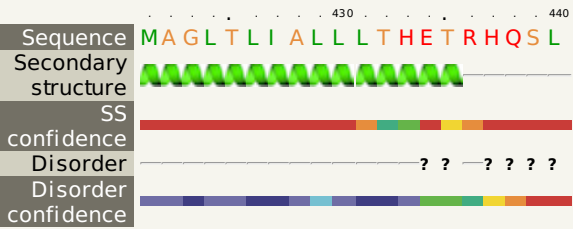


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| Date          | Thu Jan 5 11:56:15 GMT 2012 |
| Unique Job ID | 502f064e34352665            |

Protein structure and disorder analysis of the full-length protein (1-420 aa). The figure displays the full sequence in 10 blocks of 30 residues each. For each block, the amino acid sequence is shown at the top, followed by a secondary structure prediction (green cylinders for alpha-helices, red cylinders for beta-strands, and loops), an SS confidence plot (red line), a disorder prediction (colored bars), and a disorder confidence plot (blue line). The protein is highly disordered, with only a few short alpha-helices and one beta-strand predicted. The disorder confidence is generally high, indicated by the red line in the disorder confidence plots.



Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand