disorder confidence: The confidence scores for the disorder predictions are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the regions between the alpha helices and lower for the alpha helices themselves.

Zoomed-in view (Residues 70-110):

Sequence: GSRES R V T A P K G W A A T A V H Q A F D H C E G K P G S A T I G D D G K I I A K I D Y G N S G Q G D C P P


Secondary structure: The structure shows several alpha helices (green cylinders) and beta strands (blue arrows). The first alpha helix is located between residues 70 and 80. The second alpha helix is located between residues 80 and 90. The third alpha helix is located between residues 90 and 100. The fourth alpha helix is located between residues 100 and 110.

SS confidence: The confidence scores for the secondary structure elements are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the alpha helices and lower for the beta strands.


Disorder: The disorder predictions are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the regions between the alpha helices and lower for the alpha helices themselves.


Disorder confidence: The confidence scores for the disorder predictions are shown as a bar chart. The scores range from 0.0 to 1.0. The scores are generally high for the regions between the alpha helices and lower for the alpha helices themselves.

Confidence Key

High(9)  Low (0)

? Disordered (27%)

 Alpha helix (16%)

 Beta strand (32%)