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| Description   | Q9JMS4                       |
| Date          | Wed Jan 25 15:21:16 GMT 2012 |
| Unique Job ID | 4f463024f7bf1dcf             |

Figure 1 displays the protein structure and disorder analysis of the N-terminal region of the protein. The top panel shows the full sequence (1-60) with secondary structure (SS) and disorder confidence. The bottom panel shows a zoomed-in view of residues 70-80. The protein is predicted to be disordered, with a high confidence score (0.99) for the N-terminal region. The secondary structure is mostly alpha-helical, with a blue arrow indicating a predicted alpha-helix in the N-terminal region.

Confidence Key

High(9)  Low (0)

The confidence key is a horizontal bar with 10 colored segments. From left to right, the colors are: red, orange, yellow, light green, green, teal, light blue, medium blue, dark blue, and purple. The bar is labeled 'High(9)' on the left and 'Low (0)' on the right.

? Disordered

 Alpha helix

➡ Beta strand