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Protein structure visualization of the full-length protein (1-239) and its three fragments (1-60, 70-120, 130-180). Each panel shows the amino acid sequence, secondary structure (alpha-helices and beta-strands), solvent accessibility (SS), confidence scores, and disorder predictions.


Fragment 1 (1-60): Sequence: MRYDKELTENEMI RQKILQQLLEWI ECNLEHPI SIEDI AQKSGYSRRNI QLLFRNFMHVP. Secondary structure shows several alpha-helices. SS is high. Confidence is high. Disorder is predicted in the first 10 residues.

Fragment 2 (70-120): Sequence: LGEYIRKRRL CRAAILVRLTAKSMLDI ALSLHFDSQQSF SREFKKLF GCS PREYRHRD YW. Secondary structure shows several alpha-helices. SS is high. Confidence is high. Disorder is predicted in the last 10 residues.


Fragment 3 (130-180): Sequence: DLANI FPSFLIRQQKTECR LINFPETPI FGNSFKYDIEVSNKSPDEEVKLRRHHLARCM. Secondary structure shows several alpha-helices. SS is high. Confidence is high. Disorder is predicted in the first 10 residues.


Full-length protein (1-239): Sequence: KNFKTDIYFVSTFEPSTKSVDLLTVETFA GTVCEYADMPKEWTTTRGLYDPTHVI WTQA. Secondary structure shows several alpha-helices and beta-strands. SS is high. Confidence is high. Disorder is predicted in the first 10 residues.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand