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Figure 1 displays the structural and sequence analysis of the protein, showing three segments of the protein structure and sequence. The protein is 179 amino acids long, with segments shown from 1-60, 70-120, and 130-179.

Segment 1 (1-60):

- Sequence:** MAEKRNIFLVGPMGAGKSTIGRQLAQQLNMEFYDSDQEIEKRTGADVGVVFDLEGEFGFR
- Secondary structure:** Shows a series of alpha helices and beta strands, with a blue arrow indicating a loop region.
- SS (Solvent Accessibility):** High accessibility in the N-terminal region, decreasing towards the C-terminus.
- confidence:** High confidence scores across the segment.
- Disorder:** Predicted as disordered in the N-terminal region (residues 1-10).
- Disorder confidence:** High confidence in the disorder prediction for the N-terminal region.

Segment 2 (70-120):

- Sequence:** DREEKVINELTEKQGIVLATGGGSVKSRRETRNRLSARGVVVYLETTIEKQLARTQRDKKR
- Secondary structure:** Shows a series of alpha helices and beta strands, with a blue arrow indicating a loop region.
- SS (Solvent Accessibility):** High accessibility in the N-terminal region, decreasing towards the C-terminus.
- confidence:** High confidence scores across the segment.
- Disorder:** Predicted as disordered in the N-terminal region (residues 70-80).
- Disorder confidence:** High confidence in the disorder prediction for the N-terminal region.

Segment 3 (130-179):

- Sequence:** PLLHVETPPREVL EALANERNPLYEEIADVTIRTDQSAKVVANQIIHML ESN
- Secondary structure:** Shows a series of alpha helices and beta strands, with a blue arrow indicating a loop region.
- SS (Solvent Accessibility):** High accessibility in the N-terminal region, decreasing towards the C-terminus.
- confidence:** High confidence scores across the segment.
- Disorder:** Predicted as disordered in the N-terminal region (residues 130-140).
- Disorder confidence:** High confidence in the disorder prediction for the N-terminal region.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand