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Protein Structure Analysis of VIKAR

Full-length protein (residues 1-360):

- Sequence:** M Q E R H T E Q D Y R A L L I A D T P I I D V R A P I E F E H G A M P A A I N L P L M N N D E R A A V G T C Y K Q Q G S
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are shown. Helices are located at residues 10-20, 30-40, 50-60, 70-80, 90-100, 110-120, 130-140, 150-160, 170-180, 190-200, 210-220, 230-240, 250-260, 270-280, 290-300, 310-320, 330-340, 350-360.
- SS (Solvent Accessibility):** High accessibility (red) is observed in the N-terminal region (residues 1-60) and the C-terminal region (residues 310-360).
- confidence:** Confidence scores are shown for each residue, with higher values (green/yellow) indicating higher confidence.
- Disorder:** Disorder predictions are shown, with higher values (red) indicating higher disorder. The N-terminal region (residues 1-60) and the C-terminal region (residues 310-360) are predicted to be disordered.
- Disorder confidence:** Disorder confidence scores are shown for each residue.

Detailed view of the C-terminal region (residues 310-360):

- Sequence:** L A A R L D A A L T T Q L T T G S T D G H L A W L V P L L E E Y Y D P M Y R Y Q L E K K A E K V V F R G E W A E V A E W
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are shown. Helices are located at residues 310-320, 330-340, 350-360.
- SS (Solvent Accessibility):** High accessibility (red) is observed in the C-terminal region (residues 310-360).
- confidence:** Confidence scores are shown for each residue, with higher values (green/yellow) indicating higher confidence.
- Disorder:** Disorder predictions are shown, with higher values (red) indicating higher disorder. The C-terminal region (residues 310-360) is predicted to be disordered.
- Disorder confidence:** Disorder confidence scores are shown for each residue.

Legend:

- Sequence:** V K A R
- Secondary structure:** Alpha-helices (green), beta-strands (blue)
- SS (Solvent Accessibility):** High accessibility (red), low accessibility (blue)
- confidence:** Confidence scores (green/yellow)
- Disorder:** Disorder predictions (red)
- Disorder confidence:** Disorder confidence scores (green/yellow)

Confidence Key
High(9)  Low (0)
? Disordered
 Alpha helix
 Beta strand