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Description	P52135
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Figure 1 displays the protein structure and disorder analysis of the 160-residue protein. The figure is divided into three panels corresponding to different regions of the protein: residues 1-60, 70-120, and 130-160. Each panel displays the amino acid sequence, predicted secondary structure (alpha-helices in green, beta-strands in blue), sequence-sequence (SS) confidence, disorder, and disorder confidence.

Panel 1 (Residues 1-60):

- Sequence:** MKI RSLSRFVLASTMFASF TASAVPGLWQQGYGQGNAEYSVT DASGKMFTI NCTGNPDQN
- Secondary structure:** Shows several alpha-helices (green) and beta-strands (blue).
- SS confidence:** High confidence across the entire region.
- Disorder:** Low disorder, indicated by question marks.
- Disorder confidence:** High confidence across the entire region.


Panel 2 (Residues 70-120):

- Sequence:** GIYQHSVFLILAGDKTVSSHDDSTGITVVM DHKQYAI PSTLGWRNGDNAWFSFIMDIRKA
- Secondary structure:** Shows several alpha-helices (green) and beta-strands (blue).
- SS confidence:** High confidence across the entire region.
- Disorder:** Low disorder, indicated by question marks.
- Disorder confidence:** High confidence across the entire region.


Panel 3 (Residues 130-160):


- Sequence:** RQFDVYVNDQKVGSFNPDVRNAQKVLP TLA DCTND
- Secondary structure:** Shows several alpha-helices (green) and beta-strands (blue).
- SS confidence:** High confidence across the entire region.
- Disorder:** Low disorder, indicated by question marks.
- Disorder confidence:** High confidence across the entire region.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand