

Figures

Figure 1. Overview of single-particle cryo-EM for GluA2- γ 2 in complex with glutamate and cyclothiazide. **a**, Representative micrograph. **b**, Reference-free 2D class averages illustrating different particle orientations. **c**, Cryo-EM map for consensus refinement of full-length complex. **d**, Reference-free 2D class averages after subtraction of signal for ATD layer. **e**, Improved cryo-EM map for LBD-TMD region after subtraction of signal for ATD layer.

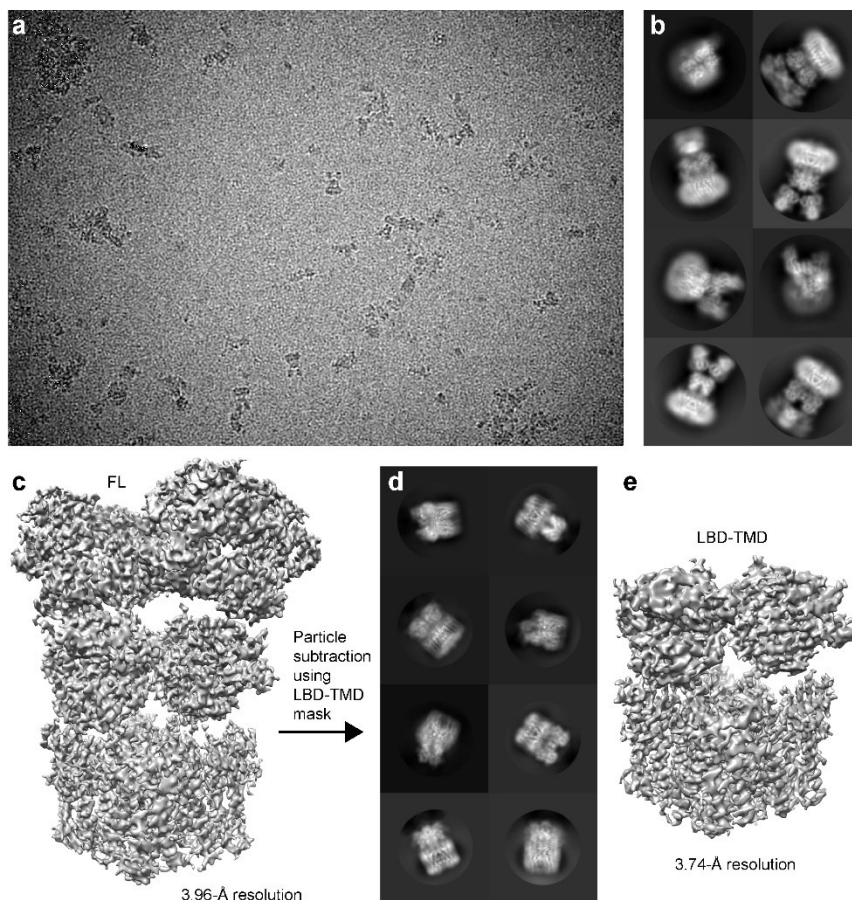


Figure 2. Overview of single-particle cryo-EM for GluA2- γ 5. **a**, Representative micrograph with example particles circled in red. **b**, Reference-free 2D class averages illustrating different particle orientations. **c**, Distribution of particle Euler angle orientations contributing to the final reconstruction, with larger red cylinders representing orientations comprising more particles. **d-g**, Local resolution presented as coloring of the cryo-EM map (**d** and **f**) and FSC curves (**e** and **g**) for the full-length (**d** and **e**) and LBD-TMD-focused (**f** and **g**) reconstructions of GluA2- γ 5_{ZK}.

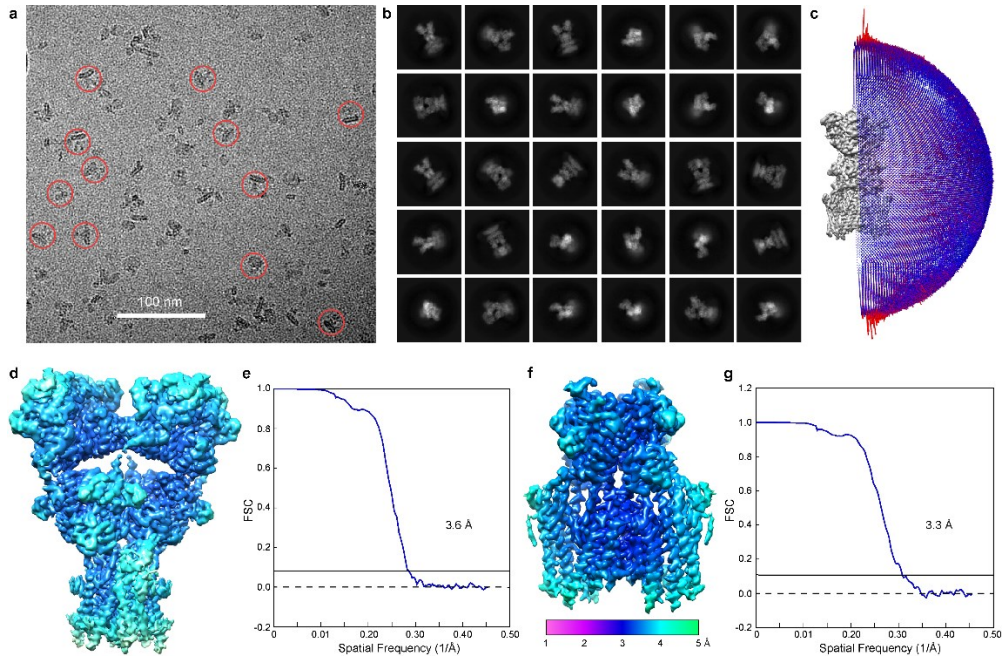


Figure 3. Overview of single-particle cryo-EM for GLR3.4. **a**, Example cryo-EM micrograph for GLR3.4 with example particles circled in red. **b**, Reference-free 2D class averages of GLR3.4 illustrating different particle orientations. **c**, Distribution of particle Euler angle orientations contributing to the final reconstruction, with larger red cylinders representing orientations comprising more particles. **d**, Local resolution mapped on the GLR3.4 density viewed parallel to the membrane either in its entirety (left) or coronally halved (right). **e**, Fourier shell correlation (FSC) curves from refinement.

