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The figure displays the protein structure analysis of the human protein sequence: MNALLSNPFKERLRKGEVQIGLWLSSTTAYMAEIAATSGYDWLLIDGEHAPNTIQDLYHQ. The analysis is presented across five rows for the full sequence (1-260 residues) and four segments of the sequence.

Sequence: MNALLSNPFKERLRKGEVQIGLWLSSTTAYMAEIAATSGYDWLLIDGEHAPNTIQDLYHQ

Secondary structure: The structure is shown as a ribbon diagram. It features several alpha-helices (green) and beta-strands (blue). The structure is primarily composed of alpha-helices, with a few beta-strands interspersed.

SS confidence: The confidence scores are shown as a bar chart. The confidence is generally high, with some lower confidence regions (yellow/green) around residues 10-20 and 40-50.


Disorder: The disorder analysis shows that the protein is mostly ordered, with some disordered regions (red) at the N-terminus and C-terminus.

Disorder confidence: The confidence scores for disorder are shown as a bar chart. The confidence is generally high, with some lower confidence regions (yellow/green) around residues 10-20 and 40-50.


Sequence segments and analysis:


- Segment 1 (Residues 1-60):** Sequence: LQAVAPYASQPVRPVEGSKPLIKQVLDTGAQTLLIPMVDTAEQARQVVSAATRYPPYGER. Secondary structure shows alpha-helices and beta-strands. SS confidence is high. Disorder is low. Disorder confidence is high.
- Segment 2 (Residues 70-120):** Sequence: GVGASVARAARWGRIVENYMAQVNDSLCLLVQVESKTALDNLDEILDVEGIDGVFIGPADL. Secondary structure shows alpha-helices and beta-strands. SS confidence is high. Disorder is low. Disorder confidence is high.
- Segment 3 (Residues 130-180):** Sequence: SASLGYPDNA GHPEVQRIETSI RRI RAAGKAAGFLAVAPDMAQQCLAWGANFVAVGVDT. Secondary structure shows alpha-helices and beta-strands. SS confidence is high. Disorder is low. Disorder confidence is high.
- Segment 4 (Residues 190-240):** Sequence: MLYS DALDQRLAMFKSGKNGPRIKGSY. Secondary structure shows alpha-helices and beta-strands. SS confidence is high. Disorder is low. Disorder confidence is high.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand