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Protein structure prediction results for a protein of length 230. The image shows three segments of the protein: residues 1-60, 70-120, and 130-180. Each segment displays the sequence, secondary structure (alpha-helices and beta-strands), and confidence scores for SS, Disorder, and Disorder confidence.

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

- Sequence: M Q Y P I N E M F Q T L Q G G E Y F T G V P A I F I R L Q G C P V G C A W C D T K H T W E K L E D R E V S L F S I L A K
- Secondary structure: Alpha-helices at residues 10-15 and 25-30; Beta-strands at residues 55-60.
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence (dark blue) for most regions, with some lower confidence (light blue) at the N-terminus.

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

- Sequence: T K E S D K W G A A S S E D L L A V I G R Q G Y T A R H V V I T G G E P C I H D L L P L T D L L E K N G F S C Q I E T S
- Secondary structure: Alpha-helices at residues 75-80, 85-90, 100-105, and 115-120; Beta-strands at residues 95-100 and 110-115.
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence (dark blue) for most regions, with some lower confidence (light blue) at the N-terminus.


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

- Sequence: G T H E V R C T P N T V V T V S P K L N M R G G Y E V L S Q A L E R A N E I K H P V G R V R D I E A L D E L L A T L T D
- Secondary structure: Alpha-helices at residues 135-140, 145-150, 160-165, and 175-180; Beta-strands at residues 155-160 and 170-175.
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence (dark blue) for most regions, with some lower confidence (light blue) at the N-terminus.


**Segment 4 (Residues 190-230):**


- Sequence: D K P R V I A L Q P I S Q K D D A T R L C I E T C I A R N W R L S M Q T H K Y L N I A
- Secondary structure: Alpha-helices at residues 195-200, 205-210, and 215-220; Beta-strands at residues 200-205 and 210-215.
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence (dark blue) for most regions, with some lower confidence (light blue) at the N-terminus.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand