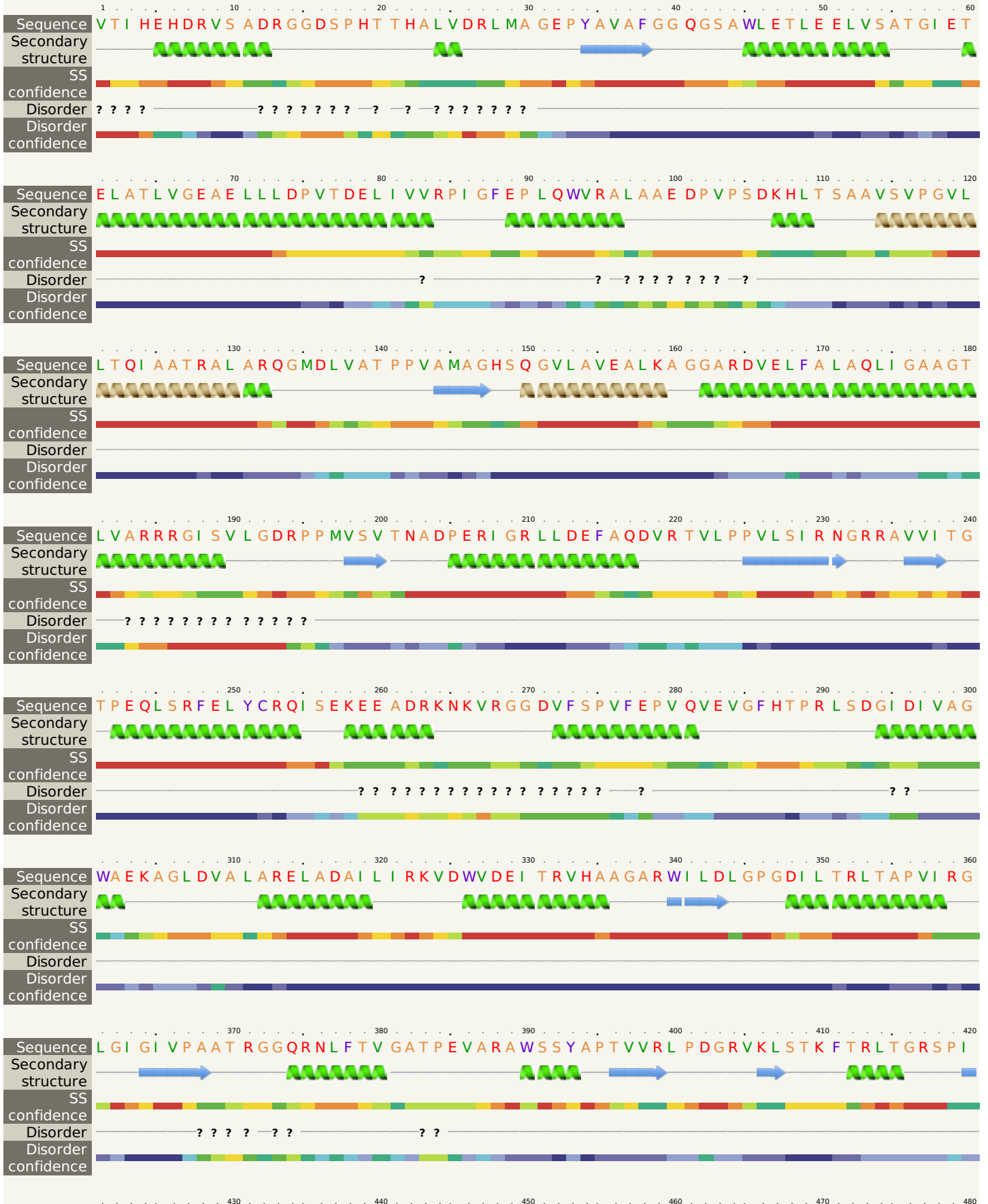
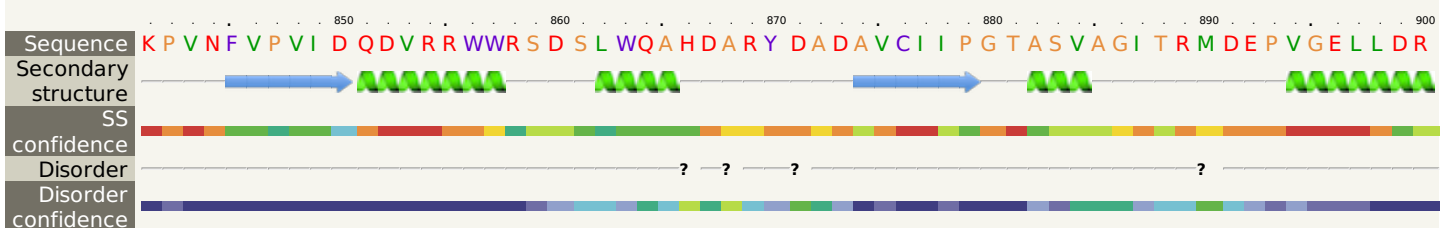
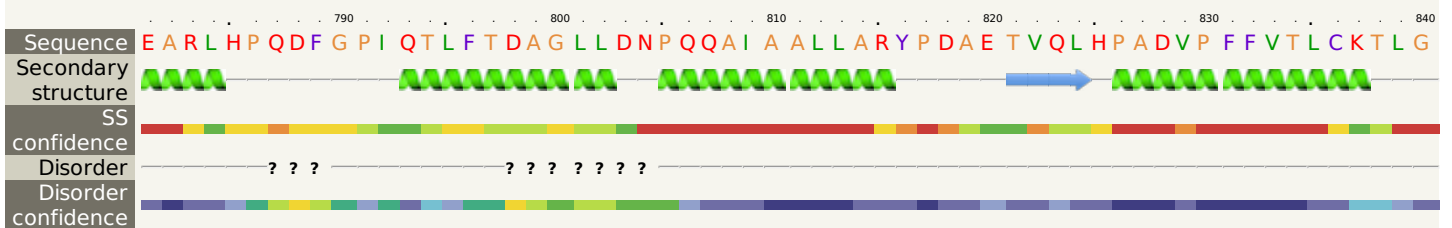
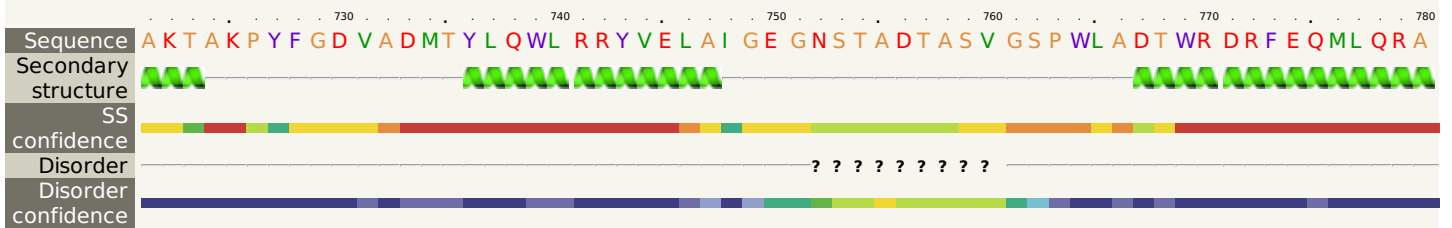
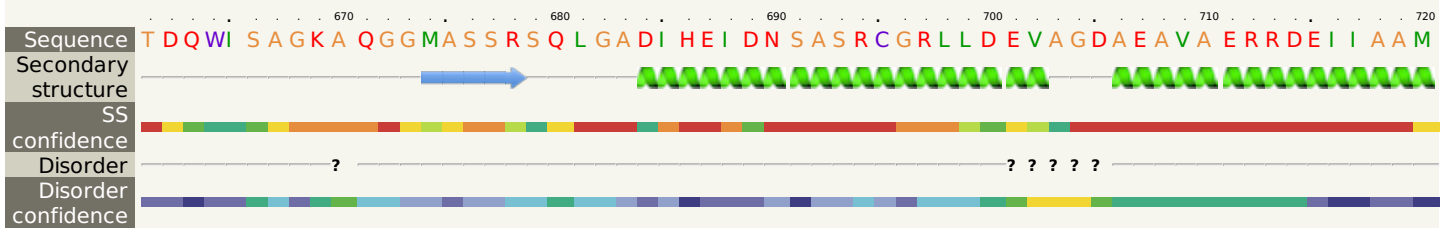
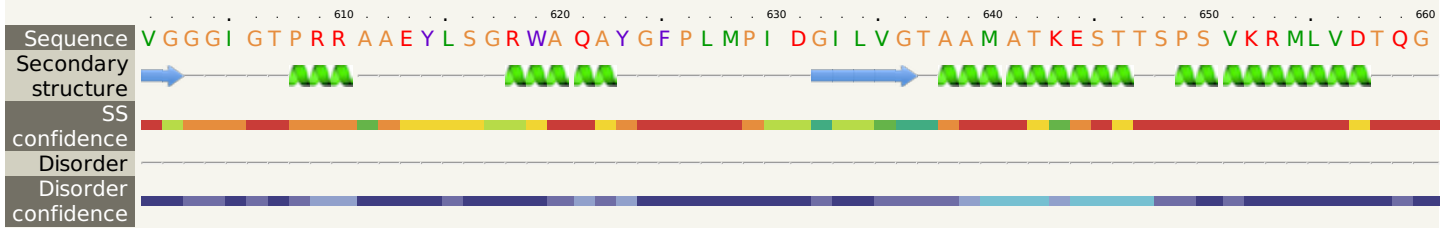
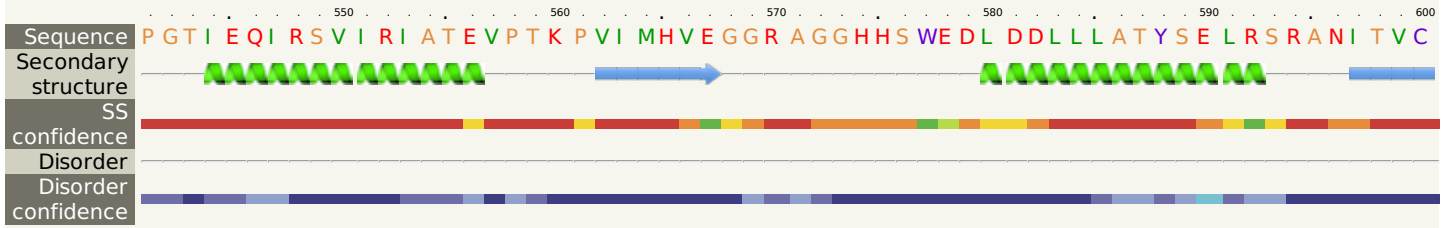
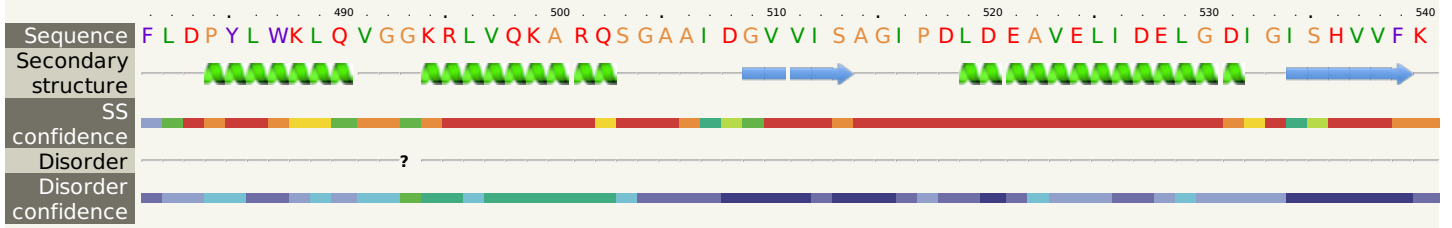
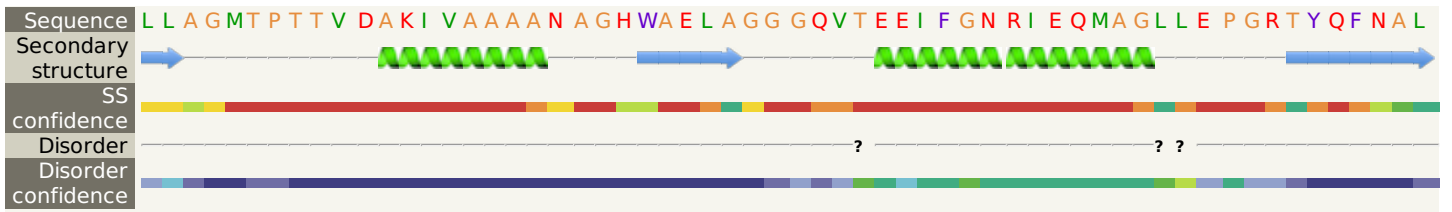


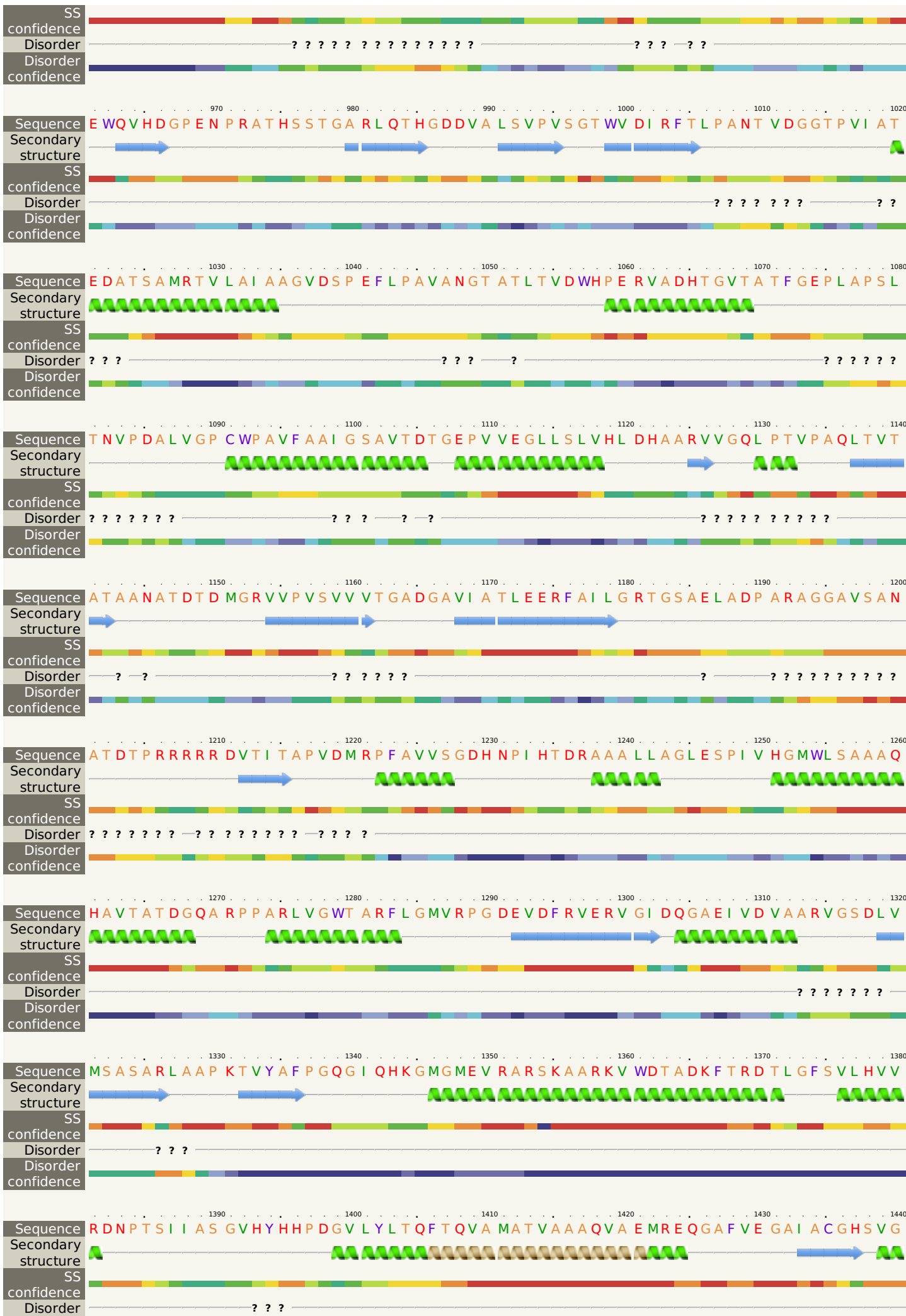
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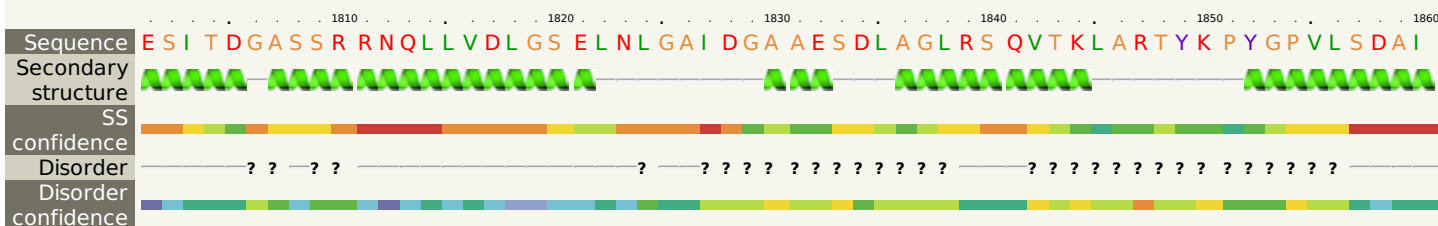
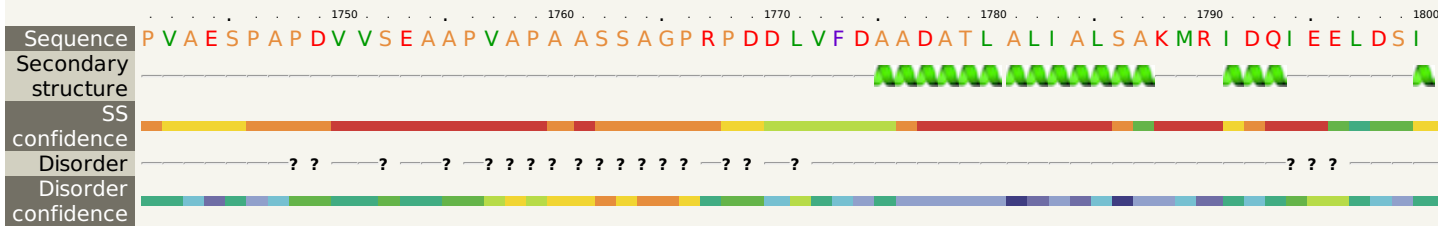
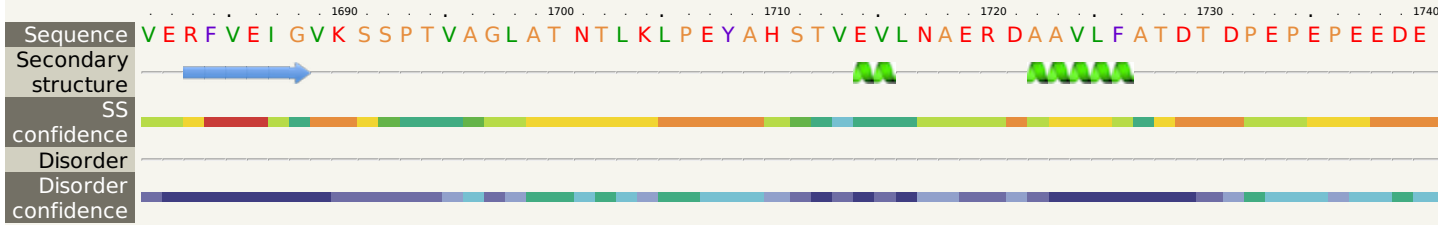
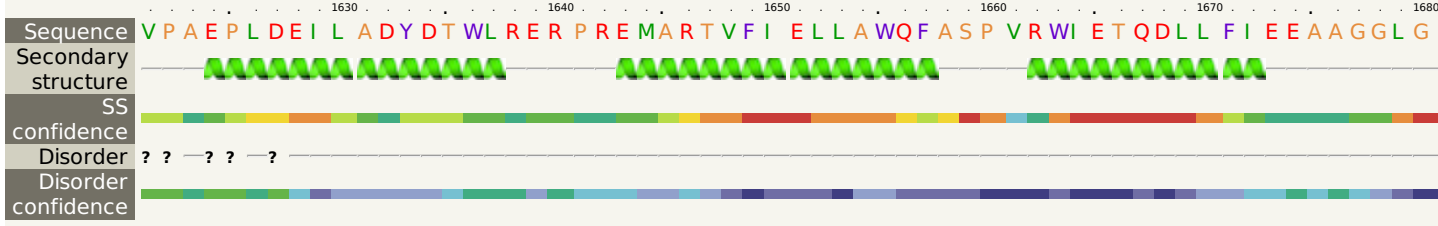
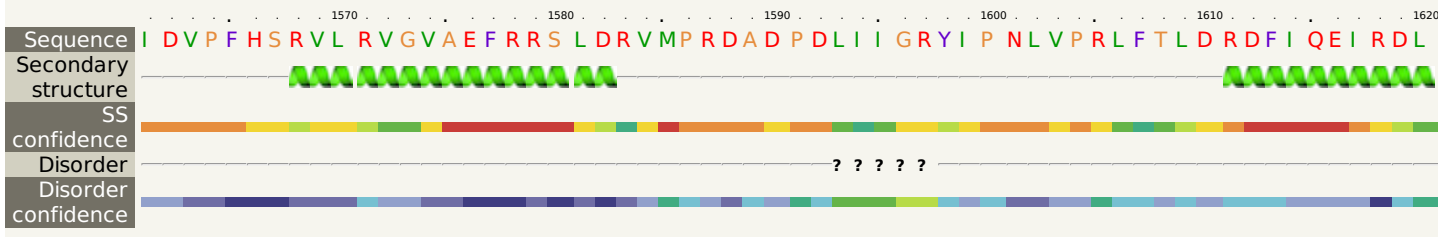
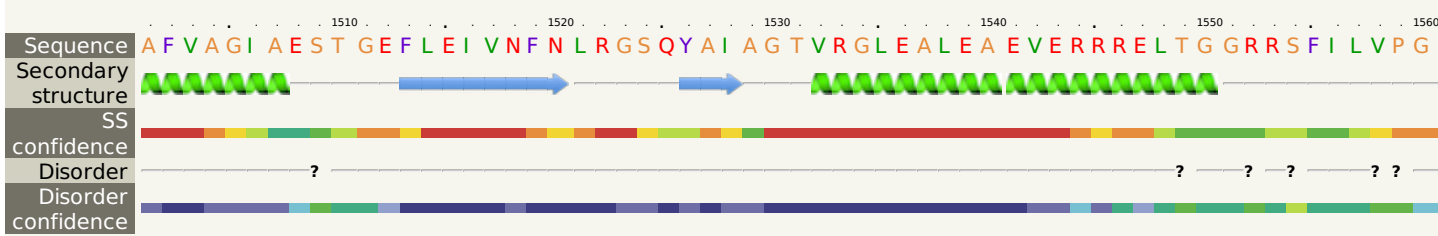
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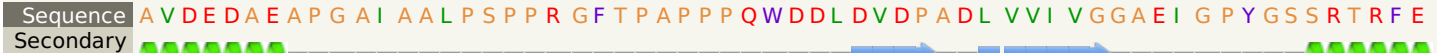
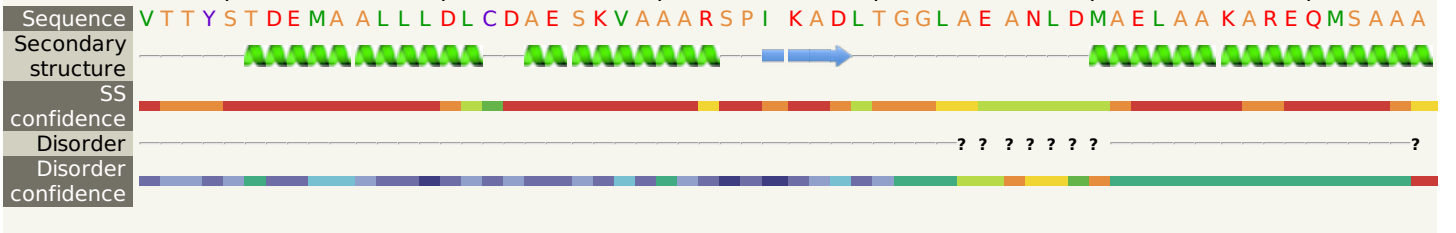
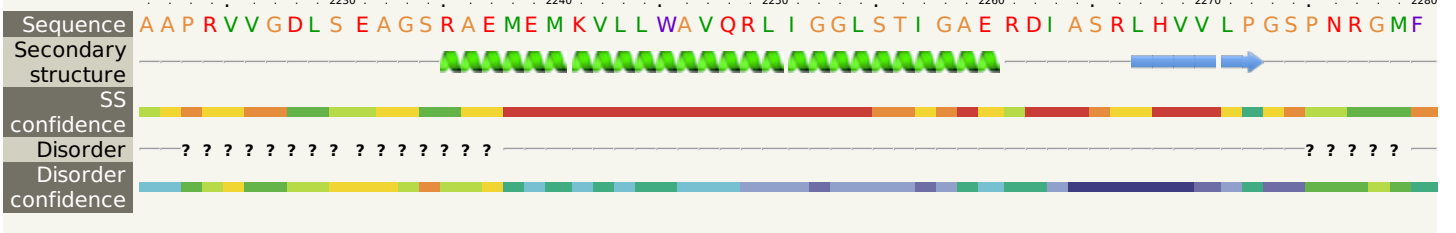
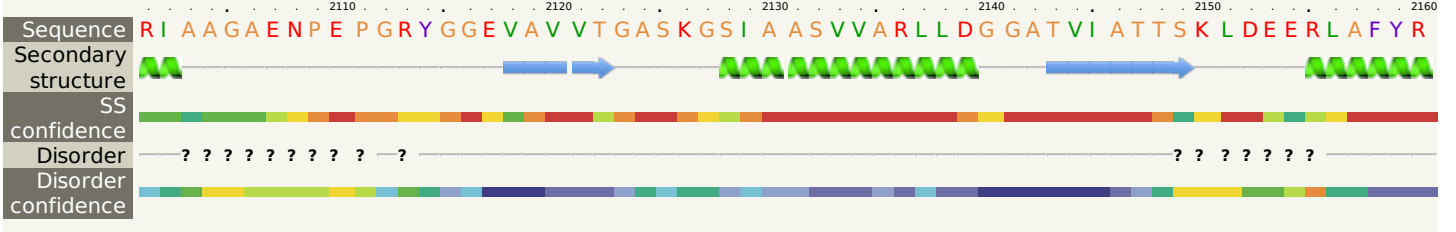
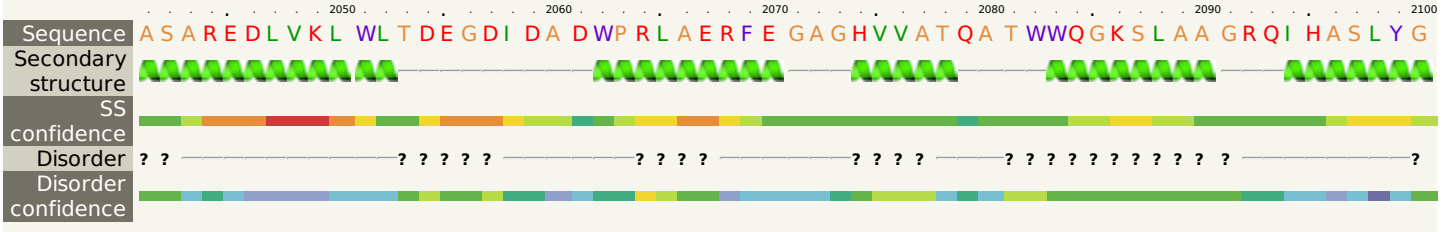
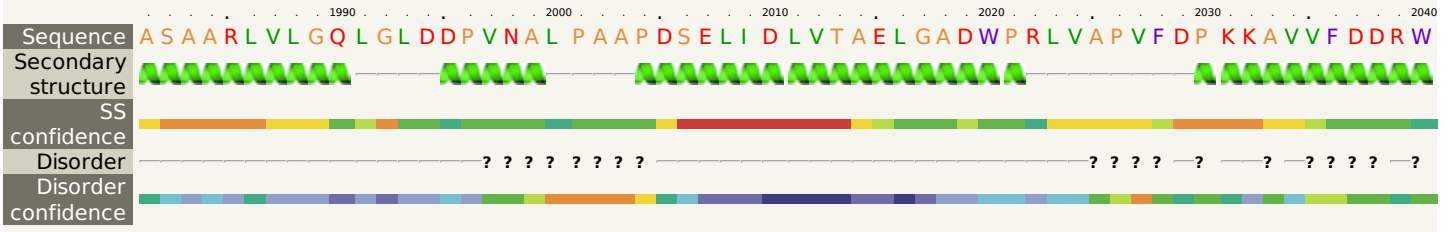
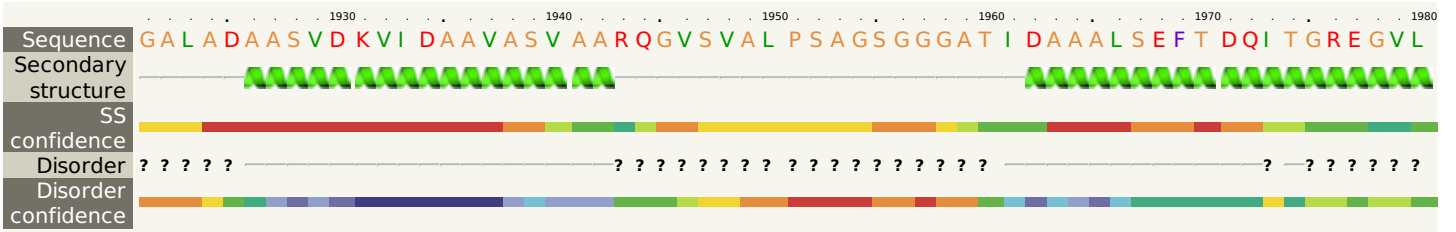
Secondary structure and disorder prediction

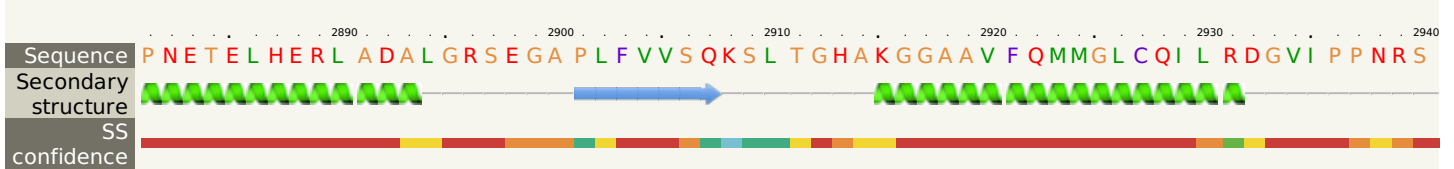
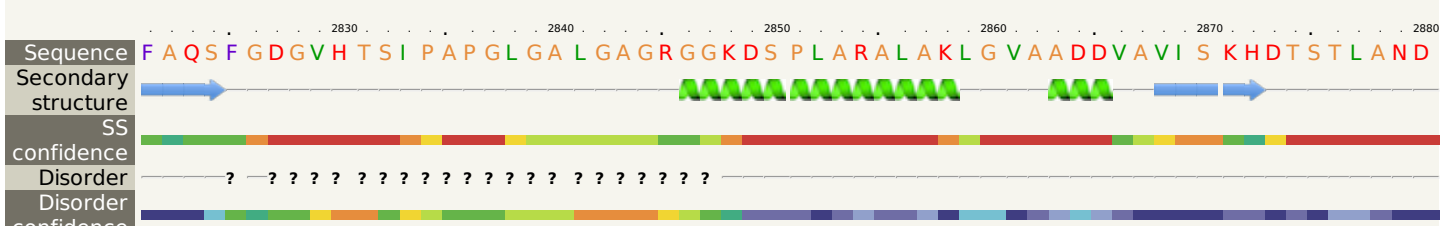
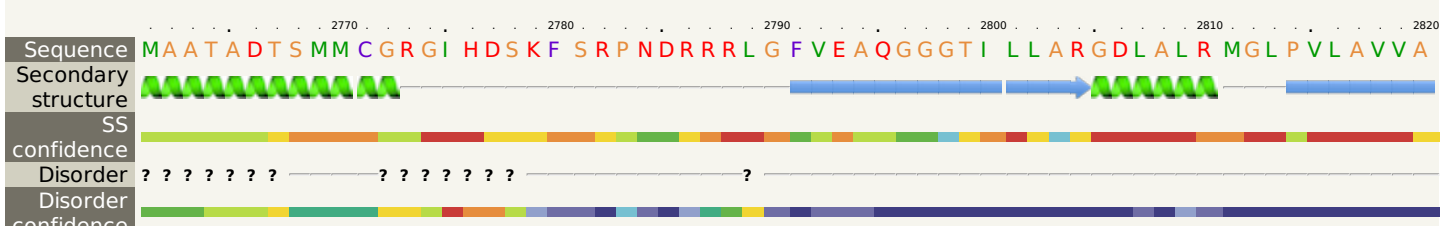
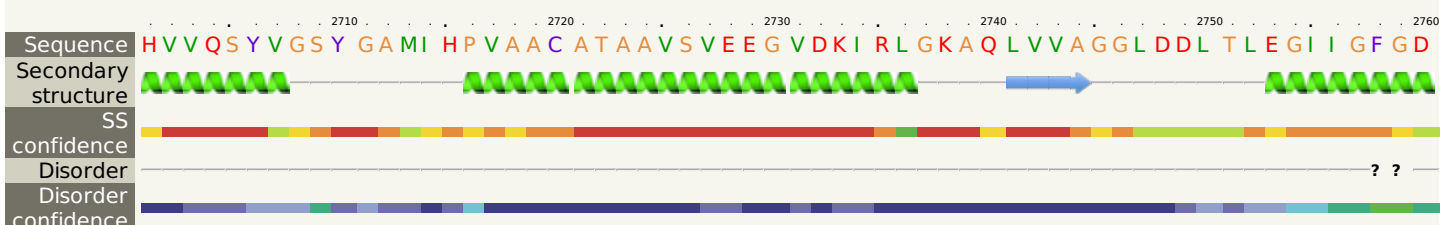
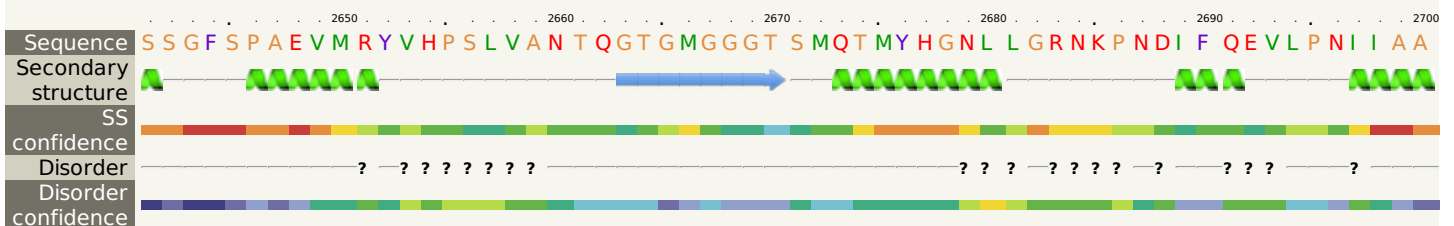
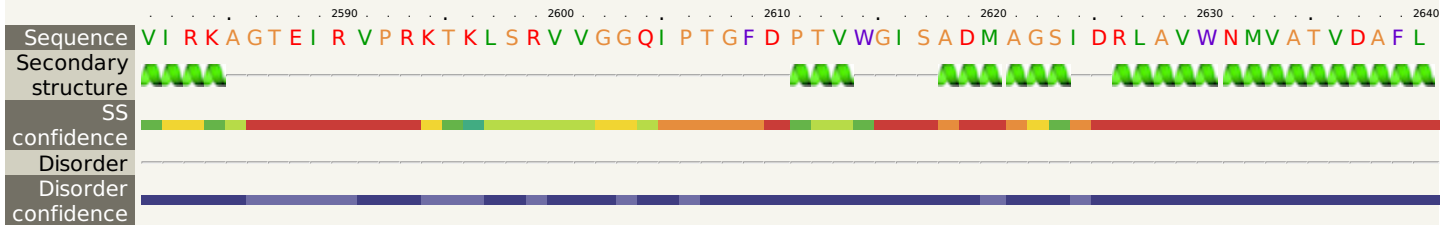
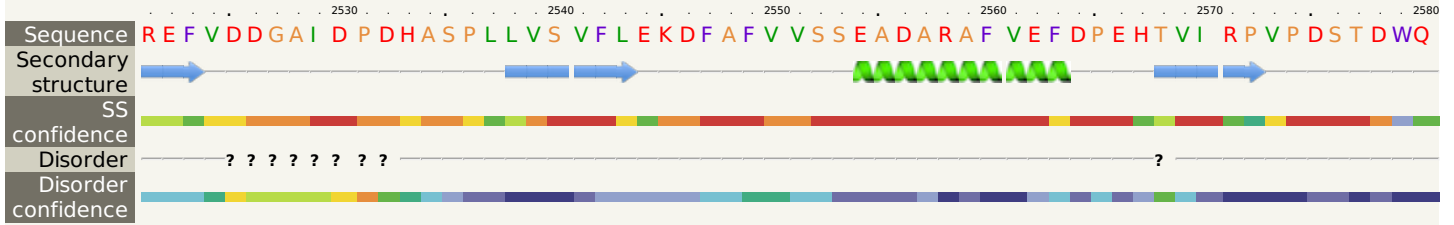
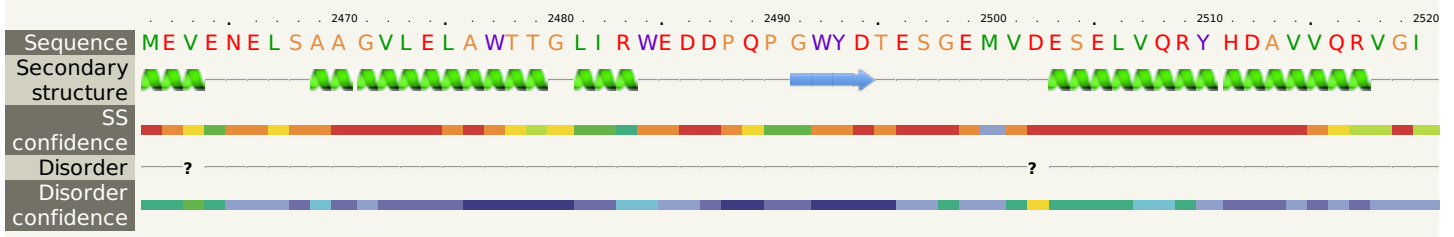
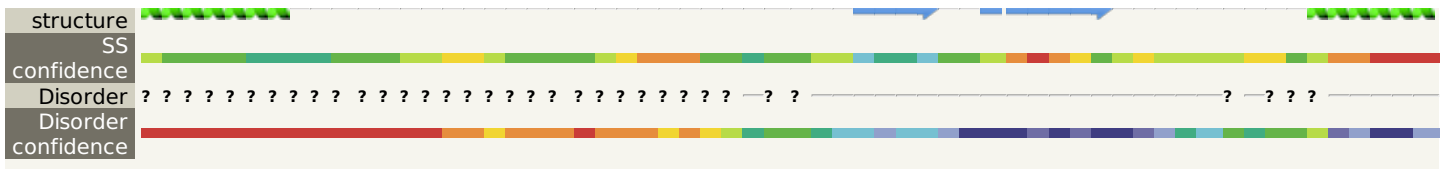


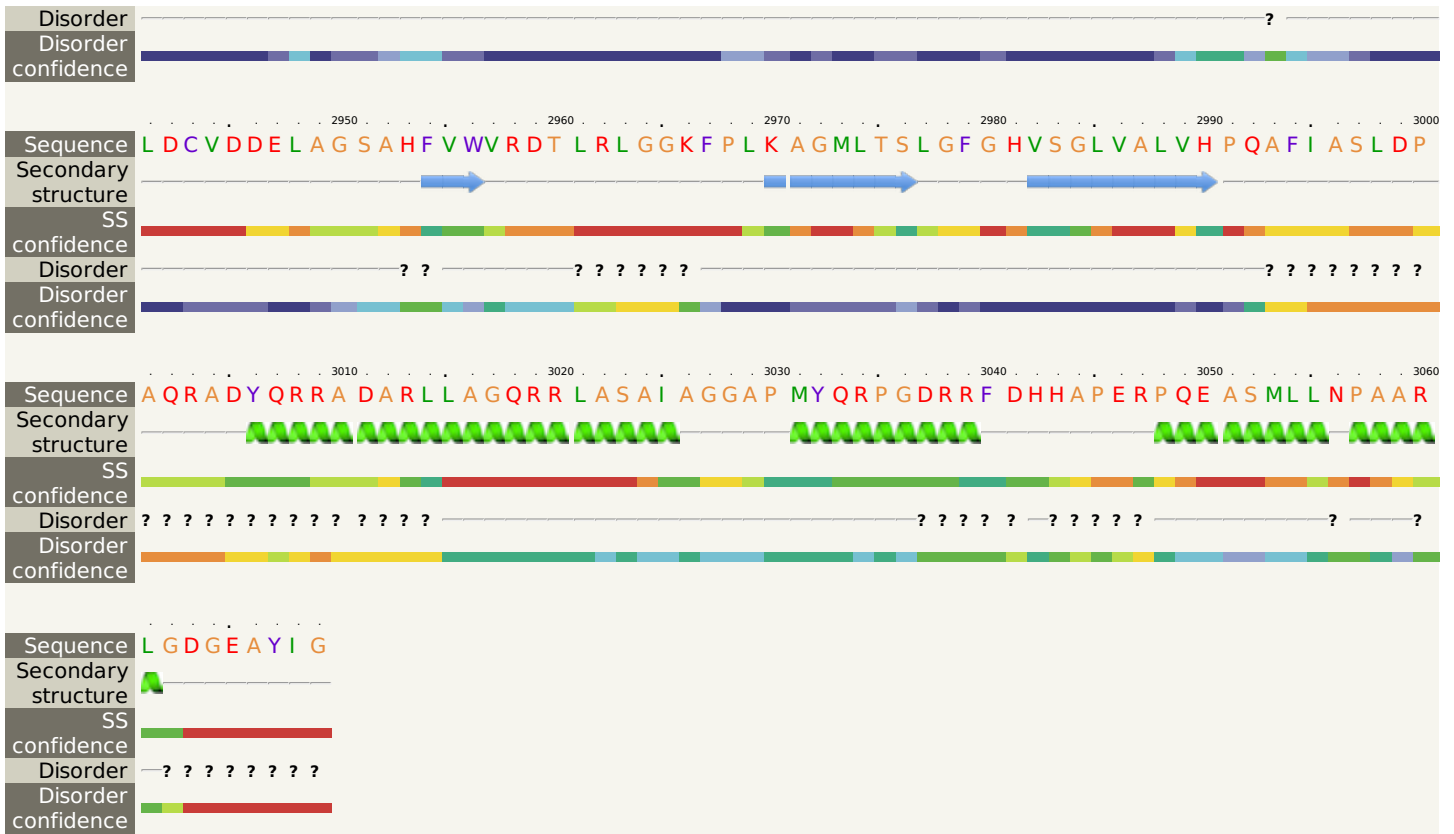












Confidence Key
High(9) Low (0)
? Disordered (20%)
Alpha helix (44%)
Beta strand (11%)
TM helix (2%)