**Figure S4. Boundaries of docking boxes.** The boundaries of the region explored for docking are highlighted for each studied receptor subtype. The docking grid was built using an inner box (ligand diameter midpoint box, boundaries shown in green) of 10 Å x 10 Å x 10 Å and an outer box (box within which all the ligand atoms must be contained, boundaries shown in purple) that extended 20 Å in each direction from the inner one. The highly conserved Asp 3.32 is shown in spheres in each receptor, as reference point. (A) $\alpha_{2B}$ model (B) $\alpha_{2C}$ model (C) 5HT$_{2B}$ crystal (D) 5HT$_{2C}$ model (E) 5HT$_7$ model and (F) $\beta_3$ model.