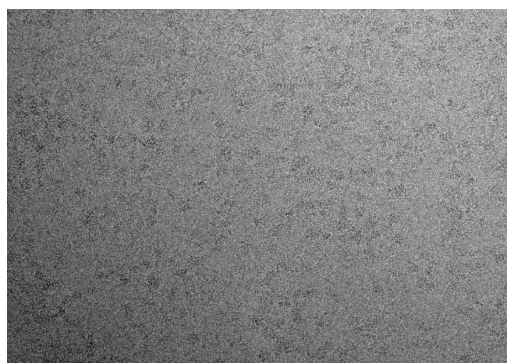


Supplementary information, Fig. S7

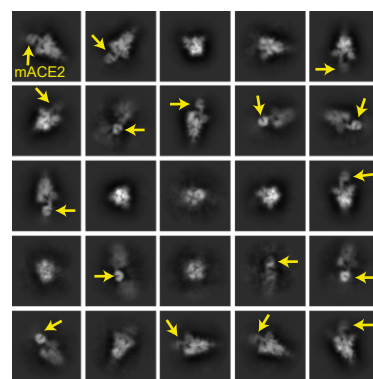
a

50 nm

b

Micrographs (6,545 movies)
Motion correction (MOTIONCOR2)
CTF estimation (CTFFIND4)
Autopick (2,260,477 particles)
2D classification (1,675,669 particles)

Hetero Refinement

c

Class 1 (483,670 particles)

Class 2 (1,191,999 particles)

Class 1
(327,560 particles)Class 2
(158,137 particles)Class 3
(187,713 particles)Class 4
(263,623 particles)Class 5
(232,817 particles)Class 6
(22,149 particles)

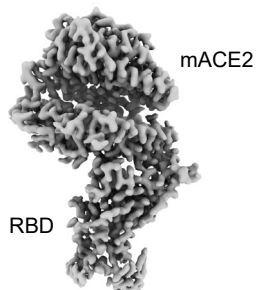
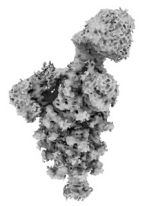
Remove duplicates (284,790 particles excluded)

Refinement (3.17 Å)

Mask on RBD-ACE2

Local refinement (2.60 Å)

Hetero Refinement

Class 4
(106,287 particles)Class 1
(136,170 particles)Class 2
(91,579 particles)Class 3
(123,465 particles)

Refinement (3.13 Å)

Refinement (3.24 Å)

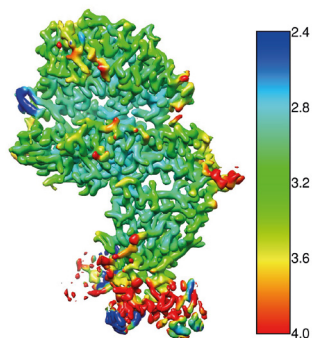
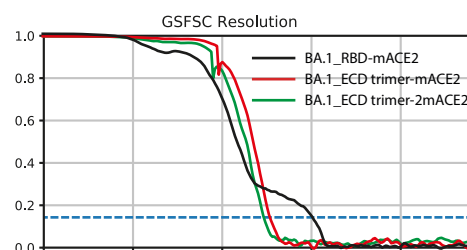
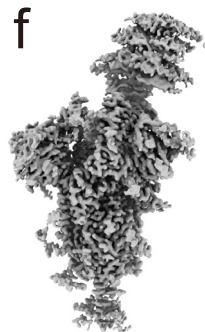
d**e****f****g**

Fig. S7 Cryo-EM data processing of the Omicron BA.1 spike protein-mACE2 complex.

(a) A representative cryo-EM micrograph of Omicron BA.1 ECD-mACE2 complex with 50 nm scale bar included as a size reference. (b) Computational processing of cryo-EM data. (c) Twenty representative reference-free two-dimensional (2D) cryo-EM class averages reveal the mACE2 density (yellow arrow). (d) Local resolution of sub-reconstructions of RBD-mACE2 (left panel) and resolution bar is shown in the right panel. (e) The FSC curves for the reconstructions. Color scheme: BA.1 RBD-mACE2, black; BA.1 ECD trimer-mACE2, red; BA.1 ECD-trimer-2mACE2, green. The resolution of the reconstructions using the Fourier shell cutoff at 0.143 is shown. (f-g) The EM maps of Omicron BA.1 ECD trimer bound to 1 mACE2 (f), 2 mACE2 (g).