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The figure displays protein structure prediction results for a protein sequence of 420 residues. The results are organized into six blocks, each corresponding to a segment of the protein. Each block contains five rows: Sequence, Secondary structure, SS confidence, Disorder, and Disorder confidence.

Block 1 (Residues 1-60): Sequence: MSKNERMVGISRRRTL... Secondary structure: Alpha helix (residues 10-30). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).

Block 2 (Residues 70-120): Sequence: GSRCALRLHVKDNEVTWVETDNTGSDEYGNHQVRACLRGRSIRRRINHPDRLNYPMKRVG... Secondary structure: Alpha helix (residues 70-80), Alpha helix (residues 85-95), Alpha helix (residues 105-115), Alpha helix (residues 115-120). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).

Block 3 (Residues 130-180): Sequence: KRGEKGKFERISWDEALDTIASLKKTVQYQNEAVYIQYSSGIVGGNMTRSSPSASAVKR... Secondary structure: Alpha helix (residues 130-145), Alpha helix (residues 155-165), Alpha helix (residues 175-180). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).




Block 4 (Residues 190-240): Sequence: LMNCYGGS LNQYGSYSTAQISCAMPYTYGSNDGNSTTDIENSKLVVMFGNNPAETRMSSGG... Secondary structure: Alpha helix (residues 190-200), Alpha helix (residues 205-215), Alpha helix (residues 220-230), Alpha helix (residues 235-240). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).

Block 5 (Residues 250-300): Sequence: GITYLEKAREKSNKMIVIDPRYTDTAAGREDEWLP I R PGTDAALVAGI A WVLINENLV... Secondary structure: Alpha helix (residues 250-260), Alpha helix (residues 265-275), Alpha helix (residues 280-290), Alpha helix (residues 295-300). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).

Block 6 (Residues 310-360): Sequence: DQPF LDKYCVGYDEKTL PADAPKNGHYKAYILGEGDDKTA KTPQWASQITGIPEDRIIKL... Secondary structure: Alpha helix (residues 310-320), Alpha helix (residues 325-335), Alpha helix (residues 340-350), Alpha helix (residues 355-360). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).

Block 7 (Residues 370-420): Sequence: AREIGTAKPAYICQGWGPQRQANGELTARAIAMLPI LTGNVGISGGNSGARESTY TITIE... Secondary structure: Alpha helix (residues 370-380), Alpha helix (residues 385-395), Alpha helix (residues 400-410), Alpha helix (residues 415-420). SS confidence: High (red). Disorder: Low (blue). Disorder confidence: High (red).



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