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Figure 1 displays the protein structure and disorder analysis of the N-terminal region of the protein, showing three segments of the sequence (residues 1-60, 70-120, and 130-160) and their corresponding structural and disorder predictions.

Segment 1 (Residues 1-60):

- Sequence:** MSHPAL TQLRAL RYCKEI PALDPQLLDVLLLED SMTKRFEQQGKTVSVTMI REGFVEQNE
- Secondary structure:** Shows a series of alpha-helices (green cylinders) and a long beta-strand (blue arrow) spanning residues 45-60.
- SS confidence:** High confidence (red) for the alpha-helices and the beta-strand.
- Disorder:** Disordered regions (red) are present at the N-terminus (residues 1-10) and between residues 20-30 and 35-45.
- Disorder confidence:** High confidence (red) for the disordered regions.

Segment 2 (Residues 70-120):

- Sequence:** IPEELPLLPKESRYWLR EILL CADGEPWLAGRTVVPVSTLSGPELALQKL GKTLGRYLF
- Secondary structure:** Shows a series of alpha-helices (green cylinders) and beta-strands (blue arrows) spanning residues 70-120.
- SS confidence:** High confidence (red) for the alpha-helices and the beta-strands.
- Disorder:** Disordered regions (red) are present at the N-terminus (residues 70-80) and between residues 85-95 and 105-115.
- Disorder confidence:** High confidence (red) for the disordered regions.

Segment 3 (Residues 130-160):

- Sequence:** TSSTLTRDFI EIGRDAGLWGRRSRLRLSGKPLLLTELF LPASPLY
- Secondary structure:** Shows a series of alpha-helices (green cylinders) and beta-strands (blue arrows) spanning residues 130-160.
- SS confidence:** High confidence (red) for the alpha-helices and the beta-strands.
- Disorder:** Disordered regions (red) are present at the N-terminus (residues 130-140) and between residues 145-155 and 160-165.
- Disorder confidence:** High confidence (red) for the disordered regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand