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Figure 1 displays the structural models of the protein, showing the sequence, secondary structure, and disorder predictions for three segments of the protein.

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

- Sequence: MWYQKTLT LSAKSRGFHLVTDEILNQLADMPRVNIGLLHLLQLHTSASLTLENENC DPTVR
- Secondary structure: Alpha-helices (green) and beta-strands (blue) are shown.
- Disorder: The protein is predicted to be disordered (red) in the N-terminal region (residues 1-10) and the C-terminal region (residues 50-60).
- Confidence: The confidence score is 0.00 for the disordered regions and 1.00 for the ordered regions.


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

- Sequence: HDMERF FLRTVPDNGNYEHDYEGADDMP SHIKSSMLGTS LVLVPVHKGR IQTGTWQGI WL G
- Secondary structure: Alpha-helices (green) and beta-strands (blue) are shown.
- Disorder: The protein is predicted to be disordered (red) in the N-terminal region (residues 70-80) and the C-terminal region (residues 110-120).
- Confidence: The confidence score is 0.00 for the disordered regions and 1.00 for the ordered regions.


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


- Sequence: EHRI HGGSRRI IATLQGE
- Secondary structure: Alpha-helices (green) and beta-strands (blue) are shown.
- Disorder: The protein is predicted to be disordered (red) in the N-terminal region (residues 130-135) and the C-terminal region (residues 138-140).
- Confidence: The confidence score is 0.00 for the disordered regions and 1.00 for the ordered regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand