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Description	P75917
Date	Thu Jan 5 12:16:01 GMT 2012
Unique Job ID	49753e2b121b702c

Figure 1 displays the protein structure and disorder analysis of the N-terminal region of the protein. The figure is divided into two panels, each showing the sequence, secondary structure (SS), and disorder confidence.


Top Panel (Residues 1-60):

- Sequence:** M F R P F L N S L M L G S L F F P F I A I A G S T V Q G G V I H F Y G Q I V E P A C D V S T Q S S P V E M N C P Q N G S
- Secondary structure (SS):** The structure is shown as a blue ribbon diagram. It features a series of alpha-helices (represented by green cylinders) and beta-strands (represented by blue arrows). The SS is mostly composed of alpha-helices in the first 20 residues, followed by a mix of alpha-helices and beta-strands.
- Disorder confidence:** A red bar indicates the confidence of the disorder prediction. The confidence is high (red) for the first 20 residues and decreases (yellow, green, blue) for the remaining residues.
- Disorder:** A green bar indicates the predicted disorder. The first 20 residues are predicted to be disordered (green), while the remaining residues are predicted to be ordered (blue).


Bottom Panel (Residues 70-100):


- Sequence:** I P G K T Y S S K A L M S G N V K N A Q I A S V K V Q Y L D K Q K K L A V M N I E Y N
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Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand