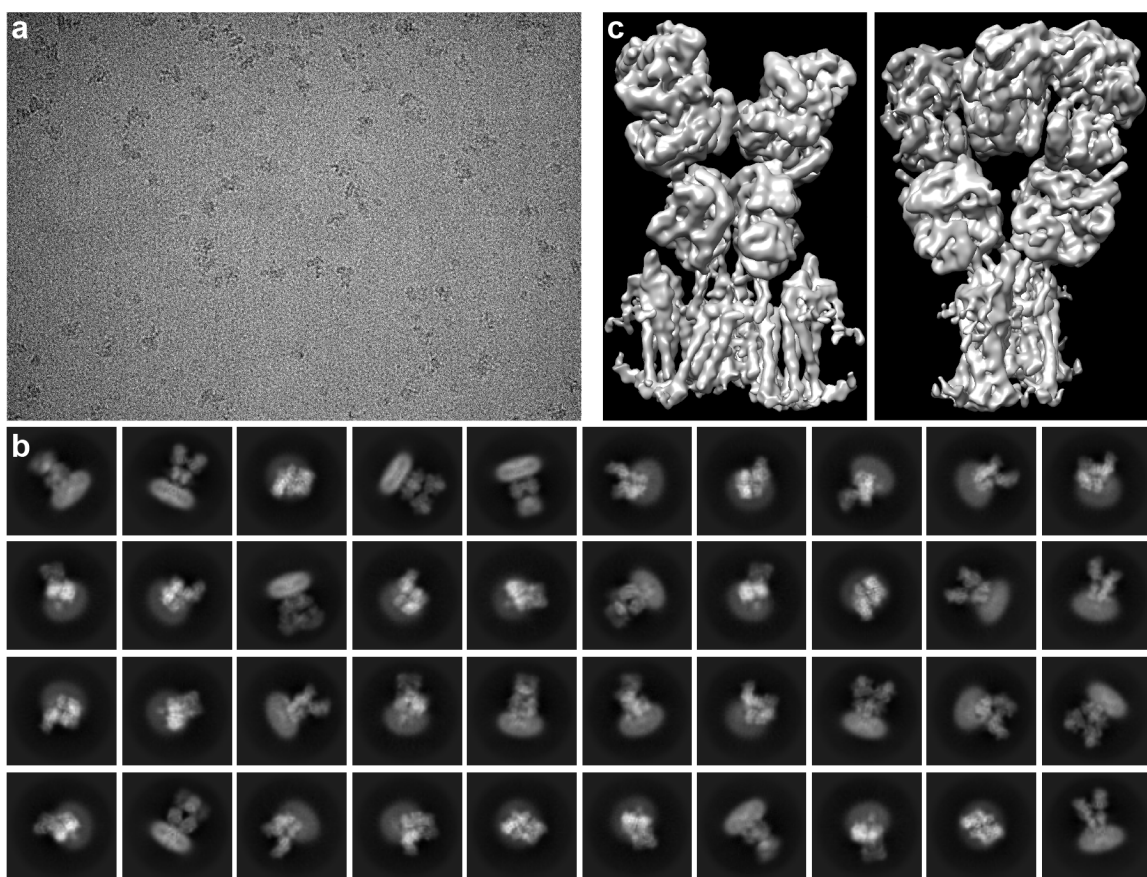
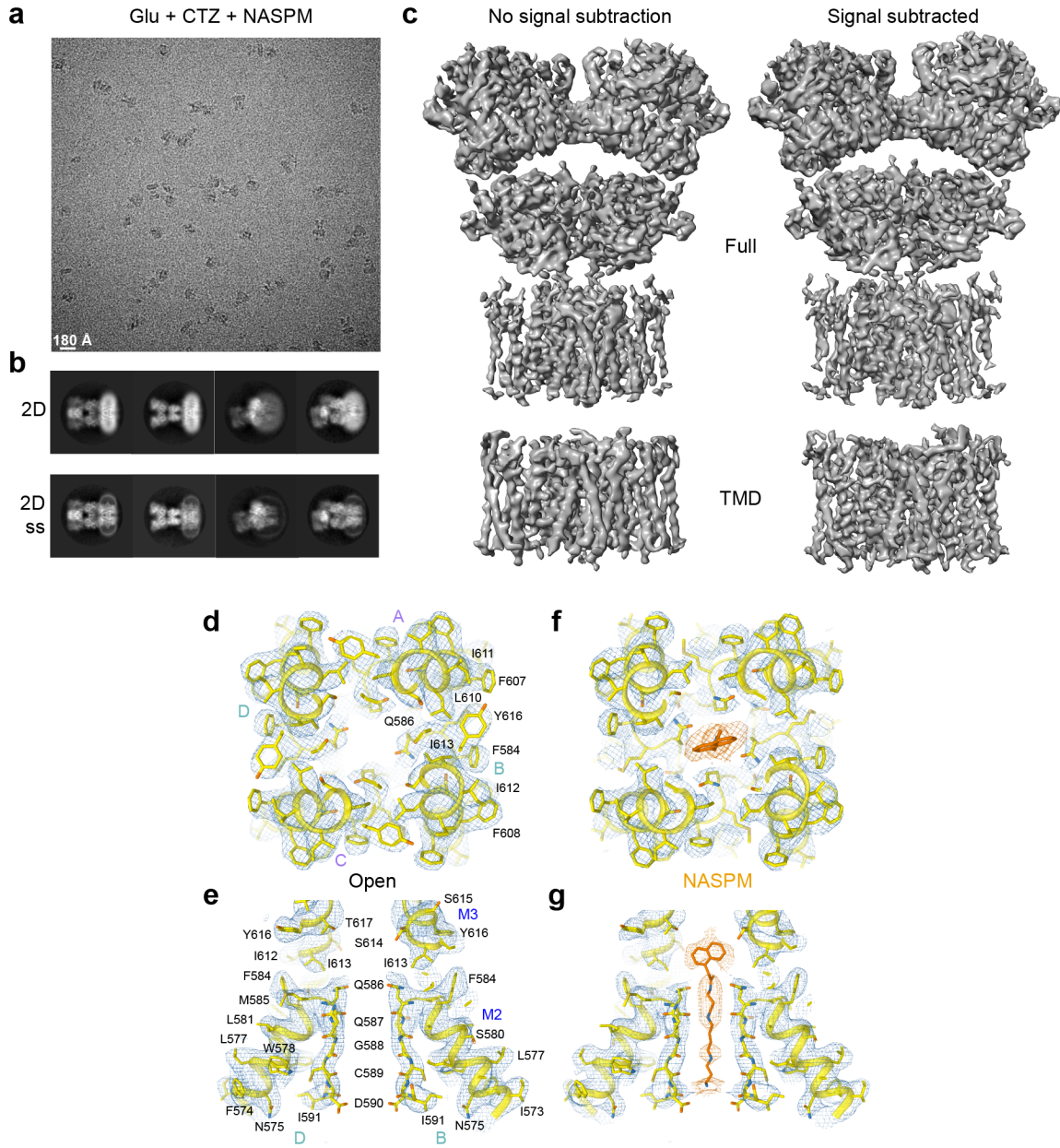


**Figure 1. Cryo-EM for GluA2-STZ in the partially activated state.** a, Example of cryo-EM micrograph. b, 2D class averages. c, 3D reconstruction of one of partially activated states at 3.99 Å resolution.



**Figure 2. Cryo-EM for GluA2-GSG1L in the desensitized state.** a, Example of cryo-EM micrograph. b, 2D class averages. c, 3D reconstruction at 4.2 Å resolution.



**Figure 3. Cryo-EM for GluA2-STZ complex bound to NASPM blocker.** **a**, Example of cryo-EM micrograph. **b**, 2D and 2D-ss (after micelle signal subtraction) class averages. **c**, 3D reconstructions for full-length structure refinement (first row) and TMD-directed refinement (second row) before (left) and after (right) micelle signal subtraction. **d-g**, Cryo-EM densities after micelle signal subtraction and focused TMD refinement for GluA2<sub>Q</sub>-STZ<sub>open</sub> (**d-e**) and GluA2<sub>Q</sub>-STZ<sub>NASPM</sub> (**f-g**) viewed extracellularly (top row; **d,f**) and parallel to the membrane, with the extracellular side up (bottom row; **e,g**). Only two of four GluA2 subunits are shown in **e** and **g**, with the front and back subunits removed for clarity. Protein density is shown as a blue mesh. The blocker NASPM and the corresponding density for it are colored orange.