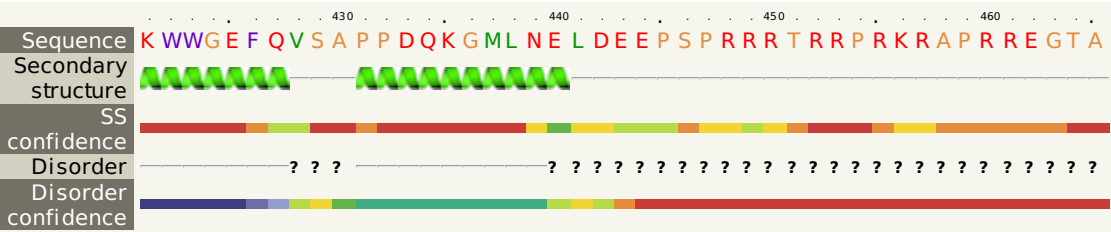


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Description	P0ABF1
Date	Thu Jan 5 11:15:21 GMT 2012
Unique Job ID	1a61aef27431177b

Protein structure prediction results for the protein sequence MFTRVANFCRKVLSREESEAEQAVARPQVTVIPREQHAISRKDISENALKVMYRLNKAAGYEAWLVGGGVDRLLGKKPKDFDVTTNATPEQVRKLFNRCLVGRRFRLAHVMFGPEIIEVATFRGHHEGNVSDRTTSQRGQNGMLLRDNI FGSIEEDAQRDRFTINSLLYSVADF TVRDYVGGMKDLKDGVI RLI GNPETRYREDPVRMLRAVRFAAKLGMRI SPETAEP I PRLATLLNDIPPARLFEESLKL LQAGYGYETYKLLCEYHLFQPLFPPTI TRYFTENGDSPMERIEQVLKNTDTRI HNDMRVNP AFLFAAMFWYP LLETAQKI AQESGLTYHDAFALAMNDVLD EACRSLAI PKRLTTLT RD I WQLQLRMSRRQGKRAWK LLEHPKFRAAYDLLALRAE VERNAE LQRLV.

The figure displays the sequence, secondary structure, SS confidence, Disorder, and Disorder confidence for the protein. The protein is 420 amino acids long. The secondary structure is shown as a ribbon diagram with alpha-helices in green and beta-strands in blue. The SS confidence is shown as a bar chart with colors representing different confidence levels. The Disorder and Disorder confidence are also shown as bar charts.



Confidence Key

High(9) [red bar] [orange bar] [yellow bar] [light green bar] [green bar] [blue bar] Low (0)

? Disordered

Alpha helix

Beta strand