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Figure 1 displays the protein structure and disorder analysis of the C-terminal region of the human protein. The figure is divided into three panels, each showing a different segment of the protein sequence (residues 1-60, 70-120, and 130-180). Each panel displays the amino acid sequence, a secondary structure prediction (SS) with alpha-helices and beta-strands, a confidence score (confidence), a disorder prediction (Disorder), and a disorder confidence score (Disorder confidence).

Panel 1 (Residues 1-60): The sequence is MSIAVTTTDPNTGTGVSSTSSSSLTGSNAADLQSSFLTLLVAQLKNQDPTNPMENNELTSQ. The secondary structure shows a long alpha-helix from residue 30 to 50 and a shorter alpha-helix from residue 55 to 60. The confidence is high (red) for the first 30 residues and lower (yellow/green) for the rest. The disorder prediction shows a high degree of disorder (red) across the entire segment.

Panel 2 (Residues 70-120): The sequence is LAQISTVSGIEKLNTTLGSI SGQIDNSQSLQASNLI GHGVMIPGTTVL AGTGSEEGAVTT. The secondary structure shows a long alpha-helix from residue 70 to 95 and a shorter alpha-helix from residue 100 to 105. The confidence is high (red) for the first 70 residues and lower (yellow/green) for the rest. The disorder prediction shows a high degree of disorder (red) across the entire segment.

Panel 3 (Residues 130-180): The sequence is TTPFGVELQQAADKVTATIT DKN GAVVRTI DIGELTAGVHSFTWDGTLTDGSTAPNGSYN. The secondary structure shows a long alpha-helix from residue 130 to 145 and a shorter alpha-helix from residue 150 to 155. The confidence is high (red) for the first 130 residues and lower (yellow/green) for the rest. The disorder prediction shows a high degree of disorder (red) across the entire segment.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand