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Figure 1 displays the protein structure and disorder analysis for the human protein. The protein is 240 residues long. The figure shows four panels of protein data, each corresponding to a different region of the protein. Each panel includes the amino acid sequence, secondary structure (SS), confidence, disorder, and disorder confidence.

The protein is predicted to be a single-domain protein with a high degree of disorder. The secondary structure is primarily alpha-helical, with a few beta-strands. The disorder analysis shows that the protein is highly disordered, with a disorder confidence of 1.0 for most of the sequence.

The panels show the following data:

- Panel 1 (Residues 1-60):** Sequence: MKI DLNADL GEGC ASDAELL TLVSSANI ACGFHAGDAQI MQACVREAI KNGVAI GAHP SF. Secondary structure: 1 alpha-helix, 1 beta-strand. Confidence: 1.0. Disorder: 1.0. Disorder confidence: 1.0.
- Panel 2 (Residues 70-120):** Sequence: PDRENFGRSAMQLPPETVYAQTLYQI GALATI ARAQGGV MRHV KPHGML YNQAAKEAQLA. Secondary structure: 1 alpha-helix, 1 beta-strand. Confidence: 1.0. Disorder: 1.0. Disorder confidence: 1.0.
- Panel 3 (Residues 130-180):** Sequence: DAI ARAVYACDPALI LVGLAGSELI RAGKQYGLTTREEVF ADRGYQADGSLVPRSQS GAL. Secondary structure: 1 alpha-helix, 1 beta-strand. Confidence: 1.0. Disorder: 1.0. Disorder confidence: 1.0.
- Panel 4 (Residues 190-240):** Sequence: IENEEQALAQTL E MVQHGRV KSI TGEWATVAAQT VCLHGDGEHALAFARRLRSAFAEKGI. Secondary structure: 1 alpha-helix, 1 beta-strand. Confidence: 1.0. Disorder: 1.0. Disorder confidence: 1.0.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand