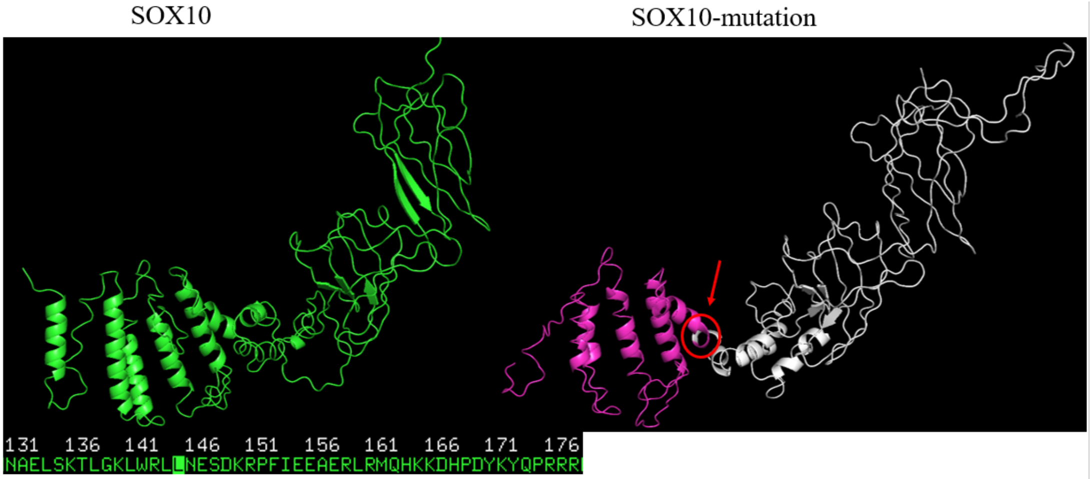
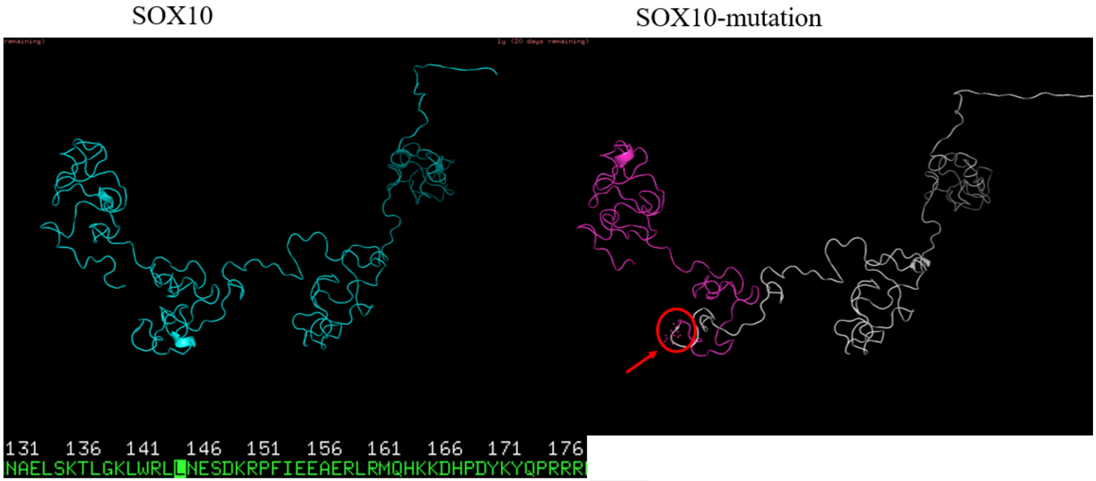


Model1: C-score=-0.99 ; RMSD = 23.083



Model2: C-score= -0.88 ; RMSD = 14.179

Appendix 1. Model1 and model2 are two 3D-structure models of the SOX10 and SOX10-mutation. The start location of the mutation is marked in red circle. The protein structure disruption caused by the mutation is shown in grey. The C-score ranges of [-5, 2]. A C-score of a higher value signifies a model with a higher confidence and vice versa. Higer RMSD means less similarity between two protein structures.