

Supplementary information, Fig. S3

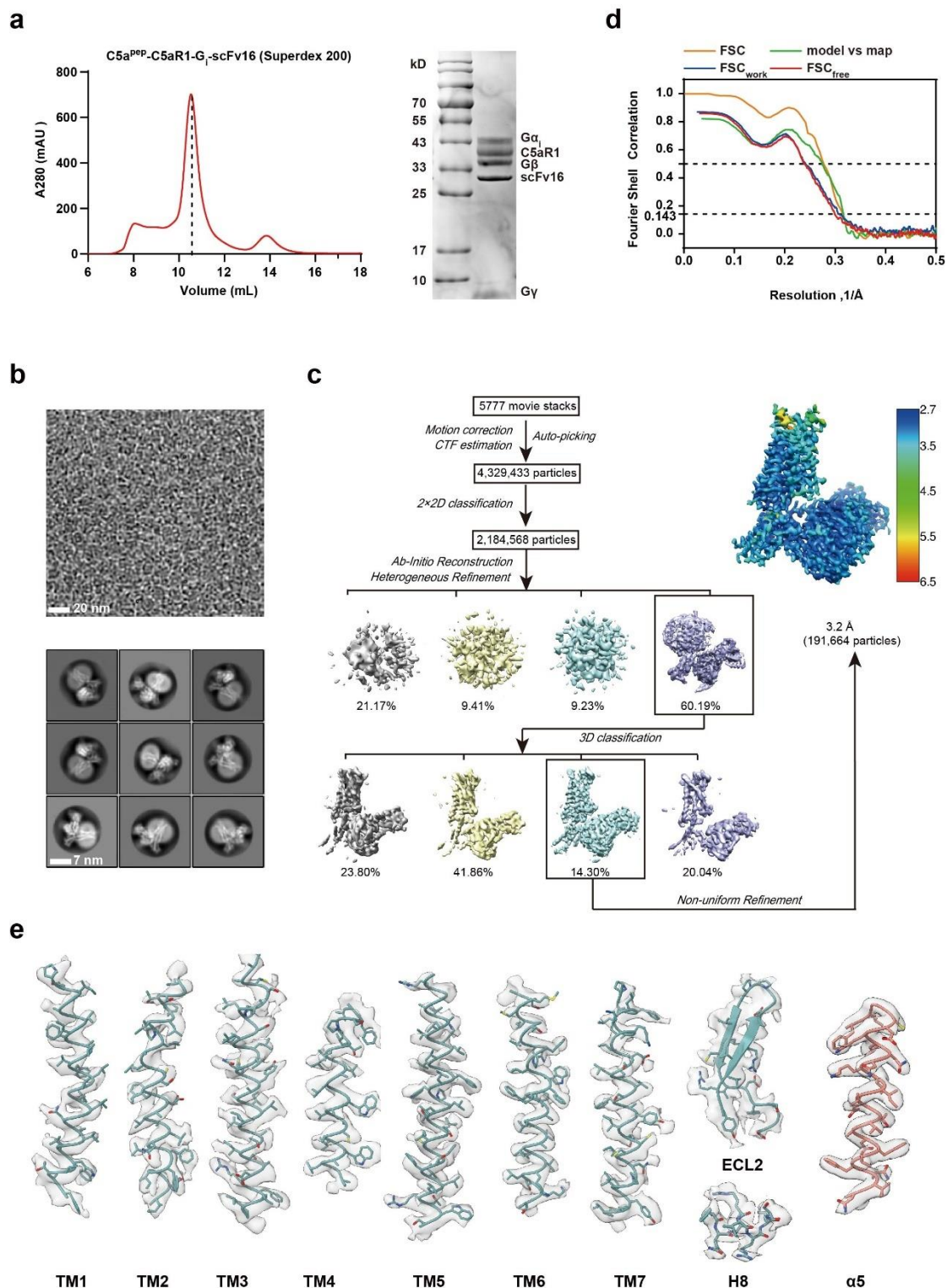


Fig. S3. Single-particle reconstruction of C5a^{pep}-C5aR1-G_i complex.

a, Representative elution profile of the purified C5a^{pep}-C5aR1-G_i 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 C5a^{pep}-C5aR1-G_i complex.

c, Cryo-EM data processing flowcharts and local resolution for the C5a^{pep}-C5aR1-G_i complex.

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

e, Cryo-EM density maps and models for transmembrane helixes TM1-TM7, ECL2 and H8 of C5a^{pep}-bound C5aR1, as well as the $\alpha 5$ helix of G α_{i1} .