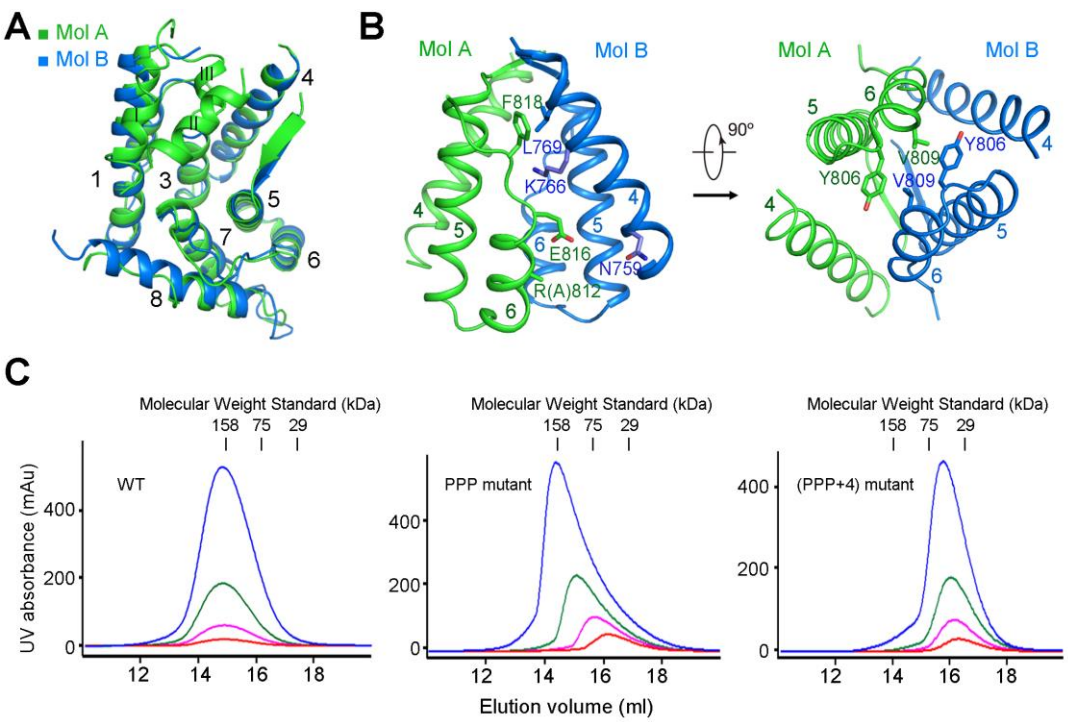

Supplementary information, Figure S5 The dimer interface of Sre1-CTD. (**A**) The two Sre1-CTD molecules in each asymmetric unit adopt almost identical conformations. Shown here is a structure overlay of these two molecules, with a pair-wise root-mean-squared deviation (RMSD) of approximately 0.63 Å over 133 Cα atoms. (**B**) The dimer interface of Sre1-CTD in two perpendicular views. (**C**) Concentration-dependent size exclusion chromatography (SEC) of WT (left), PPP mutant (middle) and the (PPP+4) mutant (right) of Sre1-CTD. The oligomerization state of the PPP mutant appears to be concentration-dependent, whereas the (PPP+4) mutant remains a monomer even at high protein concentration.