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Protein structure analysis of the N-terminal region of the protein. The figure shows three segments of the protein sequence, each with its corresponding secondary structure, solvent accessibility (SS), disorder, and disorder confidence.

Segment 1 (Residues 1-60):

- Sequence:** M A S E R S T D V Q A F I G E L D G G V F E T K I G A V L S E V A S G V M N T K T K G K V S L N L E I E P F D E N R L K
- Secondary structure:** Long alpha-helix (green) and long loop (blue).
- SS:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder confidence:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.


Segment 2 (Residues 70-120):

- Sequence:** I K H K L S Y V R P T N R G K I S E E D T T E T P M Y V N R G G R L T I L Q E D Q Q G L L T L A G E P D G K L R A A G H
- Secondary structure:** Long alpha-helix (green) and long loop (blue).
- SS:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder confidence:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.


Segment 3 (Residues 130-180):


- Sequence:** (Not explicitly shown, but residues 130-180 are indicated by the scale).
- Secondary structure:** Long alpha-helix (green) and long loop (blue).
- SS:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.
- Disorder confidence:** High confidence (red) for the alpha-helix, low confidence (yellow/green) for the loop.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand