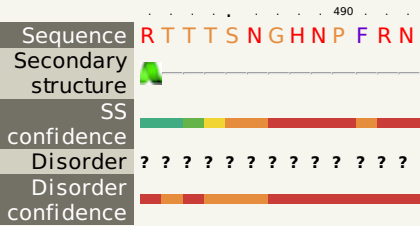
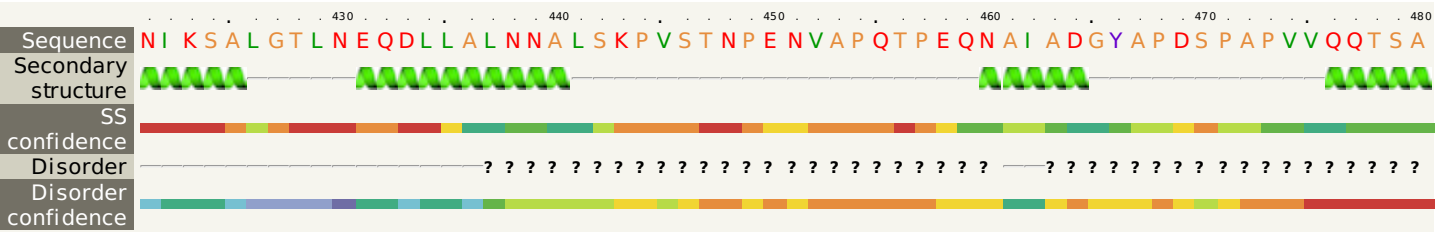


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Protein structure prediction results for the protein sequence: M K K L L P I L I G L S L S G F S S L S Q A E N L M Q V Y Q Q A R L S N P E L R K S A A D R D A A F E K I N E A R S P L L P Q L G L G A D Y T Y S N G Y R D A N G I N S N A T S A S L Q L T Q S I F D M S K W R A L T L Q E K A A G I Q D V T Y Q T D Q Q T L I L N T A T A Y F N V L N A I D V L S Y T Q A Q K E A I Y R Q L D Q T T Q R F N V G L V A I T D V Q N A R A Q Y D T V L A N E V T A R N N L D N A V E Q L R Q I T G N Y Y P E L A A L N V E N F K T D K P Q P V N A L L K E A E K R N L S L L Q A R L S Q D L A R E Q I R Q A Q D G H L P T L D L T A S T G I S D T S Y S G S K T R G A A G T Q Y D D S N M G Q N K V G L S F S L P I Y Q G G M V N S Q V K Q A Q Y N F V G A S E Q L E S A H R S V V Q T V R S S F N N I N A S I S S I N A Y K Q A V V S A Q S S L D A M E A G Y S V G T R T I V D V L D A T T T L Y N A K Q E L A N A R Y N Y L I N Q L.

The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence for each residue. The protein is 420 residues long. The secondary structure is shown as a blue ribbon diagram. The SS confidence is shown as a red bar. The disorder is shown as a green bar. The disorder confidence is shown as a blue bar.



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand