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Description	P0ABW9
Date	Thu Jan 5 11:16:35 GMT 2012
Unique Job ID	b0ef751a40698cbf

Protein structure and disorder analysis for the full-length protein (1-120). The figure shows the amino acid sequence, secondary structure (SS), confidence, disorder, and disorder confidence across the entire length. The protein is 120 residues long. The sequence is: ML DKL DAALRFQQEALNLRAQRQEVLAANI ANADTPGYQARDI DFASELKKVMQRGRDAT. The secondary structure shows several alpha-helices and beta-strands. The disorder analysis indicates regions of high confidence in disorder (red) and regions of low confidence (yellow/green).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand