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| Email | l.a.kelley@imperial.ac.uk |
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Protein structure prediction results for the protein sequence MRLTTKFS...V. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

Sequence: MRLTTKFSAFVTLLTGLTIFVTLLGCSLSFYNAIQYKFSSHRVQAVATAIDTHLVSNDFFSV
 LRPQITELMMSADIVRVDLLHGDKQVYTLARNGSYRPVGSDDLRELSVPLIKHPGMSLR
 LVYQDPMGNYFHSLLMTTAPLTGAI GFII VMLFLAVRWLQRQLAGQELLETRATRI L NGER
 GSNVLGTIYEWPPTSSALD TLLREIQNAREQHSRLDTLIRSYYAAQDVKTGLNNRLFFDN
 QLATLLEDQEKVGTHGIVMMIRLPDFNMLS DTWGHSSQVEEQFFTLTNLLSTFMMRYPGAL
 LARYHRSDFAALLPHRTLKEAESIAGQLIKAVDTLPNNKMLDRDDMIHIGICAWRSGQDT
 EQVMEHAESATRNAGLQGGNSWAIYDDSLPEKGRGNVRWRTLIEQMLSRGGPRLYQKPAV

Secondary structure: The secondary structure is represented by green cylinders (alpha-helices) and blue arrows (beta-strands). The structure shows a complex fold with multiple helices and strands, including a large alpha-helix in the C-terminal region.

SS confidence: The SS confidence is shown as a bar chart below the secondary structure, indicating the confidence level for each residue's secondary structure assignment. The confidence is generally high, with some lower confidence regions in the N-terminal and C-terminal.

Disorder: The disorder is indicated by a bar chart below the SS confidence, showing regions of predicted disorder. The protein is mostly structured, with some disordered regions in the N-terminal and C-terminal.

Disorder confidence: The disorder confidence is shown as a bar chart below the disorder, indicating the confidence level for each residue's disorder prediction. The confidence is generally high, with some lower confidence regions in the N-terminal and C-terminal.

