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Figure 1 displays protein structure and disorder analysis for the N-terminal region of the protein. The figure is divided into two panels, (a) and (b), each showing a sequence alignment, secondary structure prediction, solvent accessibility (SS), disorder prediction, and disorder confidence for a specific region of the protein.

**Panel (a):** Shows residues 1 to 60. The sequence is M N K D S T Q T W G L K R D I T P C F G A R L V Q E G H R L H F L A D R A G F T G S F S E V Q T L Q L D E A F P H F V A. The secondary structure prediction shows a series of alpha-helices (green) and beta-strands (blue). The SS is shown as a bar chart with colors representing different accessibility levels. The disorder prediction is shown as a bar chart with colors representing different disorder levels. The disorder confidence is shown as a bar chart with colors representing different confidence levels.

**Panel (b):** Shows residues 70 to 110. The sequence is H L E L M L L S C E L N P R Y A H C V T L Y R N G L T G E A D T L G S H G Y V Y I A I L N R H G F N R H L R V I. The secondary structure prediction shows a series of alpha-helices (green) and beta-strands (blue). The SS is shown as a bar chart with colors representing different accessibility levels. The disorder prediction is shown as a bar chart with colors representing different disorder levels. The disorder confidence is shown as a bar chart with colors representing different confidence levels.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand