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Protein structure and disorder analysis for the first three domains of the protein. The figure shows sequence, secondary structure, SS confidence, disorder, and disorder confidence for residues 1-60, 70-120, and 130-139.

Domain 1 (Residues 1-60): The sequence is MGLFDEVVGAFLKGDAGKYQALISWVEEQGGIQVLLLEKLQSGGLGAILSTVLSNQGNQS. The secondary structure shows a series of alpha-helices and beta-strands. The SS confidence is high (red). The disorder analysis shows that the first 10 residues are disordered, followed by a highly structured region (residues 11-58) and a disordered C-terminal region (residues 59-60).


Domain 2 (Residues 70-120): The sequence is VSGEQLESALGTNAVSDLGQKLGVDTSTASSLLAEQLPKIIDLALSPQGEVSPQANNDLLS. The secondary structure shows a series of alpha-helices and beta-strands. The SS confidence is high (red). The disorder analysis shows that the first 10 residues are disordered, followed by a highly structured region (residues 11-118) and a disordered C-terminal region (residues 119-120).


Domain 3 (Residues 130-139): The sequence is AGMELLKGLFR. The secondary structure shows a series of alpha-helices and beta-strands. The SS confidence is high (red). The disorder analysis shows that the first 10 residues are disordered, followed by a highly structured region (residues 11-138) and a disordered C-terminal region (residues 139-140).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand