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Protein structure prediction results for three protein segments. Each segment displays the amino acid sequence, secondary structure (alpha-helices and beta-strands), sequence confidence, disorder, and disorder confidence.

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

- Sequence:** M M R Q S L Q A V L P E I S G N K T S S L R K S V C S D L L T L F N S P H S A L P S L L V S G M P E W Q V H N P S D K H
- Secondary structure:** Alpha-helices (green) at positions 1-15, 40-45, and 55-60.
- SS confidence:** High confidence (red) for the helices, lower confidence (yellow/green) for loops.
- Disorder:** Disordered regions (grey) at positions 1-15, 18-35, 40-45, and 55-60.
- Disorder confidence:** High confidence (red) for the disordered regions, lower confidence (yellow/green) for helices.


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

- Sequence:** L Q S W Y C R Q L R S A L L F H E P R I A A L Q V N L K E A Y C H T L A I S L E I M L Y H D D E P L T F D L V W D N G G
- Secondary structure:** Beta-strand (green) at positions 70-85, followed by three long alpha-helices (blue) at positions 88-105, 108-120, and 123-135.
- SS confidence:** High confidence (red) for the helices, lower confidence (yellow/green) for the strand and loops.
- Disorder:** Disordered regions (grey) at positions 70-85, 88-105, 108-120, and 123-135.
- Disorder confidence:** High confidence (red) for the disordered regions, lower confidence (yellow/green) for the helices.


**Segment 3 (130):**


- Sequence:** W R S A T L E N V S
- Secondary structure:** Beta-strand (blue arrow) at positions 130-135.
- SS confidence:** High confidence (red) for the strand, lower confidence (yellow/green) for loops.
- Disorder:** Disordered regions (grey) at positions 130-135.
- Disorder confidence:** High confidence (red) for the disordered regions, lower confidence (yellow/green) for the strand.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand