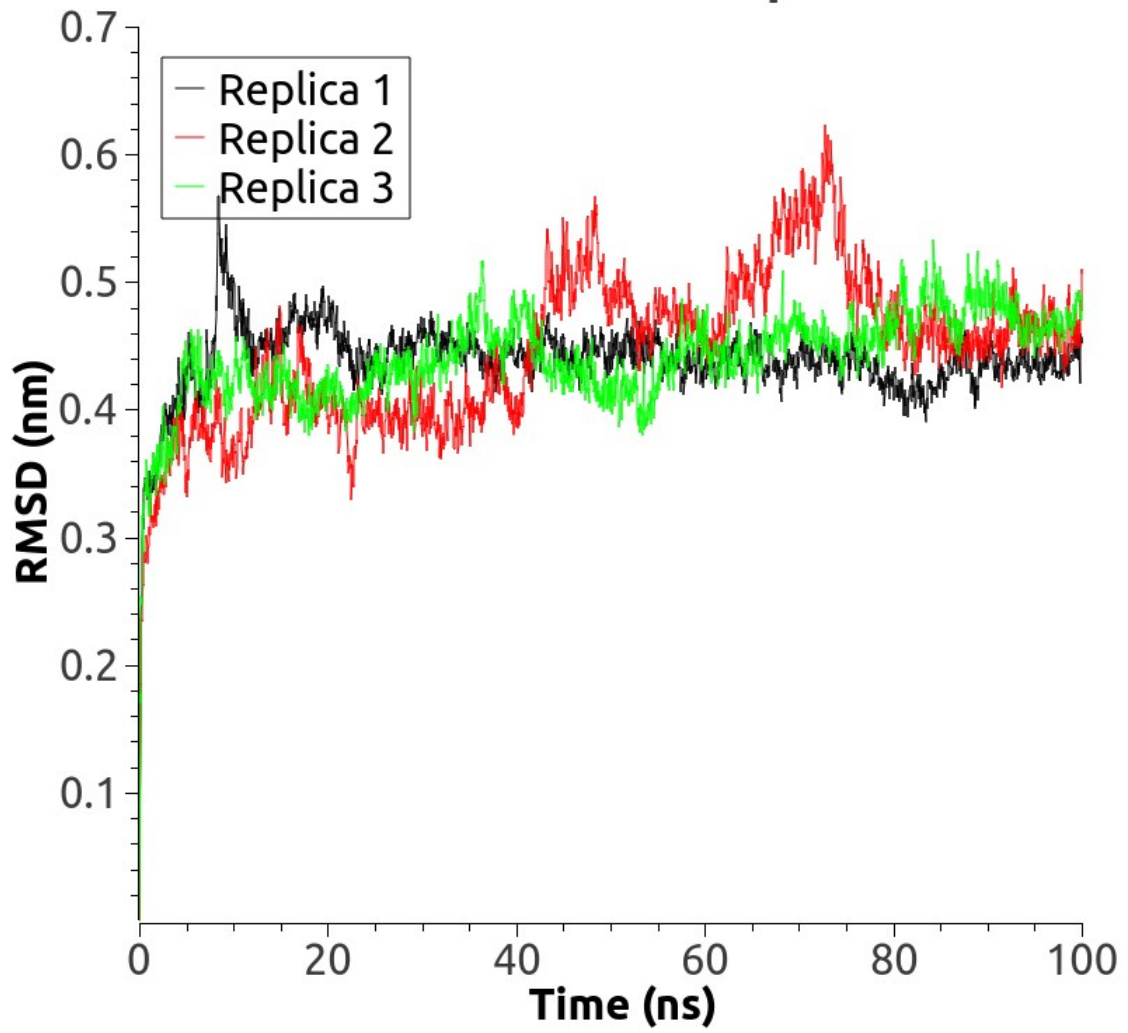


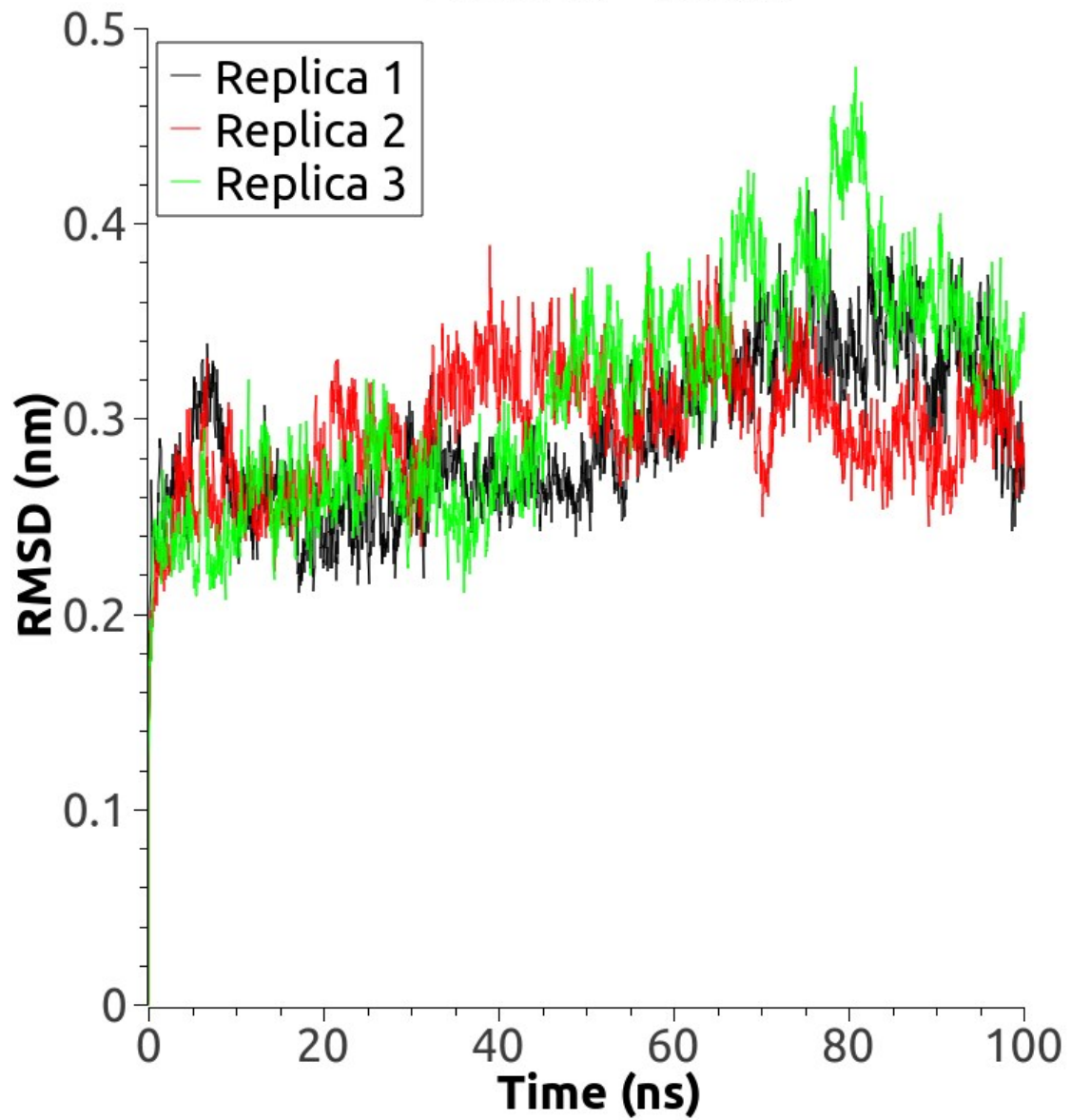
**Supplementary Figure 1.** Potential of mean forces calculated by umbrella sampling simulations for five different ligands, with NCOA1 PASB in the loop-helix-loop canonical conformation. L3 (green) has considerably lower binding energy in comparison to the other four ligands.

## NCOA1 - Loop

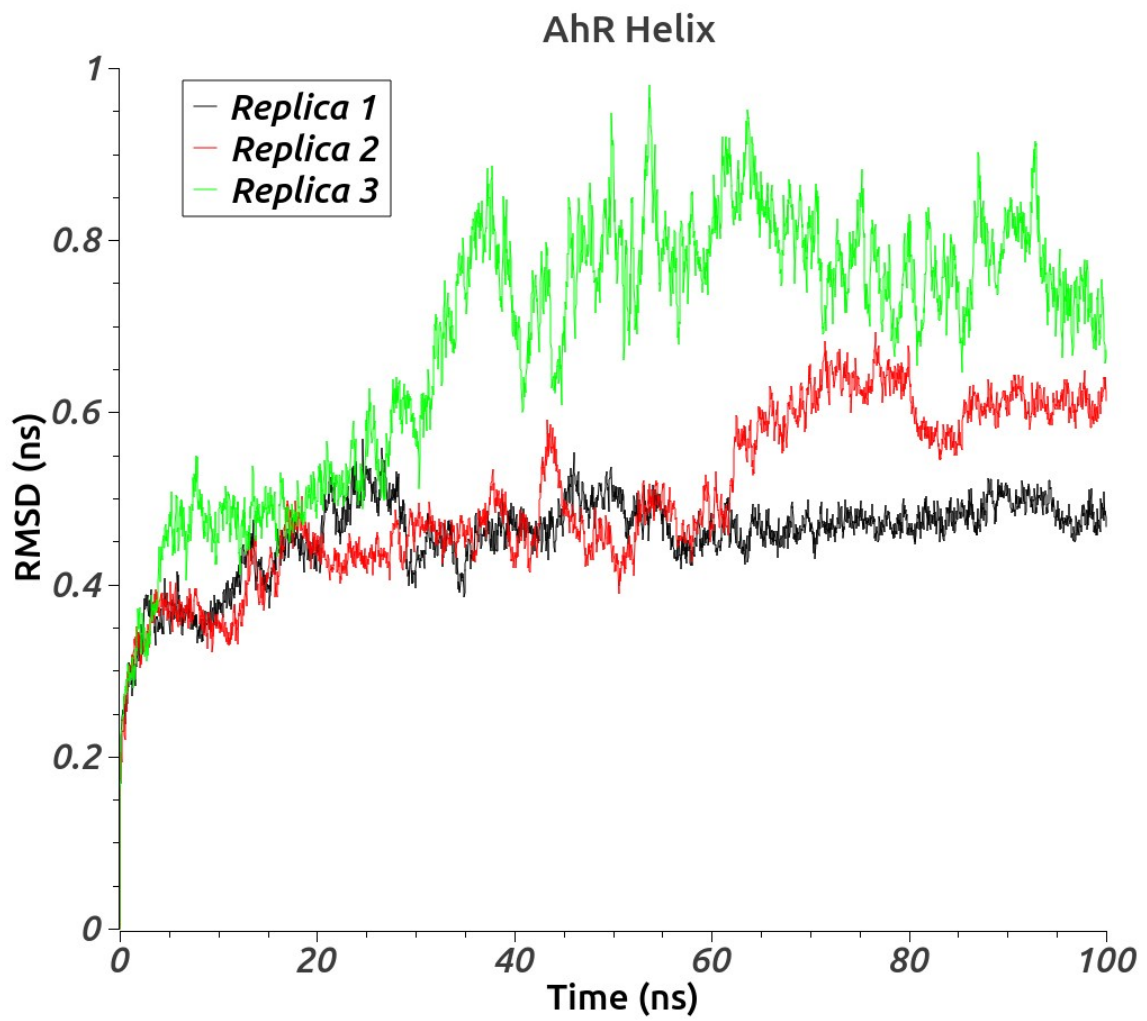


**Supplementary Figure 2.** RMSD plot for the three replicas on the partially disordered loop conformation of the PASB-NCOA1.

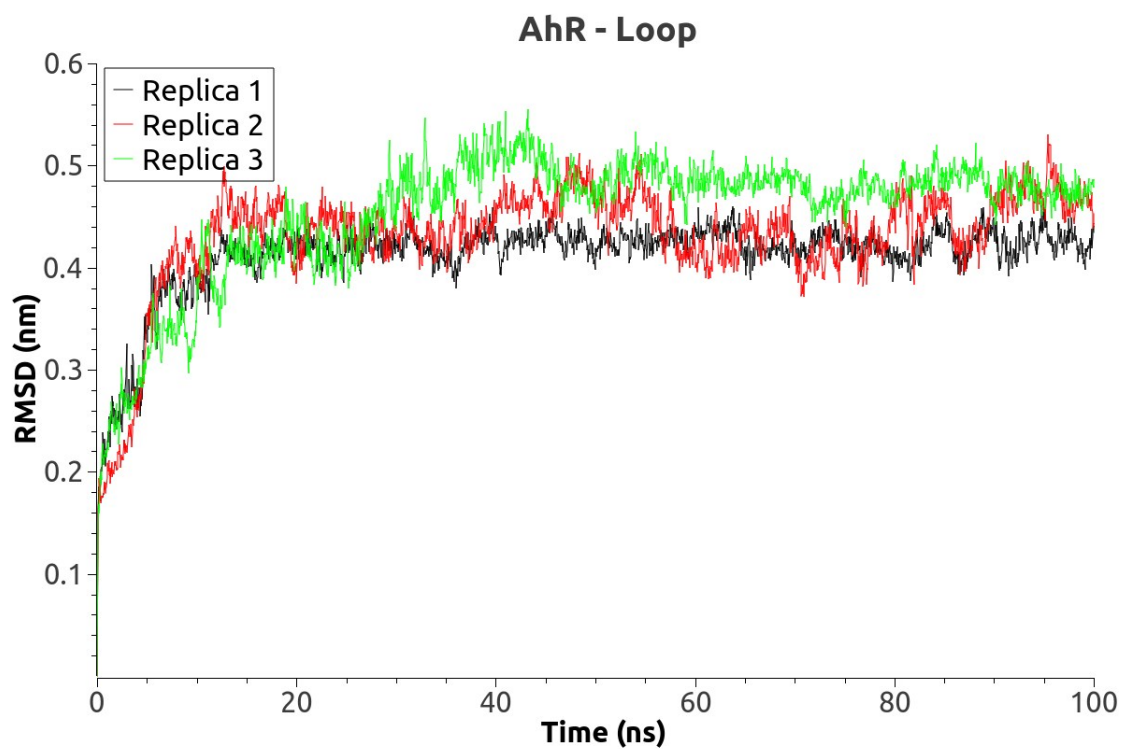
## NCOA1 - Helix



*Supplementary Figure 3. RMSD plot for the three replicas of the helix conformation of the PASB-NCOA1.*

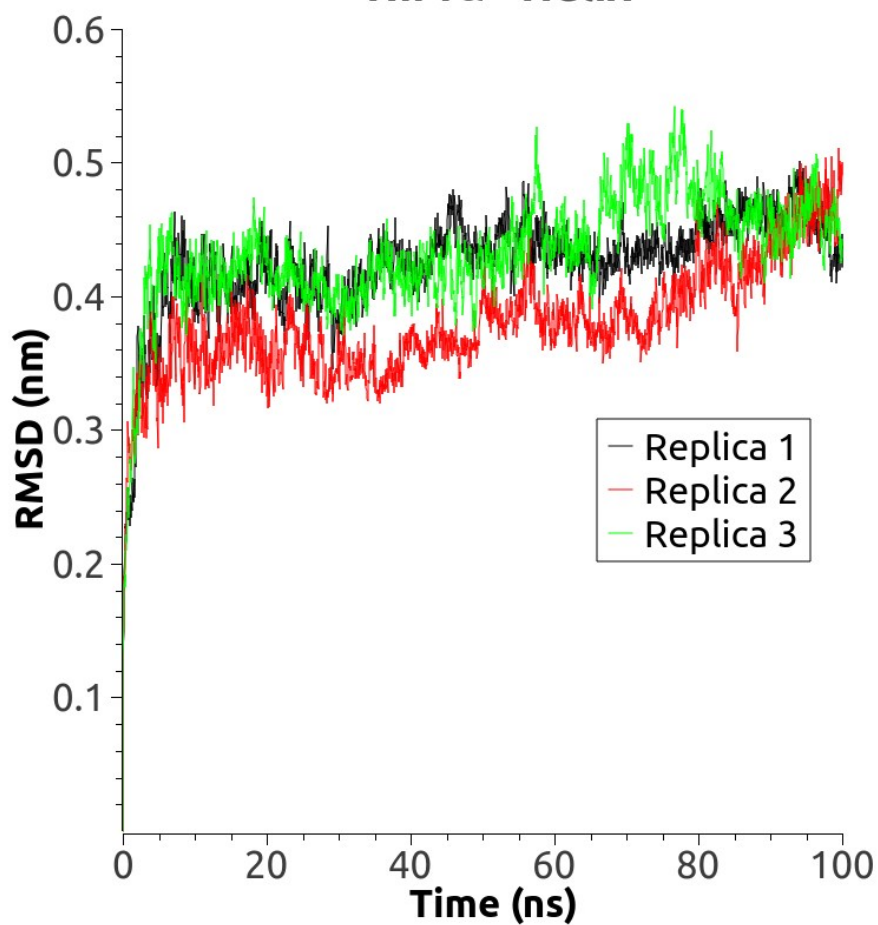


**Supplementary Figure 4.** RMSD plot for the three replicas on the helix conformation of the PASB-AhR.

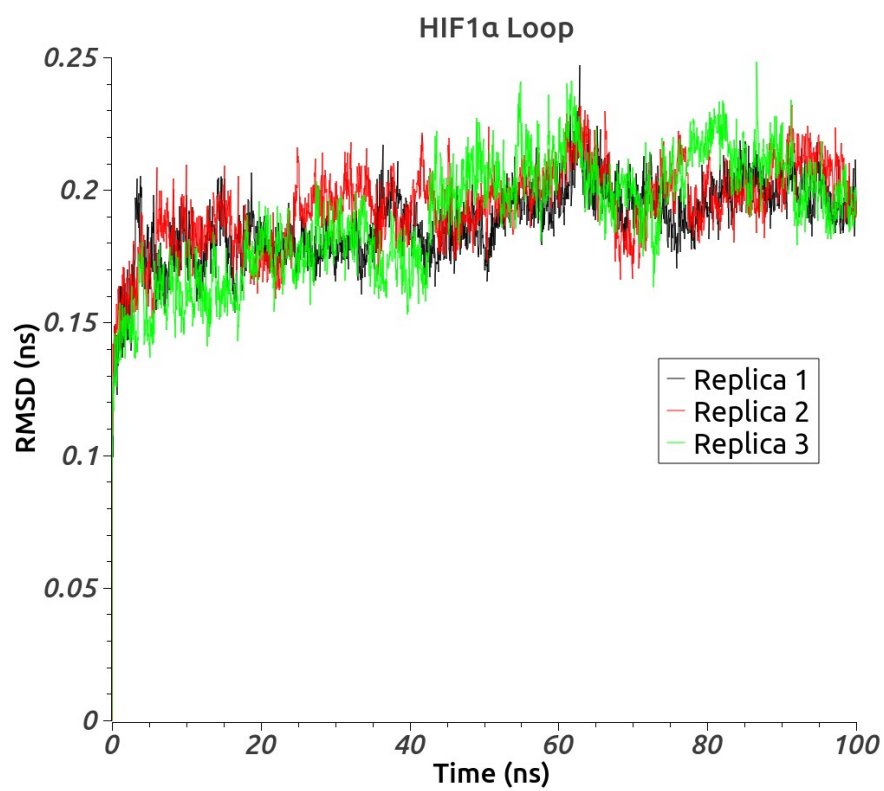


**Supplementary Figure 5.** RMSD plot for the three replicas on the loop conformation of the PASB-AhR.

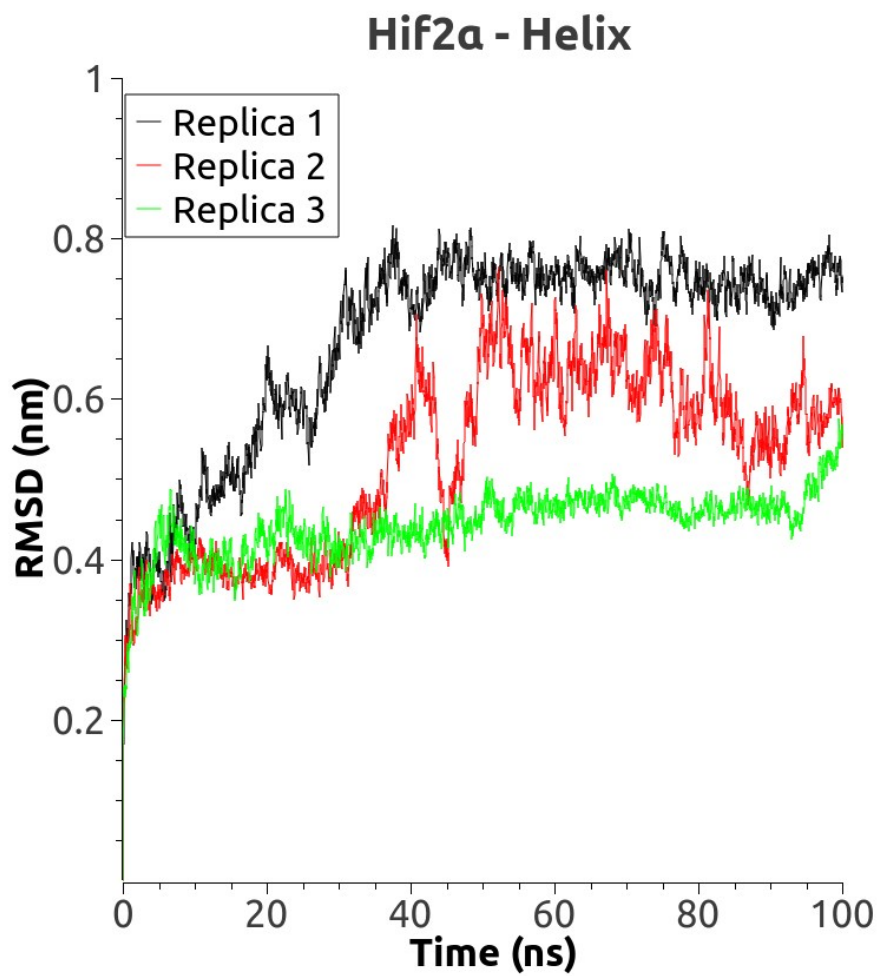
## Hif1 $\alpha$ - Helix



*Supplementary Figure 6. RMSD plot for the three replicas on the Helix conformation of the PASB-HIF1 $\alpha$ .*

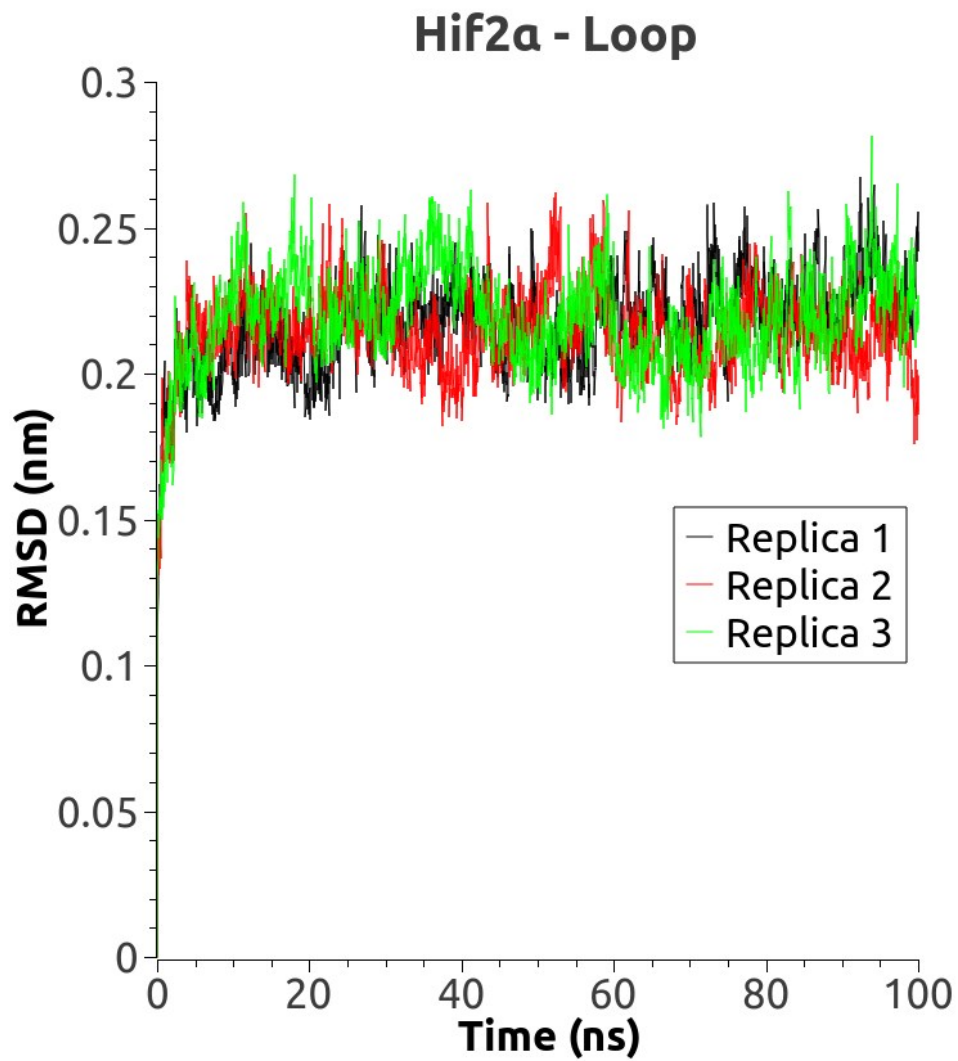


**Supplementary Figure 7.** RMSD plot for the three replicas on the loop conformation of the PASB-HIF1 $\alpha$ .



*Supplementary Figure 8. RMSD plot for the three replicas on the helix conformation of the PASB-HIF2 $\alpha$ .*





*Supplementary Figure 9. RMSD plot for the three replicas on the loop conformation of the PASB-HIF2 $\alpha$ .*