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The figure displays two panels of protein analysis. The top panel shows the full-length protein (1-60) with its sequence, secondary structure (SS), confidence, disorder, and disorder confidence. The bottom panel shows a fragment (70-100) with the same analysis. The sequence is color-coded by amino acid type. The secondary structure is represented by blue arrows for alpha-helices and green cylinders for beta-strands. The confidence is shown as a bar chart with red, yellow, and green segments. The disorder is indicated by question marks, and the disorder confidence is shown as a bar chart with red, yellow, and green segments.


**Top Panel (Full-length protein 1-60):**

- Sequence: M T V R I L A V C G N G Q G S S M I M K M K V D Q F L T Q S N I D H T V N S C A V G E Y K S E L S G A D I I I A S T H I
- Secondary structure: Alpha-helix (residues 1-10), Beta-strand (residues 11-25), Alpha-helix (residues 26-35), Beta-strand (residues 36-40), Alpha-helix (residues 41-50), Beta-strand (residues 51-60).
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow and green) segments.
- Disorder: ? ? ? (residues 1-10), ? ? ? (residues 51-60), ? (residue 60).
- Disorder confidence: High confidence (red) for most regions, with some lower confidence (yellow and green) segments.


**Bottom Panel (Fragment 70-100):**


- Sequence: A G E I T V T G N K Y V V G V R N M L S P A D F G P K L L E V I K E H F P Q D V K
- Secondary structure: Alpha-helix (residues 70-75), Beta-strand (residues 76-85), Alpha-helix (residues 86-95), Beta-strand (residues 96-100).
- SS confidence: High confidence (red) for most regions, with some lower confidence (yellow and green) segments.
- Disorder: ? ? ? ? (residues 70-75), ? ? ? (residues 76-85), ? ? ? (residues 96-100).
- Disorder confidence: High confidence (red) for most regions, with some lower confidence (yellow and green) segments.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand