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Figure 1 displays the sequence and structural analysis of the protein, showing the amino acid sequence, secondary structure (SS), confidence, disorder, and disorder confidence across four segments (1-60, 70-120, 130-180, and 190-230).


Segment 1 (1-60): Sequence: MKI ELTVNGL KIQAYQNEEI ENVHKPLLHMLAALQTVNP QRRTVVFLCAPPGTGKSTLT. Secondary structure: Alpha helix (residues 1-10), Alpha helix (residues 15-35), Alpha helix (residues 45-55), Alpha helix (residues 58-60). SS confidence: High (red/orange). Disorder: Low (blue/purple). Disorder confidence: High (red/orange).

Segment 2 (70-120): Sequence: TFW EYL AQQDPELPAI QTL P MDGF HHY NSWL DAHQLRPFK GAPETFDVAKLTENLRQVVE. Secondary structure: Alpha helix (residues 70-80), Alpha helix (residues 85-95), Alpha helix (residues 100-110), Alpha helix (residues 115-120). SS confidence: High (red/orange). Disorder: Low (blue/purple). Disorder confidence: High (red/orange).

Segment 3 (130-180): Sequence: GDCTWPQYDRQKHDPVEDALHVTAPLVI VEGNWLLLDDEK WLELASFCDFSIFIHAPAQI. Secondary structure: Alpha helix (residues 130-140), Alpha helix (residues 145-155), Alpha helix (residues 160-170), Alpha helix (residues 175-180). SS confidence: High (red/orange). Disorder: Low (blue/purple). Disorder confidence: High (red/orange).


Segment 4 (190-230): Sequence: LRERLISRK IAGGLTRQVAEAFYARTDGP NV ERLMNSRQANLI VEMTEEGRYHFTS. Secondary structure: Alpha helix (residues 190-200), Alpha helix (residues 205-220), Alpha helix (residues 225-230). SS confidence: High (red/orange). Disorder: Low (blue/purple). Disorder confidence: High (red/orange).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand