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Description	Q46843
Date	Thu Jan 5 12:35:09 GMT 2012
Unique Job ID	3229f96af4375195

Figure 1 displays the protein structure and disorder analysis of the human protein. The figure is organized into four panels, each showing a different segment of the protein (residues 1-60, 70-120, 130-180, and 190-230). Each panel includes the following information:

- Sequence:** The amino acid sequence for the segment, with residues numbered above the sequence.
- Secondary structure:** A representation of the protein's secondary structure, showing alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** A bar chart showing the confidence scores for the secondary structure predictions, with colors indicating different confidence levels (red for high, yellow for medium, green for low).
- Disorder:** A bar chart showing the disorder predictions, with red bars indicating regions of high disorder and green bars indicating regions of low disorder.
- Disorder confidence:** A bar chart showing the confidence scores for the disorder predictions, with colors indicating different confidence levels (red for high, yellow for medium, green for low).

The protein is 230 amino acids long. The first segment (1-60) shows a beta-strand followed by a large alpha-helix. The second segment (70-120) shows a beta-strand followed by a large alpha-helix. The third segment (130-180) shows a beta-strand followed by a large alpha-helix. The fourth segment (190-230) shows a beta-strand followed by a large alpha-helix. The protein is predicted to be disordered in several regions, indicated by red bars and question marks.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand