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Figure 1 displays the protein structure and disorder analysis of the human protein RPLP0. The protein is shown as a blue ribbon model, with green cylinders representing alpha-helices and blue arrows representing beta-strands. The analysis is divided into three panels, each showing a different region of the protein (1-60, 70-120, and 130-160). Each panel includes the sequence, secondary structure (SS), SS confidence, disorder, and disorder confidence.

**Panel 1 (1-60):** The sequence is MKTNRS L VVI VSLI TATL LLLTACAQPEQSSLAGDWLLTPKDKTRGLTGSIAVNIAPFRC. The secondary structure shows a large alpha-helix (residues 10-25) and a beta-strand (residues 35-45). The disorder analysis shows high disorder (red) in the N-terminal region (residues 1-10) and the C-terminal region (residues 50-60).


**Panel 2 (70-120):** The sequence is TNCRGDNL P DNTRRWQLSGGNEKELTYLHNMSAQEKVGLNPGWQCYTSFFMRVCQGKPGT. The secondary structure shows a large alpha-helix (residues 75-90) and a beta-strand (residues 105-120). The disorder analysis shows high disorder (red) in the N-terminal region (residues 70-80) and the C-terminal region (residues 110-120).


**Panel 3 (130-160):** The sequence is RPIVNE DYVSESGFFGSMMHVGI IELRRCS ENCQQELKAI NTH. The secondary structure shows a large alpha-helix (residues 135-150) and a beta-strand (residues 155-160). The disorder analysis shows high disorder (red) in the N-terminal region (residues 130-140) and the C-terminal region (residues 150-160).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand