

Supplementary information, Fig. S5

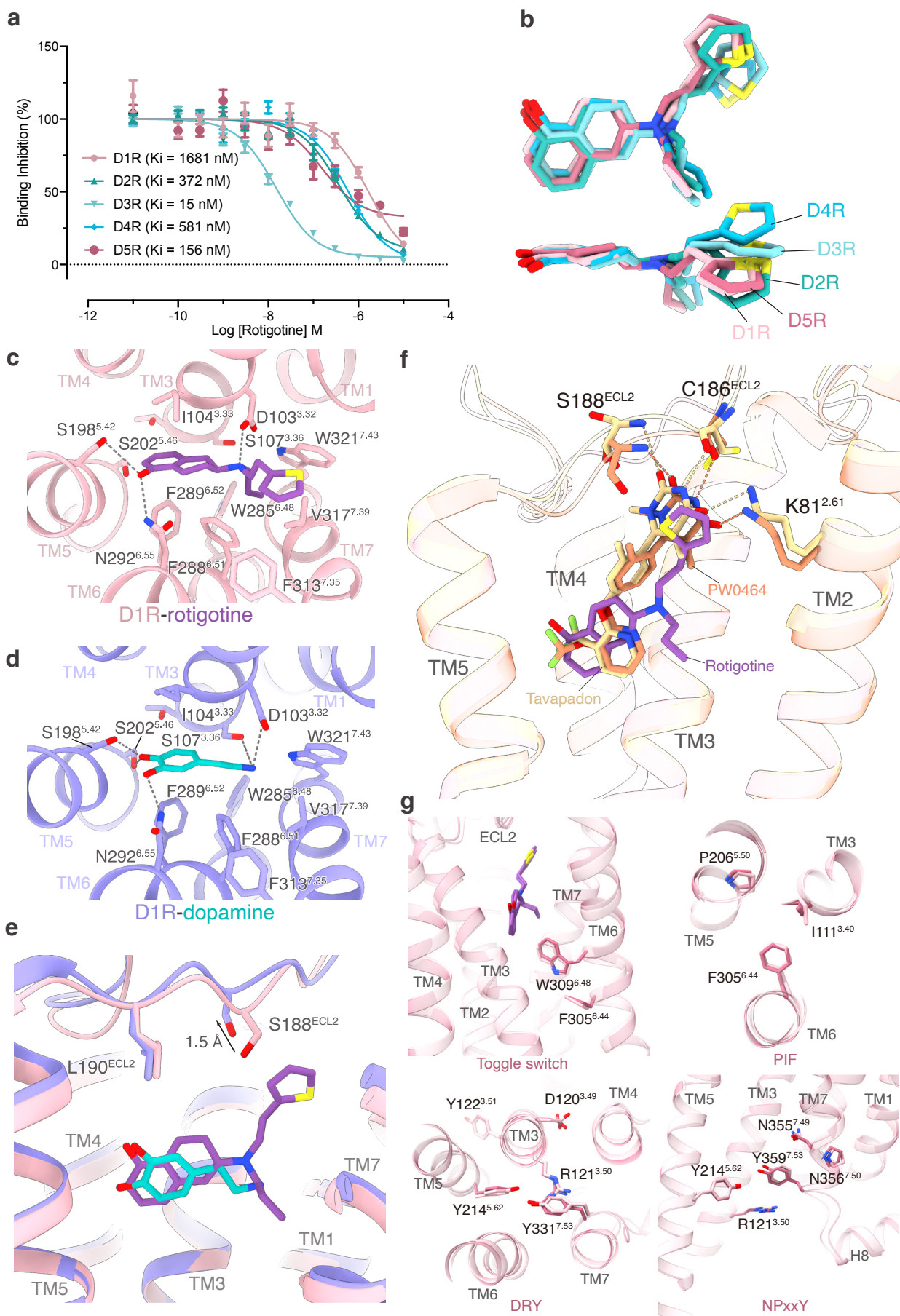


Fig. S5. Comparison of rotigotine conformation from five dopamine receptor, comparison of the binding modes of rotigotine with dopamine, tavapadon, and PW0464, and the comparison of the activation related residues between D1R and D5R. a Rotigotine competition binding curve to WT Dopamine Receptors. Graphical representation of rotigotine competition curves for wild-type receptors. Dose response curves were analyzed using “One site – Fit LogIC50” function in Graphpad Prism 8.4 software (Graphpad Software Inc., San Diego, CA). All data are presented as mean values \pm standard error of measurement (SEM) with a minimum of four technical replicates and N = 3 biological replicates. **b** Superposition of rotigotine structure from the five dopamine receptors. **c** The binding mode of rotigotine in D1R. **d** The binding mode of dopamine in D1R (PDB code: 7LJD). **e** Structural comparison of rotigotine and dopamine in D1R. **f** Structural comparison of the binding modes of rotigotine with tavapadon (PDB code: 7X2D), and PW0464 (PDB code: 7CKY) in D1R. **g** Superposition of the activation related residues of D1R and D5R.