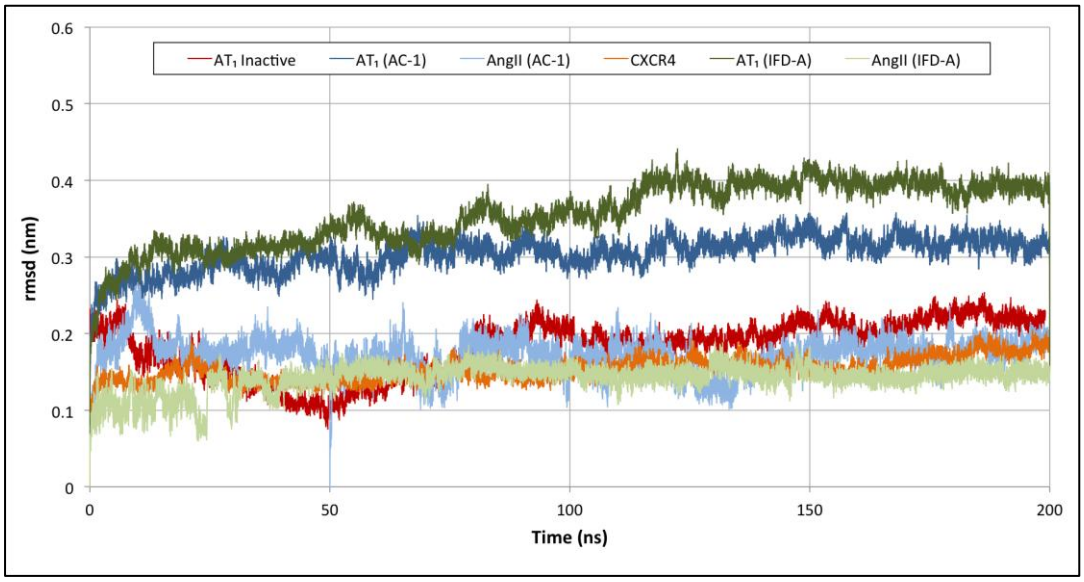

Figure S3. Root mean square deviations (rmsd) on AT_1 receptor backbone atoms (dark blue, dark green and red for AC1, IFD-A and the inactive state MD respectively) and on AngII backbone atoms (light blue and light green for AC1 and IFD-A complexes respectively), throughout the MD simulations. CXCR4 backbone atom rmsd, which was used as a control simulation, is shown in orange.