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Figure 1 displays the protein structure and disorder analysis of the C-terminal region of the human protein. The figure shows three segments of the protein sequence (residues 1-60, 70-120, and 130-180) along with their predicted secondary structures (SS) and disorder confidence scores.

**Segment 1 (Residues 1-60):**

- Sequence:** MS R F I P I E L H H A S R L L N H G P T V L I T S F D E Q S Q R R N I M A A A W S M P V E F E P P R V A I V V D K S T
- Secondary structure (SS):** Predicted structure shows a series of alpha-helices and loops.
- Disorder:** The disorder confidence is high (red bar) across the entire segment.

**Segment 2 (Residues 70-120):**

- Sequence:** W T R E L I E H N G K F G I V I P G V A A T N W T W A V G S V S G R D E D K F N C Y G I P V V R G P V F G L P L V E E K
- Secondary structure (SS):** Predicted structure shows a series of alpha-helices and loops.
- Disorder:** The disorder confidence is high (red bar) across the entire segment.


**Segment 3 (Residues 130-180):**

- Sequence:** C L A W M E C R L L P A T S A Q E E Y D T L F G E V V S A A A D A R V F V E G R W Q F D D D K L N T L H H L G A G T F V
- Secondary structure (SS):** Predicted structure shows a series of alpha-helices and loops.
- Disorder:** The disorder confidence is high (red bar) across the entire segment.


**Segment 4 (Residues 1-6):**


- Sequence:** T S G K R V T A G
- Secondary structure (SS):** Predicted structure shows a series of alpha-helices and loops.
- Disorder:** The disorder confidence is high (red bar) across the entire segment.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand