



Supplementary information, Fig. S4| The structures of active and inactive human β_1 AR are similar to those of the human β_2 AR.

a, The overall structure of the T4L- β_1 AR bound with carazolol. b, The overall structures of the T4L- β_1 AR bound with BI-167107 (cyan), norepinephrine (yellow) and epinephrine (magenta). The receptors are stabilized in active conformation by Nb6B9. c, Comparison of the PIF motif of the inactive state β_1 AR (carazolol bound, green) and β_2 AR (carazolol bound, orange. PDB code: 2RH1). d, Comparison of the PIF motif of the active state β_1 AR (BI-167107 bound, cyan) and β_2 AR (BI-167107 bound, pink. PDB code: 4LDE). e, Comparison of the positions of Y^{5.58} and Y^{7.53} of the inactive state β_1 AR (carazolol bound, green) and β_2 AR (carazolol bound, orange. PDB code: 2RH1). f, Y^{5.58} and Y^{7.53} form a water-mediated hydrogen bond in the active state β_1 AR (BI-167107 bound, cyan) and β_2 AR (BI-167107 bound, pink. PDB code: 4LDE). g, The norepinephrine binding pocket in the simulated β_2 AR-norepinephrine complex structure. h, The norepinephrine binding pocket in the β_1 AR-norepinephrine crystal structure.