



Figure 1-figure supplement 2. Cryo-EM processing.

(A) The collected data was processed using Relion 3.1. Through 2D and 3D classification, final 320,885 particles were selected for reconstruction. After sharpening, the resolution of SSTR2 complex was determined at 3.72 Å. **(B)** FSC curves of Body 1 and Body 2 as well as complete complex of SSTR2 were obtained. SSTR2 of Body1 showed better resolution than SSTR2 of complete complex, and G-proteins of Body2 showed better resolution than G-proteins of complete complex. **(C)** Euler angle distribution of the particles for the 3D reconstruction.