

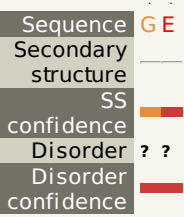
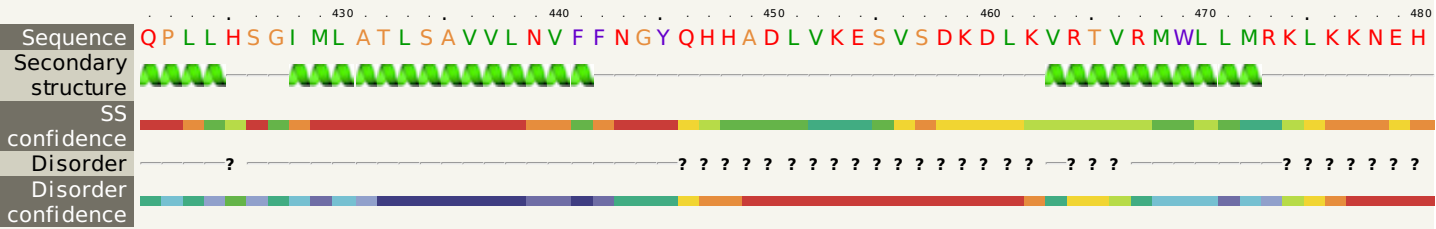
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The figure displays a detailed analysis of the protein structure across 10 segments (1-60, 61-120, 121-180, 181-240, 241-300, 301-360, 361-420). Each segment is represented by a horizontal bar with the following tracks:

- Sequence:** Amino acid sequence (e.g., MSALDSQLPSSSGQDRPTDEVDRILSPGKLIILGLQHVLMYAGAVAVPLMIGDRLGLSK).
- Secondary structure:** Alpha-helices (green cylinders) and beta-strands (green arrows).
- SS confidence:** Confidence score for secondary structure (0-100% scale).
- Disorder:** Disordered regions (red/yellow bars) and ordered regions (blue/purple bars).
- Disorder confidence:** Confidence score for disorder prediction (0-100% scale).

Key observations from the analysis:

- The protein is highly disordered, with most regions showing low confidence in secondary structure.
- Disordered regions are predominantly located in the N-terminal and C-terminal regions.
- Ordered regions are primarily found in the middle segments (e.g., segments 3, 4, 5, 6, 7, 8, 9, 10).



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