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The figure displays the protein structure prediction and disorder analysis for the protein sequence MNNNDL FQAS RRRFLAQLGGLTVAGMLGPSLLTPRRATAAQAATDAVISKEGILTGSHWG. The analysis is presented across the entire length of the protein (1-420 residues).

Sequence: MNNNDL FQAS RRRFLAQLGGLTVAGMLGPSLLTPRRATAAQAATDAVISKEGILTGSHWG

Secondary structure: The structure is primarily composed of alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 10 to 30, a loop from 30 to 40, and another long alpha-helix from 40 to 60. A large loop is present from 70 to 100, followed by several smaller alpha-helices and loops up to residue 120.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.

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

Secondary structure: The structure continues with a long alpha-helix from residue 130 to 150, followed by a loop from 150 to 160, and another long alpha-helix from 160 to 180. A large loop is present from 190 to 220, followed by several smaller alpha-helices and loops up to residue 240.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.

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

Secondary structure: The structure continues with a long alpha-helix from residue 250 to 270, followed by a loop from 270 to 280, and another long alpha-helix from 280 to 300. A large loop is present from 310 to 340, followed by several smaller alpha-helices and loops up to residue 360.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.

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

Secondary structure: The structure continues with a long alpha-helix from residue 370 to 390, followed by a loop from 390 to 400, and another long alpha-helix from 400 to 420. A large loop is present from 430 to 460, followed by several smaller alpha-helices and loops up to residue 480.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.

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

Secondary structure: The structure continues with a long alpha-helix from residue 490 to 510, followed by a loop from 510 to 520, and another long alpha-helix from 520 to 540. A large loop is present from 550 to 580, followed by several smaller alpha-helices and loops up to residue 600.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.

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

Secondary structure: The structure continues with a long alpha-helix from residue 610 to 630, followed by a loop from 630 to 640, and another long alpha-helix from 640 to 660. A large loop is present from 670 to 700, followed by several smaller alpha-helices and loops up to residue 720.

SS confidence: The confidence is generally high, indicated by the green color in the confidence bar, particularly in the regions of high secondary structure content.

Disorder: The protein is predominantly disordered, as indicated by the red color in the disorder bar. There are a few regions of low disorder (blue/green) corresponding to the structured elements.

Disorder confidence: The confidence in the disorder prediction is generally high, indicated by the green color in the confidence bar.





Confidence Key



High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand