



Figure 1-figure supplement 3. Cryo-EM structure of SSTR2 complex

(A) The cryo-EM maps of SSTR2 complex at the ligand binding pocket (i), the interface between SSTR2 and G-proteins (ii) and the G-protein (Gβ1) (iii).

(B) The atomic models of the seven transmembrane helices (TM1: 43–69 a.a., TM2: 77–105 a.a., TM3: 111–145 a.a., TM4: 156–180 a.a., TM5: 203–237 a.a., TM6: 245–281 a.a., and TM7: 288–315 a.a.) are superimposed on the cryo-EM map.