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Protein structure prediction results for the protein sequence MKLQKQLLEAVEHKQLRPLDVQFALT VAGDEHPAVTLAAALLSHDAGEGHVCLPLSRLEN. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

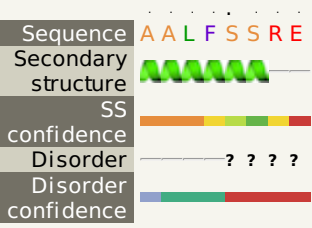
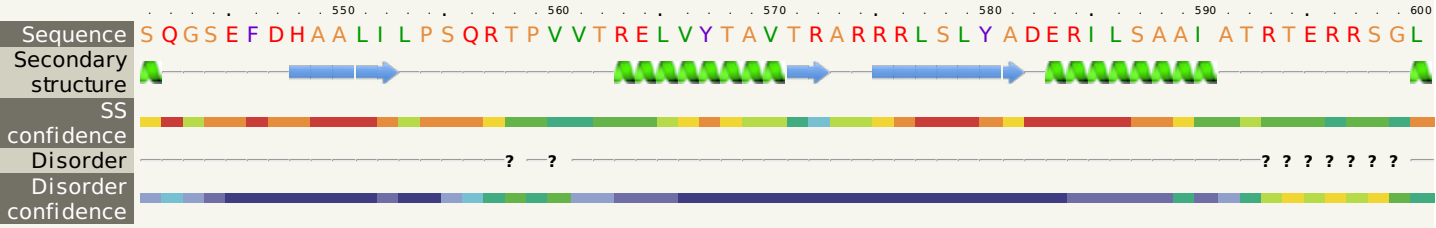
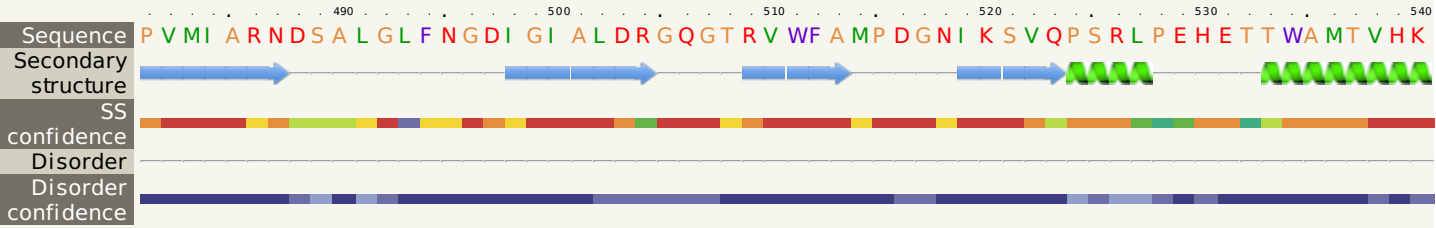
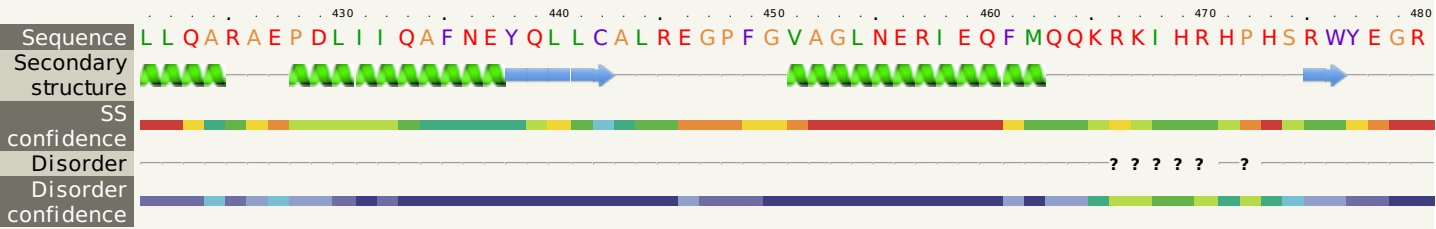
Sequence: MKLQKQLLEAVEHKQLRPLDVQFALT VAGDEHPAVTLAAALLSHDAGEGHVCLPLSRLEN

Secondary structure: Alpha helices (green cylinders) and beta strands (blue arrows) are shown. The structure is primarily composed of alpha helices, with a few beta strands interspersed.

SS confidence: A bar chart showing the confidence of the secondary structure prediction. The confidence is generally high, with some lower confidence regions (yellow and orange) around residues 10-20 and 30-40.

Disorder: A bar chart showing the disorder of the protein. The protein is mostly ordered (dark blue), with some disordered regions (light blue and yellow) around residues 10-20 and 30-40.

Disorder confidence: A bar chart showing the confidence of the disorder prediction. The confidence is generally high, with some lower confidence regions (yellow and orange) around residues 10-20 and 30-40.



Confidence Key
High(9) [Color scale from red to blue] Low (0)
? Disordered
[Alpha helix icon] Alpha helix
[Beta strand icon] Beta strand