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Figure 1 displays the schematic representation of the protein structure of the human protein, showing the sequence, secondary structure, and confidence scores across three segments.

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

- Sequence:** ML RLL E E K I A T P L G P L W V I C D E Q F R L R A V E W E E Y S E R M V Q L L D I H Y R K E G Y E R I S A T N P G
- Secondary structure:** The structure is primarily composed of alpha-helices (blue) and beta-strands (green).
- SS confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.
- Disorder:** The protein is predicted to be disordered (red) across the entire segment.
- Disorder confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.


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

- Sequence:** G L S D K L R E Y F A G N L S I I D T L P T A T G G T P F Q R E V W K T L R T I P C G Q V M H Y G Q L A E Q L G R P G A
- Secondary structure:** The structure is primarily composed of alpha-helices (blue) and beta-strands (green).
- SS confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.
- Disorder:** The protein is predicted to be disordered (red) across the entire segment.
- Disorder confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.

**Segment 3 (Residues 130-170):**


- Sequence:** A R A V G A A N G S N P I S I V V P C H R V I G R N G T M T G Y A G G V Q R K E W L L R H E G Y L L L
- Secondary structure:** The structure is primarily composed of alpha-helices (blue) and beta-strands (green).
- SS confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.
- Disorder:** The protein is predicted to be disordered (red) across the entire segment.
- Disorder confidence:** The confidence scores are high (red) for most residues, with some lower scores (yellow and green) at the C-terminus.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand