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Protein structure prediction results for a protein of 350 amino acids. The image displays six segments of the protein, each with its sequence, secondary structure (SS), confidence, disorder, and disorder confidence.

Segment 1 (1-60): Sequence: MGQQKQRNRRVVLASRPHGAPVPE NFRLEE DDVATP GEGQVLLRTVYLSLDPYMRGRMSD. Secondary structure: Alpha-helices at positions 10-15 and 25-30. SS confidence: High. Disorder: Low. Disorder confidence: High.

Segment 2 (70-120): Sequence: EPSYSPPVDI GGVMVGGTVSRVVE SNHPDY QSGDWVLGYSGWQDYDISSGDDLVLKLGDP. Secondary structure: Alpha-helices at positions 75-80 and 110-115. SS confidence: High. Disorder: Low. Disorder confidence: High.

Segment 3 (130-180): Sequence: QNP SWSLGV LGMPGF TAYMGLLDI GQPK EG ETLVVA AATGP VGATVGQI GK LKGRVVG. Secondary structure: Alpha-helices at positions 135-140 and 155-160. SS confidence: High. Disorder: Low. Disorder confidence: High.

Segment 4 (190-240): Sequence: AGGA EKCRHATEVLGF DVCL DHHADDF AEQLAKACPKGI DIYYENVGGKVFDAVLPLLNT. Secondary structure: Alpha-helices at positions 195-200 and 225-230. SS confidence: High. Disorder: Low. Disorder confidence: High.

Segment 5 (250-300): Sequence: SARIPVCGLVSSYNATELPPGPDRLPLL MATVLKKRI RLQGFII AQDYGHR IHEFQREMG. Secondary structure: Alpha-helices at positions 255-260 and 285-290. SS confidence: High. Disorder: Low. Disorder confidence: High.

Segment 6 (310-350): Sequence: QWVKEDKI HYREEITDGL ENAPQT FILLK GKGNFGKVVI RVAGDD. Secondary structure: Alpha-helices at positions 315-320 and 335-340. SS confidence: High. Disorder: Low. Disorder confidence: High.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand