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The figure shows the full-length protein structure analysis for residues 1 to 340. Each segment includes the amino acid sequence, secondary structure prediction (SS) represented by green cylinders (alpha-helices) and blue arrows (beta-strands), confidence scores, disorder predictions (indicated by question marks), and disorder confidence scores.

Segment	Residue Range	Sequence	Secondary Structure (SS)	Confidence	Disorder	Disorder Confidence
1	1 - 60	MK KVL L I I L L L V L G I AAGVG V W K V R H L A D S K L L I K E E T I F T L K P G T G R L A L G E Q L Y A D	Alpha-helix (approx. 10-30), Alpha-helix (approx. 45-55), Beta-strand (approx. 40-45), Alpha-helix (approx. 50-60)	High	Low	High
2	61 - 120	K I I N R P R V F Q W L L R I E P D L S H F K A G T Y R F T P Q M T V R E M L K L L E S G K E A Q F P L R L V E G M R L	Alpha-helix (approx. 65-75), Beta-strand (approx. 80-90), Alpha-helix (approx. 95-105), Beta-strand (approx. 110-115), Alpha-helix (approx. 120-125)	High	Low	High
3	121 - 180	S D Y L K Q L R E A P Y I K H T L S D D K Y A T V A Q A L E L E N P E W I E G W F W P D T W M Y T A N T D V A L L K R	Alpha-helix (approx. 125-135), Alpha-helix (approx. 140-150), Beta-strand (approx. 160-165), Alpha-helix (approx. 175-185)	High	Low	High
4	181 - 240	A H K K M V K A V D S A W E G R A D G L P Y K D K N Q L V T M A S I I E K E T A V A S E R D K V A S V F I N R L R I G M	Alpha-helix (approx. 185-195), Alpha-helix (approx. 200-210), Alpha-helix (approx. 215-225), Alpha-helix (approx. 230-240)	High	Low	High
5	241 - 300	R L Q T D P T V I Y G M G E R Y N G K L S R A D L E T P T A Y N T Y T I T G L P P G A I A T P G A D S L K A A A H P A K	Alpha-helix (approx. 245-255), Alpha-helix (approx. 260-265), Alpha-helix (approx. 285-295)	High	Low	High
6	301 - 340	T P Y L Y F V A D G K G G H T F N T N L A S H N K S V Q D Y L K V L K E K N A Q	Beta-strand (approx. 305-315), Beta-strand (approx. 320-325), Alpha-helix (approx. 325-335)	High	Low	High

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand