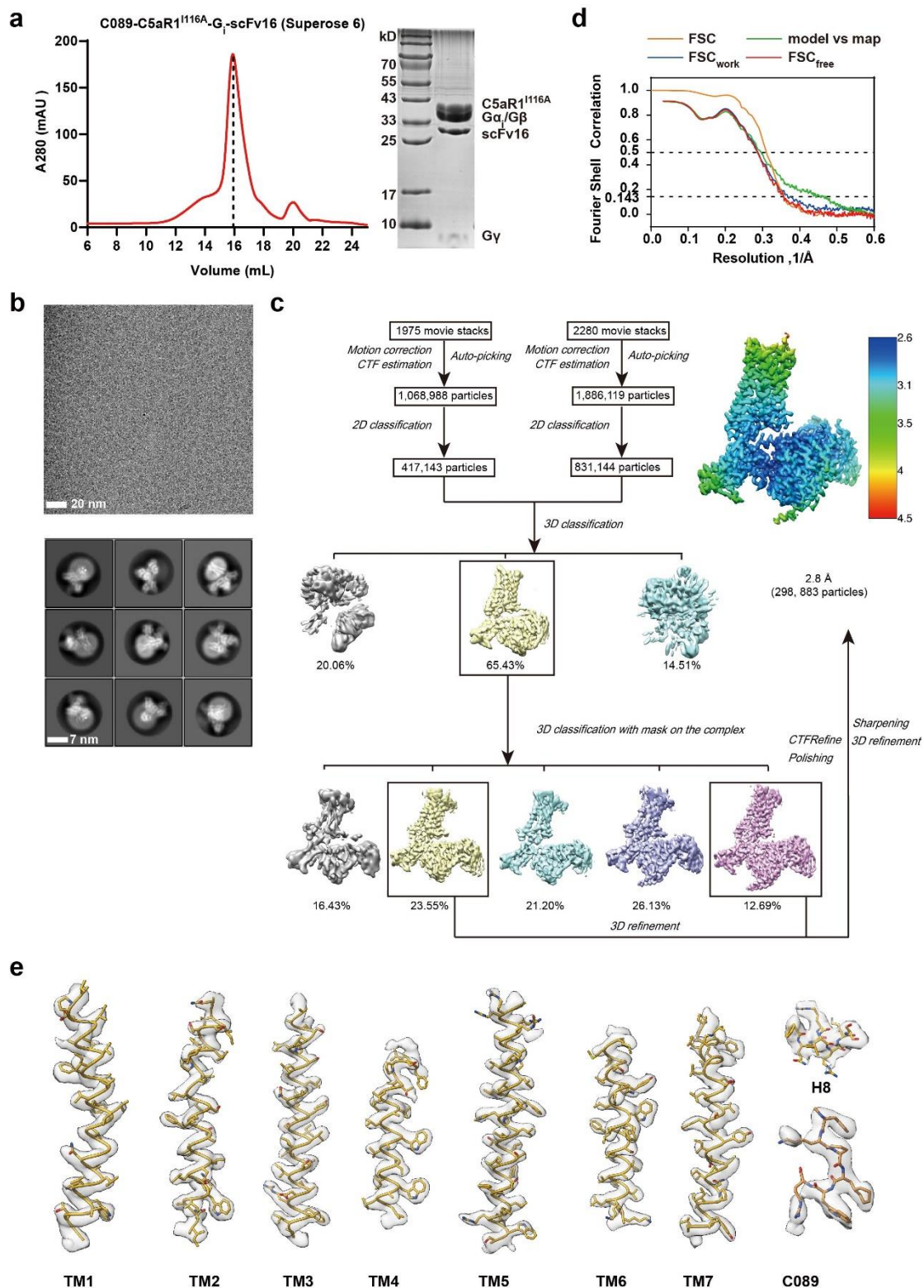


## Supplementary information, Fig. S13



**Fig. S13. Single-particle reconstruction of C089-C5aR1<sup>I116A</sup>-G<sub>i</sub> complex.**

**a**, Representative elution profile of the purified C089-C5aR1<sup>I116A</sup>-G<sub>i</sub> complex (left panel) and SDS-PAGE of the size-exclusion chromatography peak (right panel).

- b**, Representative cryo-EM micrographs (upper panel) and 2D classification averages (lower panel) of the C089-C5aR1<sup>I116A</sup>-G<sub>i</sub> complex.
- c**, Cryo-EM data processing flowcharts and local resolution for the C089-C5aR1<sup>I116A</sup>-G<sub>i</sub> complex.
- d**, Gold-standard FSC curve (orange), the model-vs-map curve (green), FSC<sub>work</sub> (blue) and FSC<sub>free</sub> (red) validation curve of C089-C5aR1<sup>I116A</sup>-G<sub>i</sub> complex. The marginal gap between the FSC<sub>work</sub> and FSC<sub>free</sub> validation curve indicate no over-fitting of the model.
- e**, Cryo-EM density maps and models for transmembrane helices TM1-TM7 and H8 of C5aR1, as well as the ligand C089.