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The figure displays protein structure prediction results for a protein sequence, organized into eight segments corresponding to residues 1-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, and 430-480.

Segment 1 (Residues 1-60):

- Sequence: M A N F F I R R P I F A W V L A I I L M M A G A L A I L Q L P V A Q Y P T I A P P A V S V S A N Y P G A D A Q T V Q D T
- Secondary structure: Alpha-helices at positions 1-10, 15-25, 30-35, 45-55, and 60-65.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 2 (Residues 70-120):

- Sequence: V T Q V I E Q N M N G I D N L M Y M S S T S D S A G S V T I T L T F Q S G T D P D I A Q V Q V Q N K L Q L A T P L L P Q
- Secondary structure: Alpha-helices at positions 70-75, 85-95, 100-110, and 115-120.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 3 (Residues 130-180):

- Sequence: E V Q Q Q G I S V E K S S S S Y L M V A G F V S D N P G T T Q D D I S D Y V A S N V K D T L S R L N G V G D V Q L F G A
- Secondary structure: Beta-strands at positions 130-135, 140-150, 155-165, 170-180, and 185-190.
- SS confidence: High confidence regions (red) correspond to the strand segments.
- Disorder: Disordered regions (blue) are located between strands.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 4 (Residues 190-240):

- Sequence: Q Y A M R I W L D A D L L N K Y K L T P V D V I N Q L K V Q N D Q I A A G Q L G G T P A L P G Q Q L N A S I I A Q T R F
- Secondary structure: Alpha-helices at positions 190-200, 205-215, 220-230, and 235-240.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 5 (Residues 250-300):

- Sequence: K N P E E F G K V T L R V N S D G S V V R L K D V A R V E L G G E N Y N V I A R I N G K P A A G L G I K L A T G A N A L
- Secondary structure: Alpha-helices at positions 250-255, 265-275, 280-290, 295-300, and 305-310.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 6 (Residues 310-360):

- Sequence: D T A K A I K A K L A E L Q P F F P Q G M K V L Y P Y D T T P F V Q L S I H E V V K T L F E A I M L V F L V M Y L F L Q
- Secondary structure: Alpha-helices at positions 310-320, 325-335, 340-350, 355-360, and 365-370.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

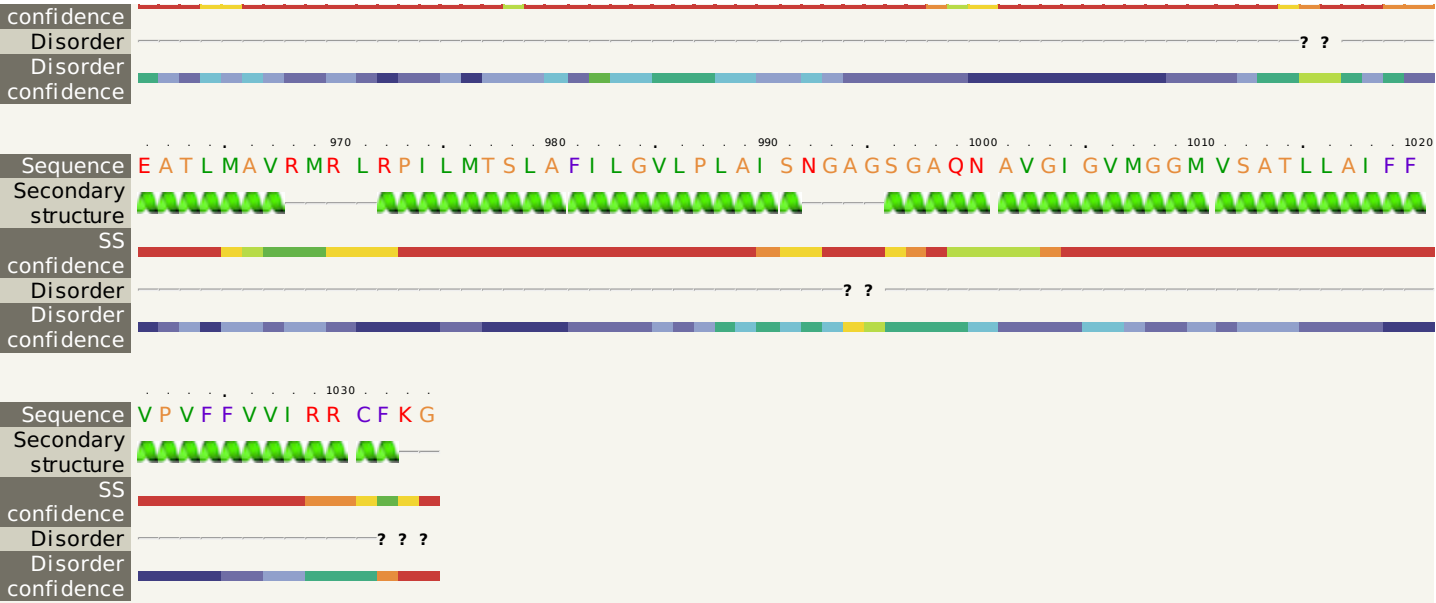
Segment 7 (Residues 370-420):

- Sequence: N M R A T L I P T I A V P V V L L G T F A I L A A F G Y S I N T L T M F G M V L A I G L L V D D A I V V V E N V E R V M
- Secondary structure: Alpha-helices at positions 370-380, 385-395, 400-410, 415-420, and 425-430.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.

Segment 8 (Residues 430-480):

- Sequence: (Continuation of the sequence)
- Secondary structure: Alpha-helices at positions 430-440, 445-455, 460-470, and 475-480.
- SS confidence: High confidence regions (red) correspond to the helical segments.
- Disorder: Disordered regions (blue) are located between helices.
- Disorder confidence: Low confidence (purple) in disordered regions.





Confidence Key
High(9) Low (0)
? Disordered
 Alpha helix
 Beta strand