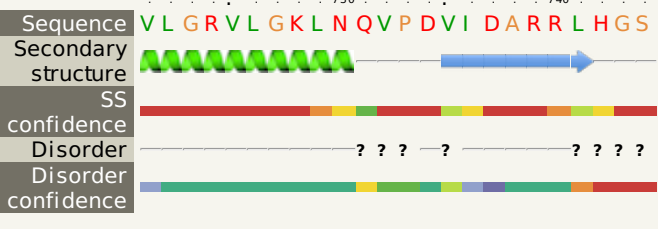
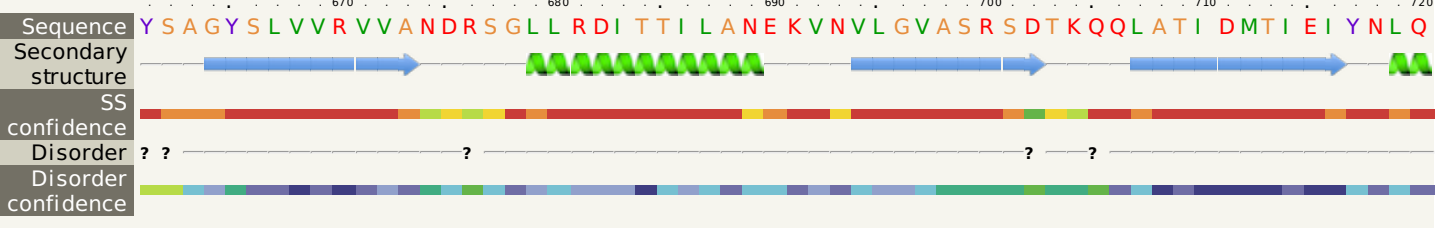
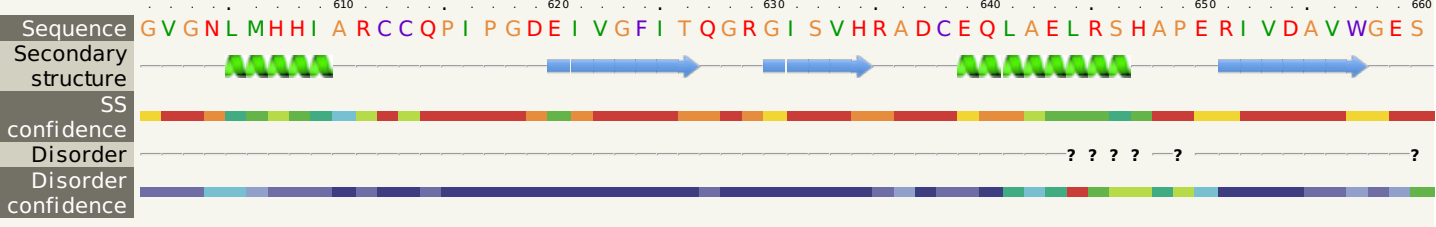
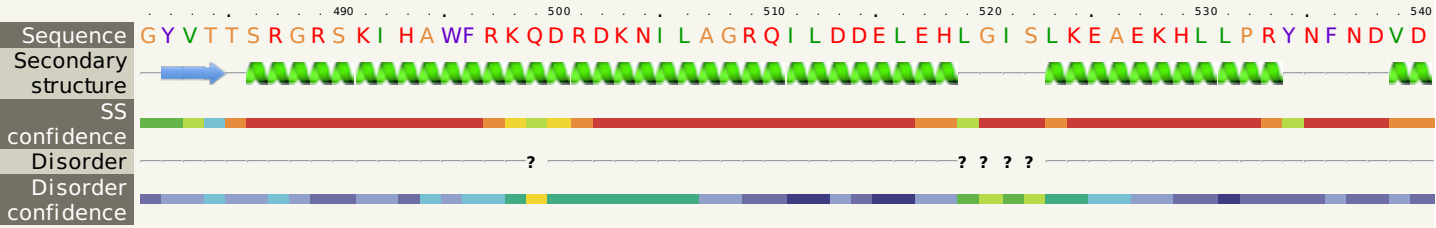
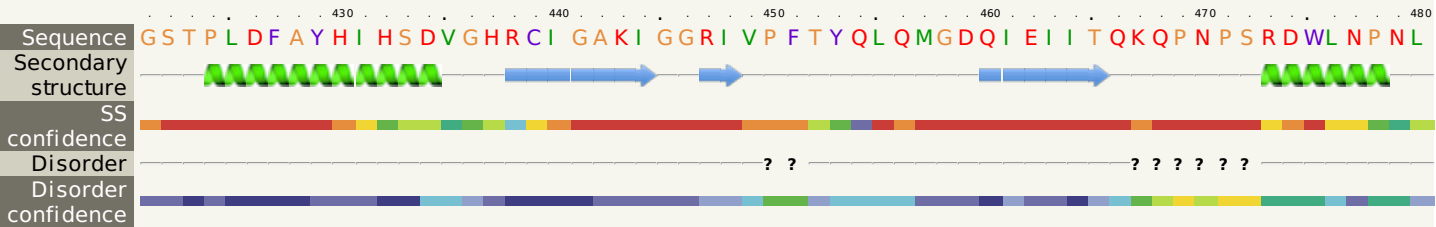


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Description	P0AG20
Date	Thu Jan 5 11:27:53 GMT 2012
Unique Job ID	d7085604ab271c15

The figure displays the protein structure analysis for the full-length protein (1-420). The analysis includes the following components:

- Sequence:** The amino acid sequence is shown in a color-coded format (e.g., MVAVRSAHI, NKAGEF, DPEKWI, ASLGI, TSQKSCECLAET, WAYCYCLQQT, QGHPPDAS, LLLWRGV).
- Secondary structure:** The predicted secondary structure is shown as a series of green bars representing alpha-helices and blue bars representing beta-strands.
- SS (Solvent Accessibility):** The solvent accessibility is shown as a series of colored bars (red, yellow, green, blue) indicating the degree of exposure of each residue.
- confidence:** The confidence score for the secondary structure prediction is shown as a series of colored bars (red, yellow, green, blue).
- Disorder:** The predicted disorder is shown as a series of colored bars (red, yellow, green, blue) indicating the degree of disorder.
- Disorder confidence:** The confidence score for the disorder prediction is shown as a series of colored bars (red, yellow, green, blue).

The analysis shows that the protein is highly disordered, with a high percentage of residues predicted to be disordered (indicated by the red and yellow bars in the Disorder and Disorder confidence tracks). The secondary structure is primarily composed of alpha-helices, with some beta-strands and loops. The solvent accessibility is generally low, suggesting a compact structure.



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