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Description	P42913
Date	Thu Jan 5 12:02:12 GMT 2012
Unique Job ID	3901190eee014967

Figure 1 displays the protein structure and disorder analysis of the protein. The protein is shown as a blue ribbon structure with green alpha-helices and red beta-strands. The disorder analysis shows regions of high confidence (red) and low confidence (green/yellow) for disorder prediction.


The protein structure is shown in four segments, with the following amino acid sequences and disorder analysis results:


- Segment 1 (Residues 1-60):** Sequence: MNKVT KTAI AGL LALF AGNAAAT DGEI VFDGEI LKSACEI NDS DKKI EVAL GHYNAEQFR. Secondary structure: 1 alpha-helix, 1 beta-strand. SS confidence: 0.95. Disorder: 0.95. Disorder confidence: 0.95.
- Segment 2 (Residues 70-120):** Sequence: NIGERSPKIPFTIPLVNCPTGWEHDNGNVEASFRLWLETRDNGTVPNFPNLAKVGSFAG. Secondary structure: 1 alpha-helix, 1 beta-strand. SS confidence: 0.95. Disorder: 0.95. Disorder confidence: 0.95.
- Segment 3 (Residues 130-180):** Sequence: IAAATGVGIRIDDAESGNI MPLNAMGNDNTVYQIPAESNGI VNVDLI AYYVSTVVPSEITP. Secondary structure: 1 alpha-helix, 1 beta-strand. SS confidence: 0.95. Disorder: 0.95. Disorder confidence: 0.95.
- Segment 4 (Residues 190-200):** Sequence: GEADAI VNVTL DYR. Secondary structure: 1 alpha-helix. SS confidence: 0.95. Disorder: 0.95. Disorder confidence: 0.95.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand