Supplementary information, Fig. S2

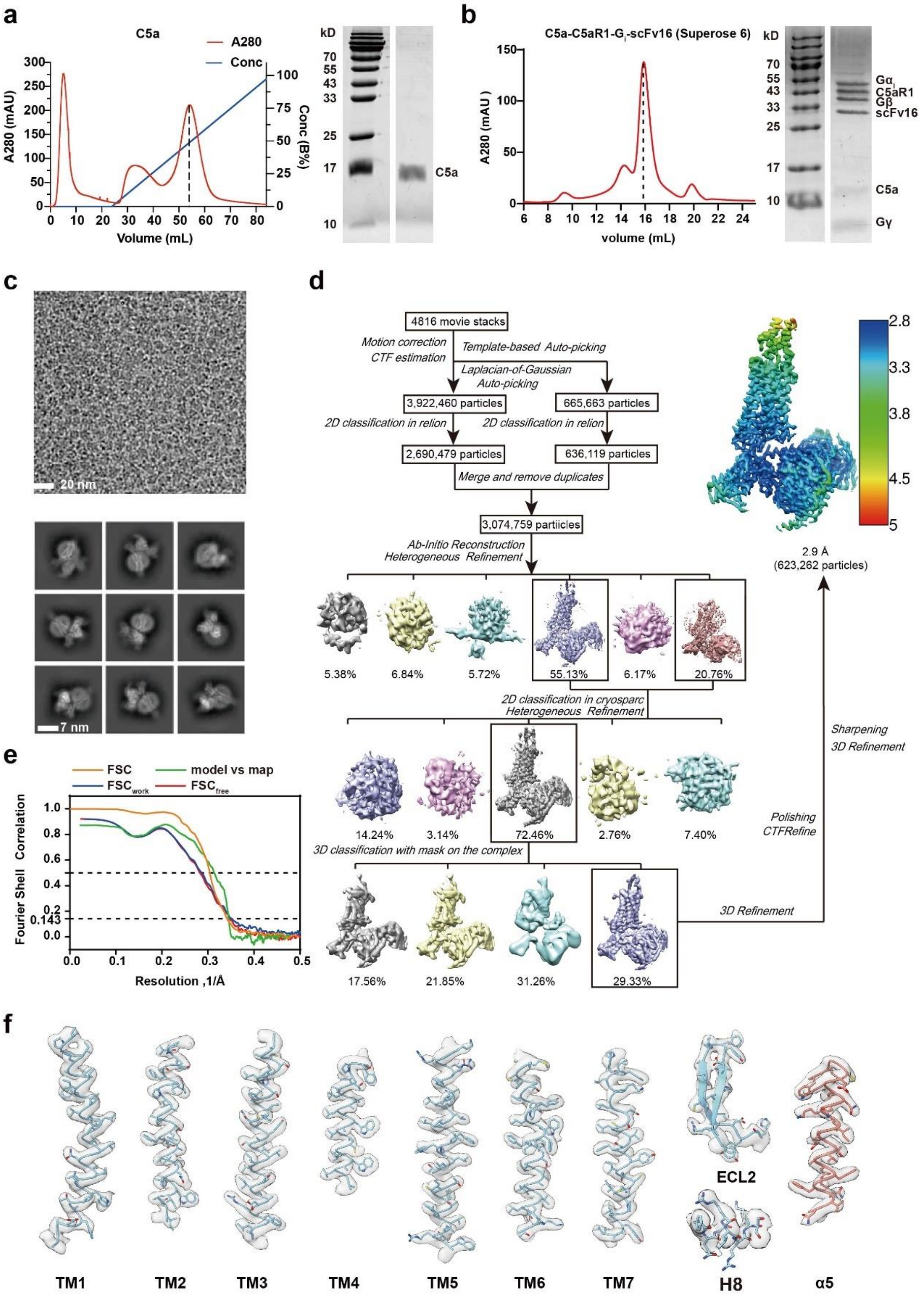

Fig. S2. Single-particle reconstruction of C5a-C5aR1-G$_i$ complex.

a, Representative elution profile of the purified C5a (left panel) and SDS–PAGE of the ion-exchange column chromatography peak (right panel).

b, Representative elution profile of the purified C5a-C5aR1-G_i complex (left panel) and SDS–PAGE of the size-exclusion chromatography peak (right panel).

c, Representative cryo-EM micrographs (upper panel) and 2D classification averages (lower panel) of the C5a-C5aR1-G_i complex.

d, Cryo-EM data processing flowcharts and local resolution for the C5a-C5aR1-G_i complex.

e, Gold-standard Fourier shell correlation (FSC) curve (orange), the model-vs-map curve (green), FSC_{work} (blue) and FSC_{free} (red) validation curve of C5a-C5aR1-G_i complex. The marginal gap between the FSC_{work} and FSC_{free} validation curve indicate no over-fitting of the model.

f, Cryo-EM density maps and models for transmembrane helixes TM1-TM7, ECL2 and H8 of C5a-bound C5aR1, as well as the α5 helix of $G\alpha_{i1}$.