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| Description | P0ABU5 |
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Protein structure prediction results for three protein segments. Each segment shows the amino acid sequence, secondary structure (SS) with confidence, disorder, and disorder confidence.

Segment 1 (Residues 1-60):

- Sequence: MKKI GVI LSGCGVYDGSEI HEAVLTLLAI SRSGAQAVCFAPDKQQVDVI NHLTGEAMTET
- Secondary structure: SS (blue arrows for loops, green cylinders for alpha-helices)
- SS confidence: Red (low), Green (high)
- Disorder: ? ? ?
- Disorder confidence: Red (low), Green (high)

Segment 2 (Residues 70-120):

- Sequence: RNVLI EAARI TRGEI RPLAQADAAELDALI VPGGF GAAK NLSNFASLGS ECTVDRELKAL
- Secondary structure: SS (blue arrows for loops, green cylinders for alpha-helices)
- SS confidence: Red (low), Green (high)
- Disorder: ? ?
- Disorder confidence: Red (low), Green (high)


Segment 3 (Residues 130-180):

- Sequence: AQAMHQAGKPLGFMCIA PAMLPKIFDFPLRLTIGTDI DTAEVLEEMGA EHVP CPVDDI VV
- Secondary structure: SS (blue arrows for loops, green cylinders for alpha-helices)
- SS confidence: Red (low), Green (high)
- Disorder: ? ?
- Disorder confidence: Red (low), Green (high)


Segment 4 (Residues 190-210):


- Sequence: DEDNKI VTTTPAYMLAQNI AE AASGI DKLVS RVLVLAE
- Secondary structure: SS (blue arrows for loops, green cylinders for alpha-helices)
- SS confidence: Red (low), Green (high)
- Disorder: ? ?
- Disorder confidence: Red (low), Green (high)

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand