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Figure 1 displays the protein structure and disorder analysis of the N-terminal region of the protein. The figure is divided into two main sections, each showing a sequence alignment, secondary structure (SS), and disorder confidence.


**Top Section (Residues 1-60):**

- Sequence:** M F C V I Y R S S K R D Q T Y L V E K K D D F S R V P E E L M K G F G Q P Q L A M I L P L D G R K K L V N A D I E K V
- Secondary structure (SS):** The structure is shown as a blue ribbon diagram. It features several alpha-helices (represented by green cylinders) and a beta-strand (represented by a blue arrow). The structure is predominantly alpha-helical.
- Disorder confidence:** A scale from 0 (blue) to 1 (red) is shown below the sequence. The confidence is generally low (blue/green) for the first 30 residues and increases (yellow/red) for the last 30 residues.


**Bottom Section (Residues 70-90):**


- Sequence:** K Q A L T E Q G Y Y L Q L P P P P E D L L K Q H L S V M G Q K T D D T N K
- Secondary structure (SS):** The structure is shown as a blue ribbon diagram. It features several alpha-helices (represented by green cylinders) and a beta-strand (represented by a blue arrow). The structure is predominantly alpha-helical.
- Disorder confidence:** A scale from 0 (blue) to 1 (red) is shown below the sequence. The confidence is generally low (blue/green) for the first 30 residues and increases (yellow/red) for the last 30 residues.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand