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

The figure displays the protein structure prediction results, showing the sequence, secondary structure, SS confidence, disorder, and disorder confidence for each residue.

Residue ranges shown: 1-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-410.

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