


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Protein structure and disorder analysis of the full-length protein (1-270 aa). The figure shows the full sequence in five segments, each with its corresponding secondary structure (SS) and disorder confidence. The protein contains several alpha-helices and beta-strands, with some regions marked as disordered. The disorder confidence is shown as a scale from 0 (red) to 1 (blue).


Segment	Sequence (1-270 aa)	Secondary structure	Disorder confidence
1	1-60: MQNITQSVFVQGMIKATTTDAWLGWDERNGGNLTLRLDDADIAPYHDNFHHQQPRYIPLSQ	Alpha-helices at positions 10-25, 30-35, 40-50, 55-60	Disordered regions at positions 1-9, 26-29, 36-39, 41-54, 51-54, 61-69
2	70-120: PMPLLANTPFIVTGSGKFFRNVQLDPAANLGIKVDSDGAGYHILWGLTNEAVPTSELP	Alpha-helices at positions 80-85, 110-115	Disordered regions at positions 70-69, 121-129
3	130-180: HFLSHCERIKATNGKDRVIMHCHATNLIALTIVLENDTAVFTRQLWEGSTECCLVVPDGV	Alpha-helices at positions 135-140, 145-150, 155-160, 165-170	Disordered regions at positions 130-134, 171-180
4	190-240: GILPVMVPGTDEIGQATAQEMQKHS LVLWPFHGVFGSGPTLDETFGLI DTAEKSAQVLVK	Alpha-helices at positions 195-200, 205-210, 215-220, 225-230	Disordered regions at positions 190-194, 231-240
5	250-270: VYSMGGMKQTI SREELIALGKRFGVTPLASALAL	Alpha-helices at positions 255-260, 265-270	Disordered regions at positions 250-254, 271-270

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand