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Description	P0A7W7
Date	Thu Jan 5 11:06:21 GMT 2012
Unique Job ID	38ebc4dc7d2516f7

Protein structure analysis of the C-terminal region of the protein, showing three segments: residues 1-60, 70-120, and 130-135. Each segment displays the amino acid sequence, secondary structure (alpha-helices and beta-strands), and confidence scores for disorder and confidence.

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

- Sequence: MS MQDPI ADMLTRI R N GQAANKAAVT MP S SKLKVAI ANVLKEEGFIEDFKVEGDTKPELE
- Secondary structure: Alpha-helices (green) and beta-strands (blue).
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.


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

- Sequence: L T LKYFQGKAVVESI QRVS RPGLRI Y KRKDEL PKVMAGLGI AVVSTSGVMTDRAARQAG
- Secondary structure: Alpha-helices (green) and beta-strands (blue).
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.


**Segment 3 (Residues 130-135):**


- Sequence: L G G E I I C Y V A
- Secondary structure: Alpha-helices (green) and beta-strands (blue).
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.
- Disorder confidence: High confidence (red) for most regions, with some lower confidence (yellow/green) in the middle.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand