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The figure displays the protein structure of the full-length protein (1-360) and a fragment (DITEKQ). The protein is shown in six segments, with the sequence, secondary structure, and disorder confidence scores for each segment.

**Full-length protein (1-360):**

- Segment 1 (1-60):** Sequence: MRGKKRI GLL FLLI AVVVGGGGLLLA QKVL HKTS DTA FCL SCHS MSKP FEE YQGT VHF SN. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).
- Segment 2 (61-120):** Sequence: QKGI RAECADCHI PKSGMDYL FAKL KASKDI YHEF VSGKI DSDDKFEAHRQEMAETVWKE. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).
- Segment 3 (121-180):** Sequence: LKATDSATCRSCHSF DAMDI ASQSESAQKMHNKAQK DSET CI DCHKGI AHFPPEI KMDDN. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).
- Segment 4 (181-240):** Sequence: AAHELESQAATSVTNGAHI YPFKTSHI GELATVNP GTDLTVVDASGKQPI VLLQGYQM QG. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).
- Segment 5 (241-300):** Sequence: SENTLYLAAGQRLALATLSEEGI KALT VNGEWQADEYGNQWRQASLQGAL TDPALADRKP. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).
- Segment 6 (301-360):** Sequence: LWQYAEKLDDTYCAGCHAPI AADHYTVNAWPSI AKGMGARTSMS ENELDI LTRYFYQYNAK. Secondary structure: 10 alpha-helices. Disorder confidence: High (red).

**Fragment (DITEKQ):**

- Sequence: DITEKQ
- Secondary structure: 1 alpha-helix
- Disorder confidence: High (red)

Confidence Key  
High(9)  Low (0)  
? Disordered  
 Alpha helix  
 Beta strand