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Figure 1 displays the protein structure and disorder analysis for a 120-residue protein. The protein is composed of three alpha-helices (green) and three beta-strands (blue). The disorder analysis shows regions of high confidence (red) and low confidence (green/yellow) for disorder prediction.

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

- Sequence: METLI AISRWLAKQHVVTVWCVQQEGELWCANAFYLFDAQKVAFYILTEEEKTRHAQMSGPQ
- Secondary structure: Alpha-helix (1-10), Beta-strand (11-20), Alpha-helix (21-30), Beta-strand (31-40), Alpha-helix (41-50), Beta-strand (51-60)
- SS confidence: High (red) for most regions, low (green/yellow) for some regions.
- Disorder: ? ? ?
- Disorder confidence: High (red) for most regions, low (green/yellow) for some regions.


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

- Sequence: AAVAGTVNGQPKTVALIRGVQFKGEIRRLERGEESDLARKAYNRRFPVARMLSAPVWEIRL
- Secondary structure: Beta-strand (70-80), Alpha-helix (81-90), Alpha-helix (91-100), Alpha-helix (101-110), Alpha-helix (111-120)
- SS confidence: High (red) for most regions, low (green/yellow) for some regions.
- Disorder: ? ? ?
- Disorder confidence: High (red) for most regions, low (green/yellow) for some regions.


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


- Sequence: DEI KFTDNTLGFGKKMIWLRDSGTEQA
- Secondary structure: Beta-strand (130-140)
- SS confidence: High (red) for most regions, low (green/yellow) for some regions.
- Disorder: ? ? ? ? ? ? ?
- Disorder confidence: High (red) for most regions, low (green/yellow) for some regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand