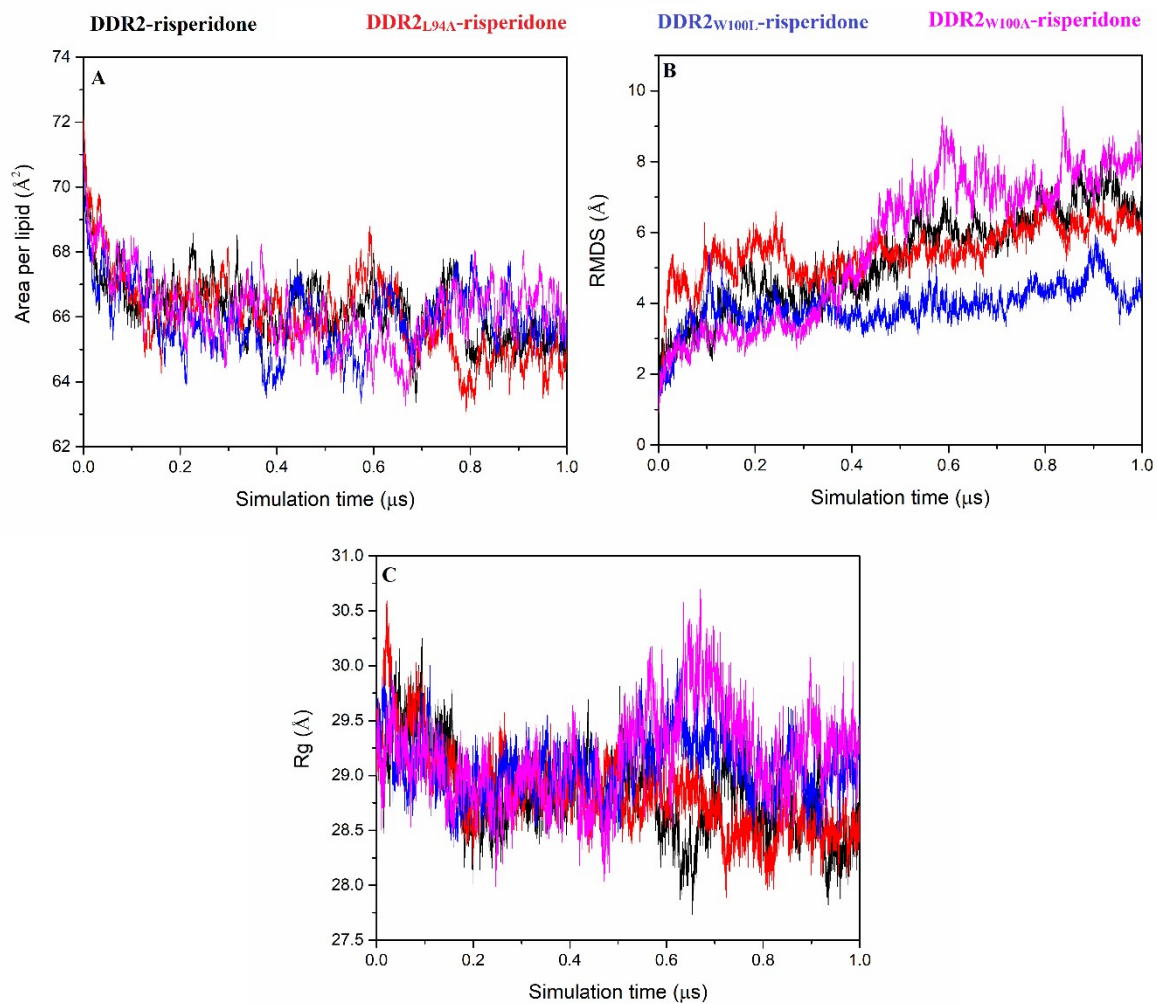
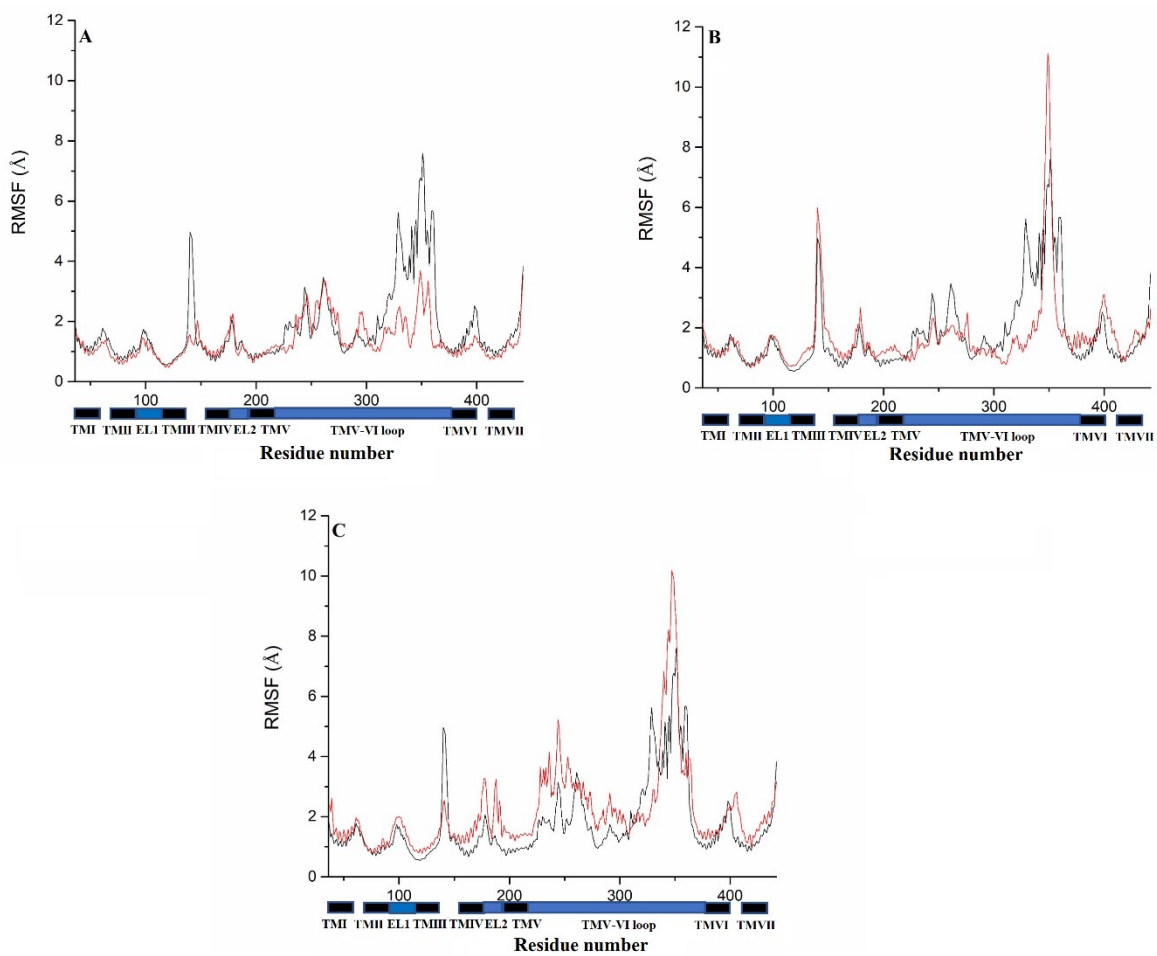


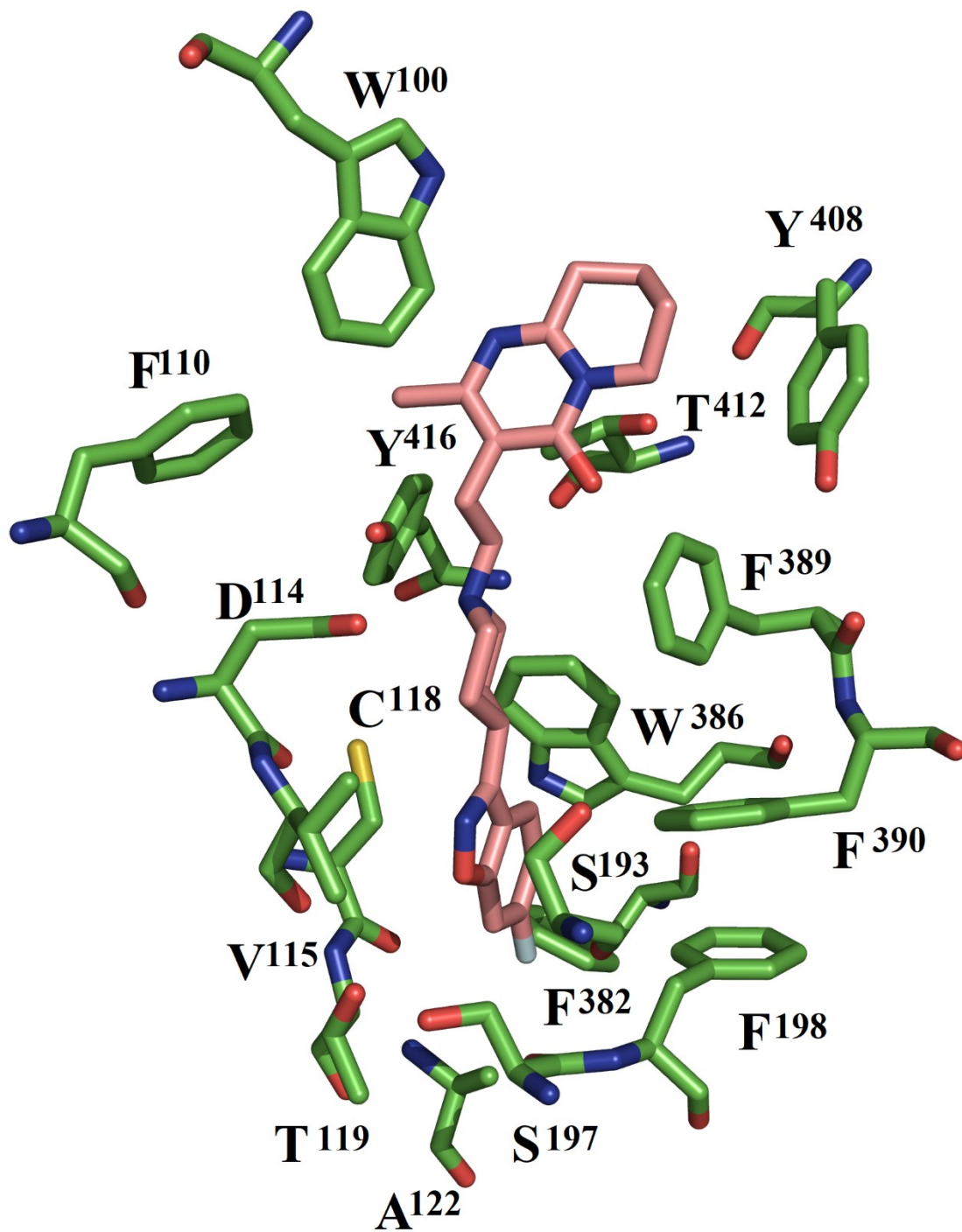
## SUPPLEMENTARY MATERIAL



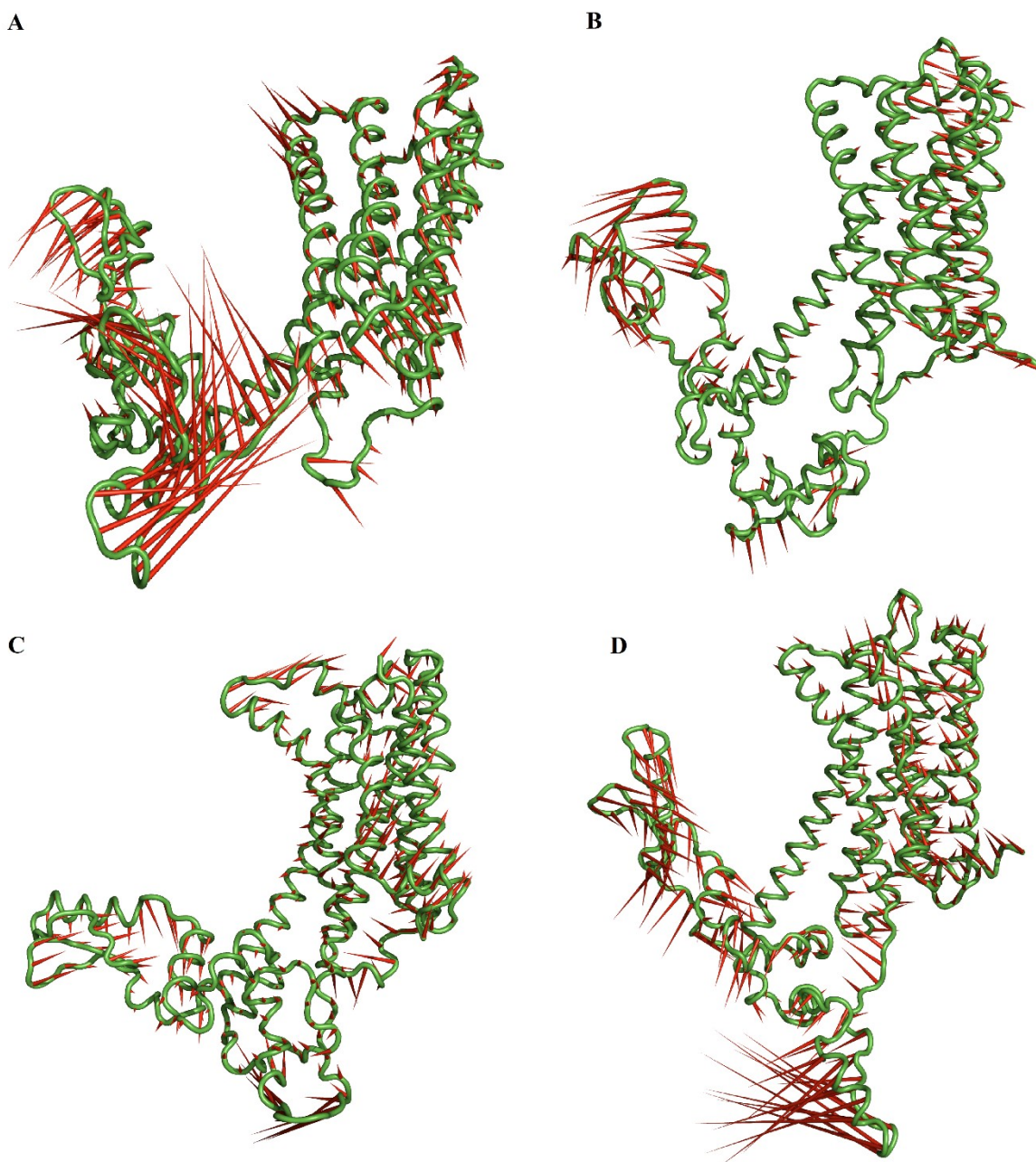
**Fig. S1.** Area per lipid, RMSD and radius of gyration (Rg) values of wild-type and mutant DDR2-risperidone systems. Area per lipid (A), RMSD (B), and Rg (C) values of DDR2<sub>WT</sub>-risperidone (black line), DDR2<sub>L94A</sub>-risperidone (red line), DDR2<sub>W100L</sub>-risperidone (blue line) and DDR2<sub>W100A</sub>-risperidone (magenta line).



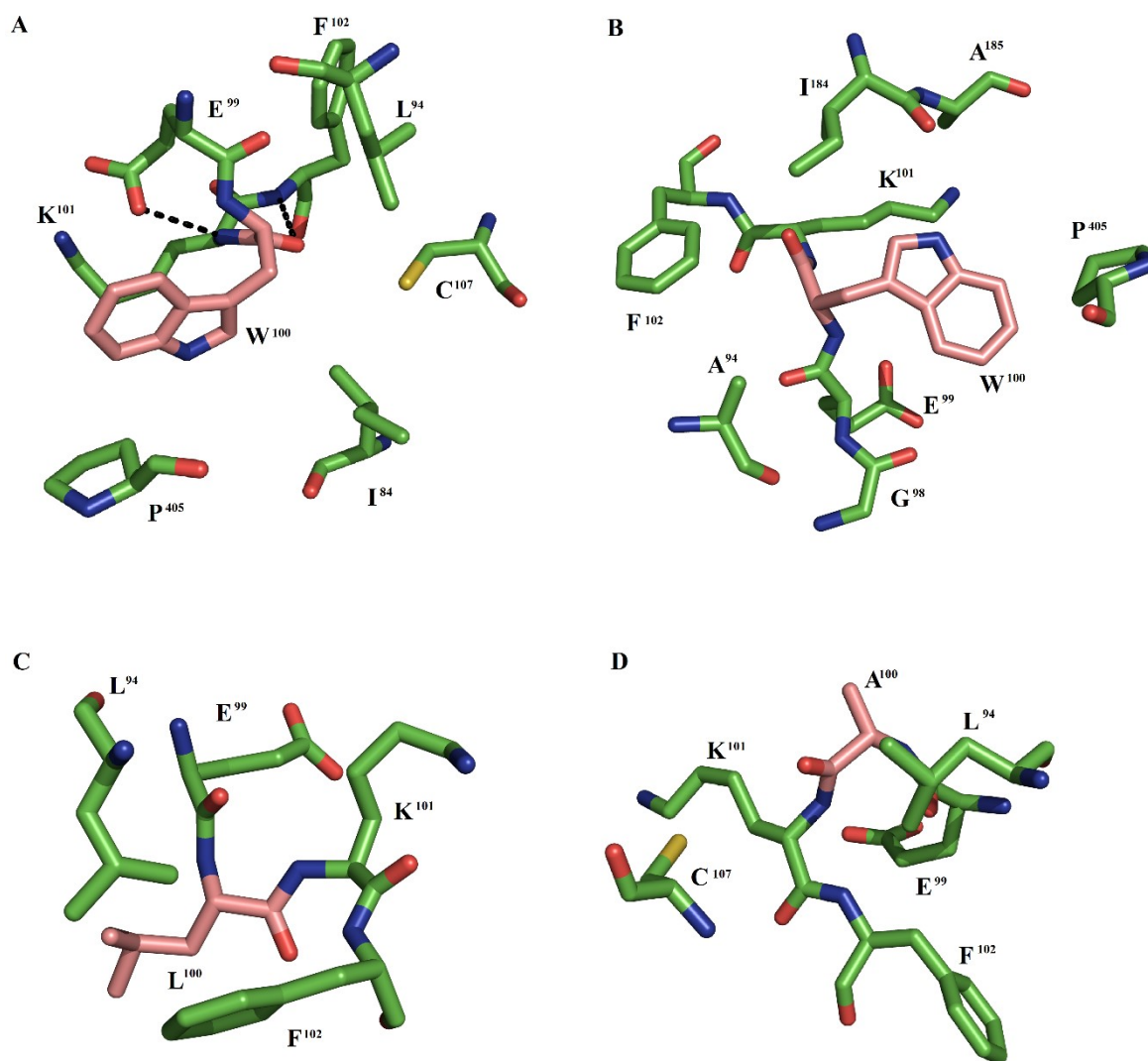
**Fig. S2.** RMSF analysis of wild-type and mutant DDR2-risperidone systems. A) RMSF values of the DDR2<sub>WT</sub>-risperidone (black line) and DDR2<sub>L94A</sub>-risperidone (red line) systems. B) RMSF values of the DDR2<sub>WT</sub>-risperidone (black line) and DDR2<sub>W100L</sub>-risperidone (red line) systems. C) RMSF values of the DDR2<sub>WT</sub>-risperidone (black line) and DDR2<sub>W100A</sub>-risperidone (red line) systems.



**Fig. S3.** Protein–ligand interactions of the cocrystallized ligand (risperidone) in DDR2 (PDB entry 6CM4, chain A).



**Fig. S4.** Graphic depiction of the projection on wild-type and mutant DRD2-ligand systems. Depiction of the two extreme projections along PC1 vs. PC2 for DDR2<sub>WT</sub>-risperidone (A), DDR2<sub>L94A</sub>-risperidone (B), DDR2<sub>W100L</sub>-risperidone (C) and DDR2<sub>W100A</sub>-risperidone (D). Porcupine drawings indicate the magnitude and direction of movements.



**Fig. S5.** Interactions around 4 Å of residue at 100 positions of wild type and mutant DDR2-risperidone systems. DDR2<sub>WT</sub>-risperidone (A), DDR2<sub>L94A</sub>-risperidone (B), DDR2<sub>W100L</sub>-risperidone (C) and DDR2<sub>W100A</sub>-risperidone (D). Residue at 100 position and residues around 4 Å of it are in salmon and green stick representations.