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

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

- Sequence: MT S R R D W Q L Q Q L G I T Q W S L R R P G A L Q G E I A I A I P A H V R L V M V A N D L P A L T D P L V S D V L R A
- Secondary structure: Alpha helices (green) and beta strands (blue).
- SS confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.
- Disorder: Low confidence (green) for residues 1-10, 15-20, 25-30, 35-40, 45-50, 55-60.
- Disorder confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.

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

- Sequence: L T V S P D Q V L Q L T P E K I A M L P Q G S H C N S W R L G T D E P L S L E G A Q V A S P A L T D L R A N P T A R A A
- Secondary structure: Alpha helices (green) and beta strands (blue).
- SS confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.
- Disorder: Low confidence (green) for residues 70-80, 85-90, 95-100, 105-110, 115-120.
- Disorder confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.

**Segment 3 (Residues 130-140):**


- Sequence: L W Q Q I C T Y E H D F F P R N D
- Secondary structure: Alpha helix (green).
- SS confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.
- Disorder: Low confidence (green) for residues 130-140.
- Disorder confidence: High confidence (red) for most residues, with some medium (yellow) and low (green) confidence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand