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Description	P08622
Date	Thu Jan 5 11:01:33 GMT 2012
Unique Job ID	40570adf5ff47076

Protein structure prediction results for the protein sequence MAKQDY...KSF... The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the full length of the protein (residues 1 to 370).




**Sequence:** MAKQDY...KSF... (Residues 1 to 370)

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and loops (blue arrows). Key features include a large alpha-helical region from residue 10 to 30, a long loop from 30 to 40, and a large alpha-helical region from 40 to 60. The structure continues with a mix of helices and loops, ending with a short alpha-helical region from 360 to 370.

**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 several 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 red color in the confidence bar.

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