

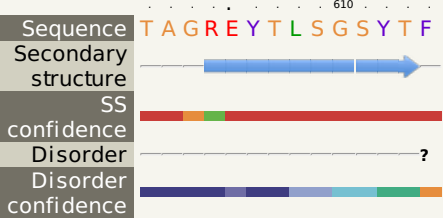
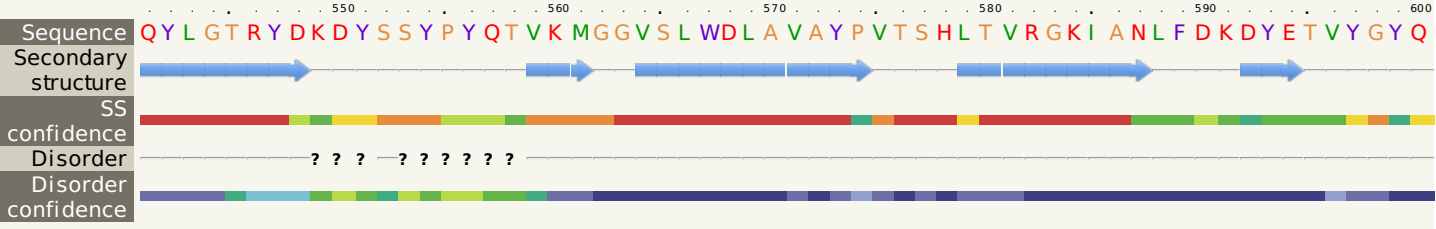
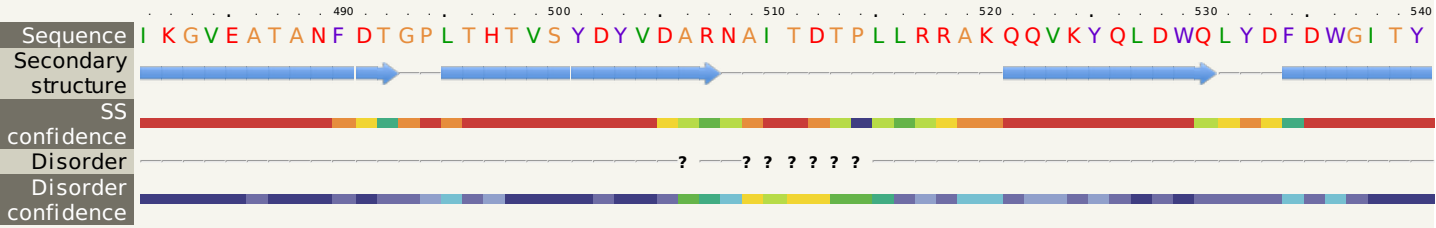
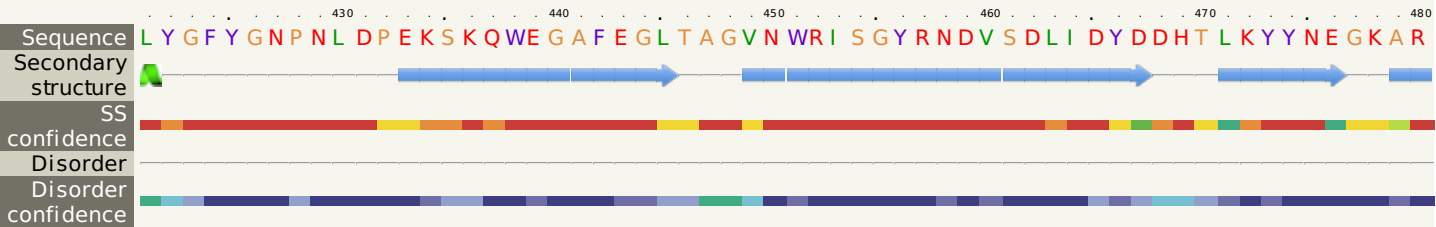
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The figure displays a protein structure prediction and disorder analysis for a protein sequence. The sequence is shown in a color-coded format, with residues grouped into segments. The analysis includes secondary structure prediction (SS), confidence scores, and disorder analysis (Disorder) for the entire sequence.

Sequence: MIKKASLLTACSVTAFSAWAQDTSPDTLVVTANRFEQPRSTVLAPT TVVTRQDIDRWQSTSVNDVLRRLPGVDITQNGGSGQLSSI FIRGTNASHVLVLIDGVRLNLAGVSGSADLSQFRIALVQRVEYIRGPRSAVYGSDAIGGVVNIITTRDEPGTEISAGWGSNSYQNYDVSTQQQLGDKTRVTLGLGDYAHTHGYDVVAYGNTGTQAQTDNDGFLSKTLYGALEHNFTDAWSG FVRGYGYNRTNYDAYYSPGSPLL DTRKLYSQSWDAGLRYNGELIKSQLITSYSHSKDYNYPHYGRYDSSATLDEMKQYTVQWANNVIVGHGSI GAGVDWQQTTPGTGYVEDGYDQRNTGIYLTGLQQVGDFTFEGAARSDDNSQFGRHGTWQTSAGWEFIEGYRFIASYGTSYKAPNLGQ

Secondary structure prediction (SS): The structure is shown as a series of blue arrows (alpha-helices) and green cylinders (beta-strands) along the sequence. The prediction is highly confident, with many regions marked as "SS confidence".

Disorder analysis: The disorder analysis is shown as a series of colored bars (red, yellow, green, blue, purple) along the sequence. The analysis indicates regions of high disorder (red/yellow) and low disorder (green/blue/purple). The disorder analysis is highly confident, with many regions marked as "Disorder confidence".



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand