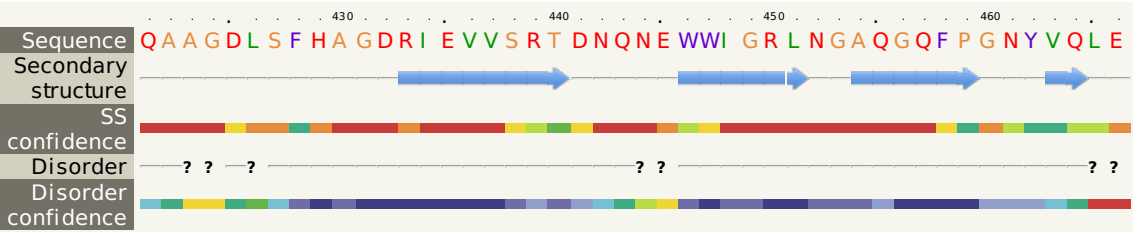


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Protein structure and disorder analysis of the full-length protein (1-420 aa). The figure displays the amino acid sequence, secondary structure (SS), confidence scores, and disorder predictions across the entire protein length. The sequence is color-coded by amino acid type. The secondary structure is shown as a green ribbon model. The confidence scores are represented by a red bar. The disorder predictions are shown as a blue bar with question marks indicating regions of uncertainty. The protein is divided into four segments, each 100 residues long, with the final segment being 20 residues shorter (420 total).

Segment	Residue Range	Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
1	1-100	MSWKGF TKALARTPQTLRSKFNVGEITKDPITYEDAGR RFKSL ETEAKKLA EDAKKYTDAL	Alpha-helix (1-20), Alpha-helix (21-30), Alpha-helix (31-40), Alpha-helix (41-50), Alpha-helix (51-60), Alpha-helix (61-70), Alpha-helix (71-80), Alpha-helix (81-90), Alpha-helix (91-100)	High	Low	High
2	101-200	NGLLNHQI GFADACIEIYKPI SGRASDPESYEQEGNAEGI EAAEAYKEI VYDLQKNLASE	Alpha-helix (101-110), Alpha-helix (111-120), Alpha-helix (121-130), Alpha-helix (131-140), Alpha-helix (141-150), Alpha-helix (151-160), Alpha-helix (161-170), Alpha-helix (171-180), Alpha-helix (181-190), Alpha-helix (191-200)	High	Low	High
3	201-300	MDVINTRI VNPTGELLKIVKDVDKLLKRDHKQLDYDRHRSSF KKLQEKKDKSLKDEKKL	Alpha-helix (201-210), Alpha-helix (211-220), Alpha-helix (221-230), Alpha-helix (231-240), Alpha-helix (241-250), Alpha-helix (251-260), Alpha-helix (261-270), Alpha-helix (271-280), Alpha-helix (281-290), Alpha-helix (291-300)	High	Low	High
4	301-420	YEAETAF EQSSQEY EYNEMLKEELPKLFA LAQSFIAPLF QGFYMQNLNVYYVLY EKMSH	Alpha-helix (301-310), Alpha-helix (311-320), Alpha-helix (321-330), Alpha-helix (331-340), Alpha-helix (341-350), Alpha-helix (351-360), Alpha-helix (361-370), Alpha-helix (371-380), Alpha-helix (381-390), Alpha-helix (391-400), Alpha-helix (401-410), Alpha-helix (411-420)	High	Low	High



Confidence Key
High(9) [red bar] [orange bar] [yellow bar] [green bar] [light blue bar] [dark blue bar] Low (0)
? Disordered
Alpha helix
Beta strand