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Protein structure prediction results for the protein sequence MS DYKSTLNL PETGFP MRGDL AKREP GMLAR WTDDDLYGI I RAAKKGKKT F I L HDGPPYA. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

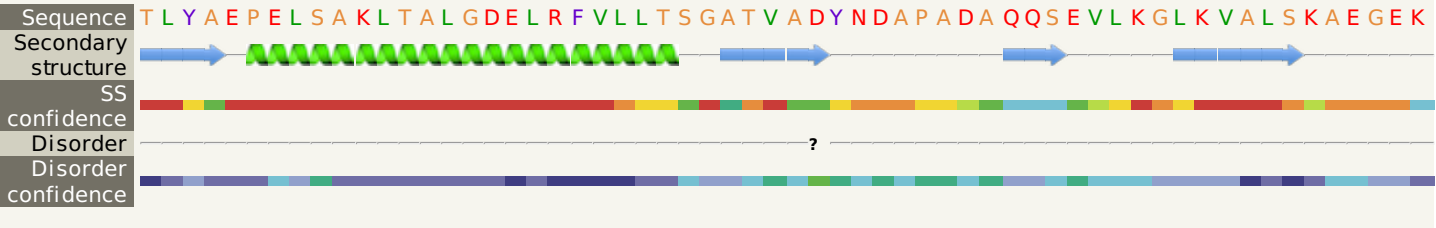
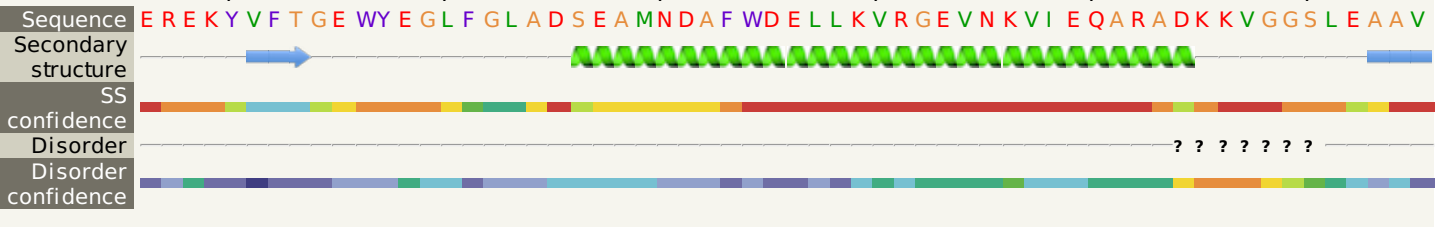
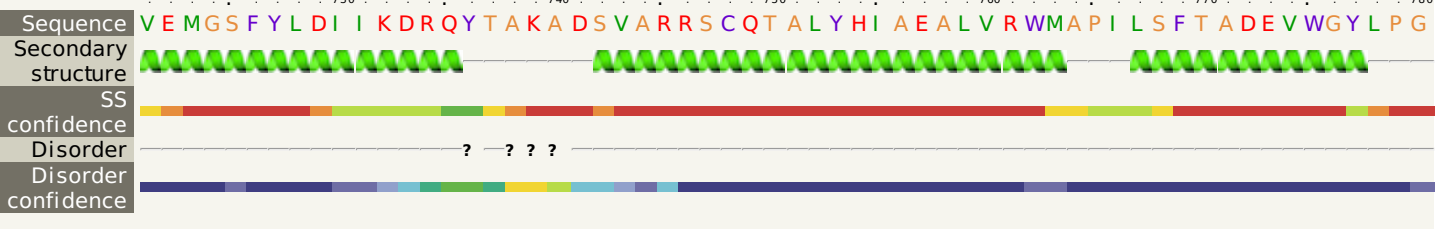
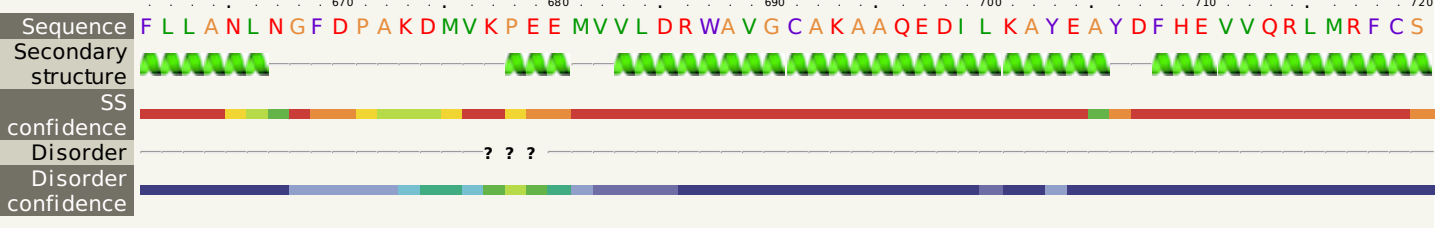
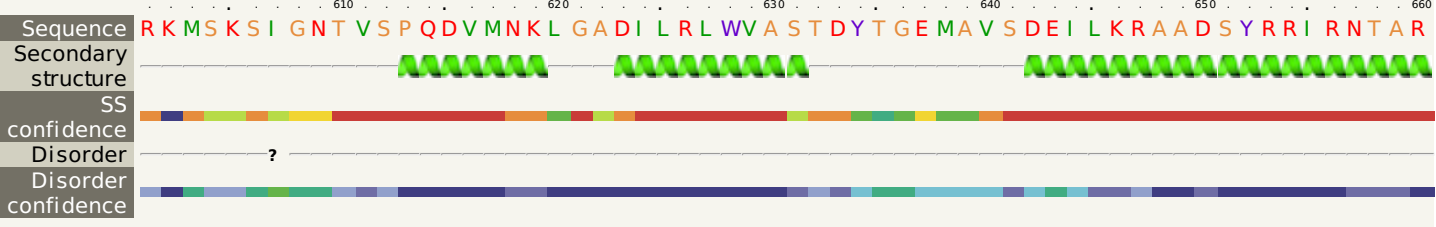
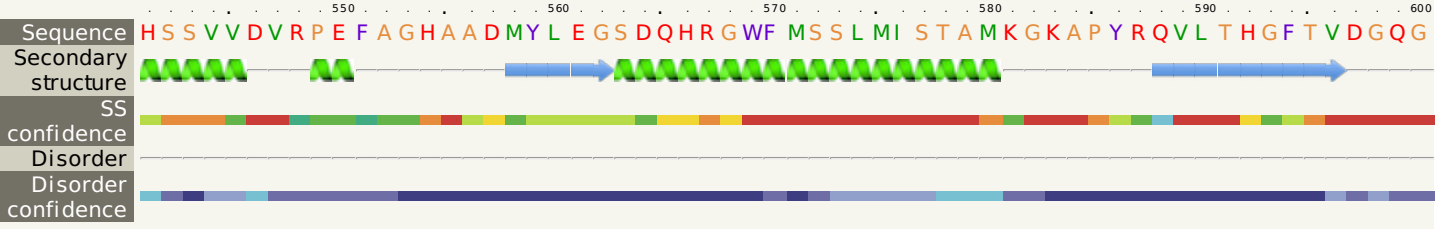
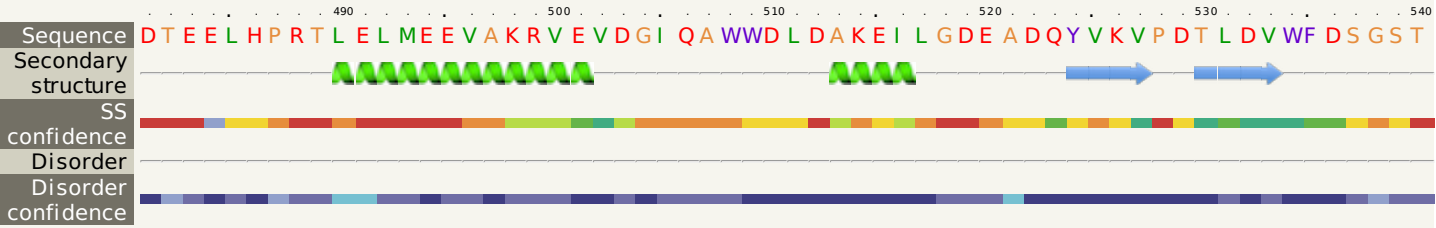
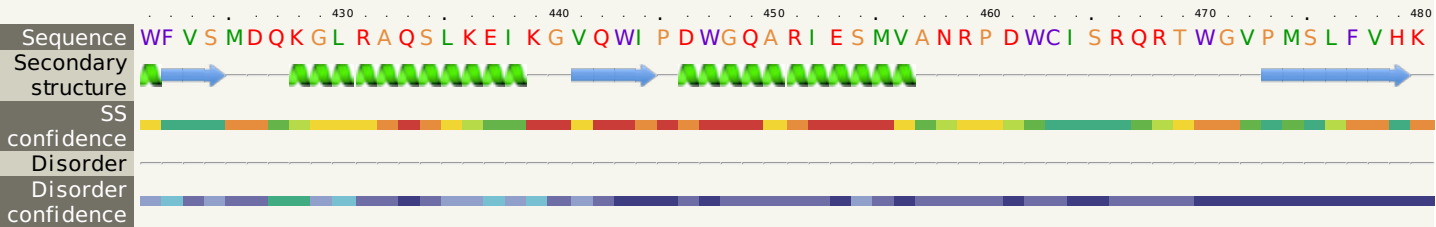
Sequence: MS DYKSTLNL PETGFP MRGDL AKREP GMLAR WTDDDLYGI I RAAKKGKKT F I L HDGPPYA

Secondary structure: The structure is shown as a series of green arrows representing alpha-helices and blue arrows representing beta-strands. The structure is primarily composed of alpha-helices, with a few beta-strands interspersed.

SS confidence: The confidence is shown as a series of colored bars (red, yellow, green, blue) indicating the reliability of the secondary structure prediction. The confidence is generally high, with some lower confidence regions (yellow and red) interspersed.

Disorder: The disorder is shown as a series of colored bars (red, yellow, green, blue) indicating the predicted disorder of the protein. The protein is predominantly disordered, with some ordered regions (green and blue) interspersed.

Disorder confidence: The confidence is shown as a series of colored bars (red, yellow, green, blue) indicating the reliability of the disorder prediction. The confidence is generally high, with some lower confidence regions (yellow and red) interspersed.





Confidence Key
High(9) [red bar] [orange bar] [yellow bar] [light green bar] [green bar] [dark green bar] [blue bar] Low (0)
? Disordered
Alpha helix
Beta strand