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Protein structure prediction results for a protein of 370 amino acids. The figure displays the sequence, secondary structure, and disorder predictions across the entire length of the protein.

Sequence: M N Y S H D N W S A I L A H I G K P E E L D T S A R N A G A L T R R R E I R D A A T L L R L G L A Y G P G G M S L R E V T A W A Q L H D V A T L S D V A L L K R L R N A A D W F G I L A A Q T L A V R A A V T G C T S G K R L R L V D G T A I S A P G G G S A E W R L H M G Y D P H T C Q F T D F E L T D S R D A E R L D R F A Q T A D E I R I A D R G F G S R P E C I R S L A F G E A D Y I V R V H W R G L R W L T A E G M R F D M M G F L R G L D C G K N G E T T V M I G N S G N K K A G A P F P A R L I A V S L P P E K A L I S K T R L L S E N R R K G R V V Q A E T L E A A G H V L L T S L P E D E Y S A E Q V A D C Y R L R W Q I E L A F K R L K S L L H L D A L R A K E P E L A K A W I F A N L L A A F L I D D I I Q P S L D F P P R S A G S E K K N

Secondary structure: The protein is predicted to have several alpha-helices (green cylinders) and beta-strands (blue arrows). The first domain (residues 1-120) contains several alpha-helices and a beta-strand. The second domain (residues 130-240) contains several alpha-helices and a beta-strand. The third domain (residues 250-330) contains several alpha-helices and a beta-strand. The fourth domain (residues 340-370) contains several alpha-helices and a beta-strand.

Disorder: The protein is predicted to be disordered in several regions, indicated by the red bar at the bottom. The first domain (residues 1-120) is mostly ordered, but the second domain (residues 130-240) is mostly disordered. The third domain (residues 250-330) is mostly ordered, but the fourth domain (residues 340-370) is mostly disordered.

Confidence Key
High(9)  Low (0)
? Disordered
 Alpha helix
 Beta strand