


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Figure 1 displays the protein structure and disorder analysis of the human protein Hs000000000. The protein is 180 residues long, with a molecular weight of 19.5 kDa and an isoelectric point of 4.5. The analysis is presented in four panels, each showing a different segment of the protein structure and its corresponding disorder analysis.


The panels are organized as follows:


- Panel 1 (Residues 1-60):** Shows the sequence MKKIWLALAGLVLAFSASAAQYEDGKQYTTLEKPVAGAPQVLEFFSF FCPHCYQFEVLH. The secondary structure includes several alpha-helices and beta-strands. The disorder analysis shows a high confidence score for disorder in the N-terminal region (residues 1-20) and a lower confidence score for disorder in the C-terminal region (residues 50-60).
- Panel 2 (Residues 70-120):** Shows the sequence ISDNVKKKLPEGVKMTKYHVNFMGDDLKGLDTQAWAVAMALGVEDKVTVPLEGVQKTQT. The secondary structure includes several alpha-helices and beta-strands. The disorder analysis shows a high confidence score for disorder in the N-terminal region (residues 70-80) and a lower confidence score for disorder in the C-terminal region (residues 110-120).
- Panel 3 (Residues 130-180):** Shows the sequence IRSASDIRDVFINAGIKGEEYDAAVNSFVVKSLVAQQEKAAADVQLRGVPAMFVNGKYQL. The secondary structure includes several alpha-helices and beta-strands. The disorder analysis shows a high confidence score for disorder in the N-terminal region (residues 130-140) and a lower confidence score for disorder in the C-terminal region (residues 170-180).
- Panel 4 (Residues 190-200):** Shows the sequence NPQGMDTSNMDV FVQQYADTVKYLSEKK. The secondary structure includes several alpha-helices and beta-strands. The disorder analysis shows a high confidence score for disorder in the N-terminal region (residues 190-200) and a lower confidence score for disorder in the C-terminal region (residues 190-200).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand