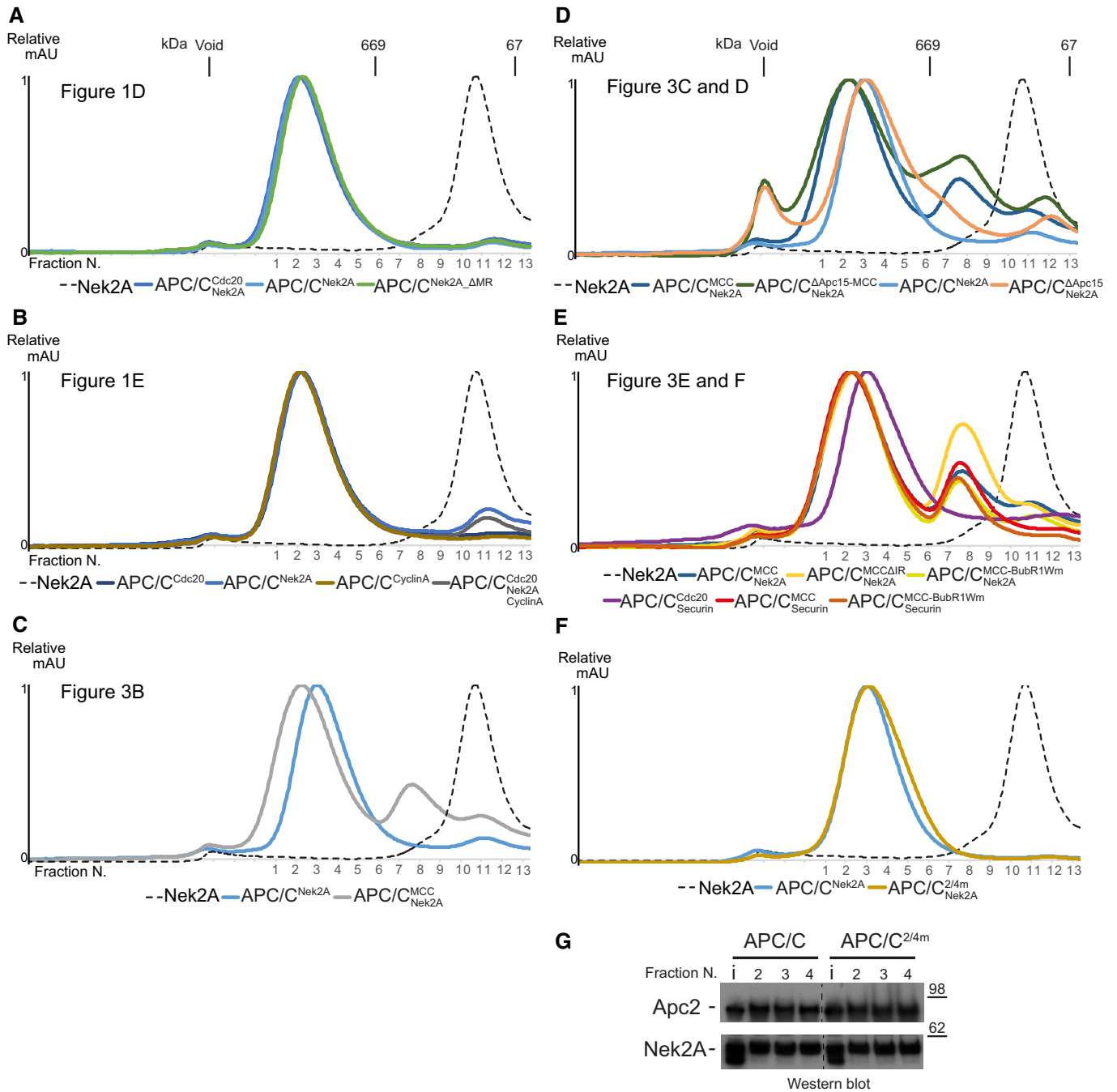


## Expanded View Figures



**Figure EV1. Binding studies defining the binding mode of Nek2A to the APC/C and APC/C<sup>MCC</sup> complexes.**

A–E Size-exclusion chromatograms of APC/C complexes in this study. The corresponding peak fractions SDS–PAGE gels are shown in the main figures. F, G Size-exclusion chromatography chromatograms (F) and SDS–PAGE gels (G) of either APC/C wild-type or 2/4 m complexes with Nek2A.

Source data are available online for this figure.

**Figure EV2. APC/C–Nek2A complex sample preparation and cryo-EM analysis.**

- A SDS–PAGE gels (stained with Coomassie blue) of the gel filtration peak fraction from the APC/C–Nek2A complex preparation used in this study. Western blot against Nek2A confirms the presence of the Nek2A 301–406 construct.
- B A typical cryo-EM micrograph of APC/C–Nek2A representative of 6,448 micrographs. Scale bar: 500 Å.
- C Gallery of two-dimensional class averages of APC/C<sup>Nek2A</sup> showing different views representative of 50 two-dimensional classes. Scale bar: 150 Å.
- D Fourier shell correlation (FSC) curves are shown for all the cryo-EM reconstructions of APC/C<sup>Nek2A</sup> determined in this study.
- E Fourier shell correlation (FSC) curves are shown for all the cryo-EM reconstructions of APC/C<sup>MCC</sup> determined in this study using cryo-EM data as published [14].

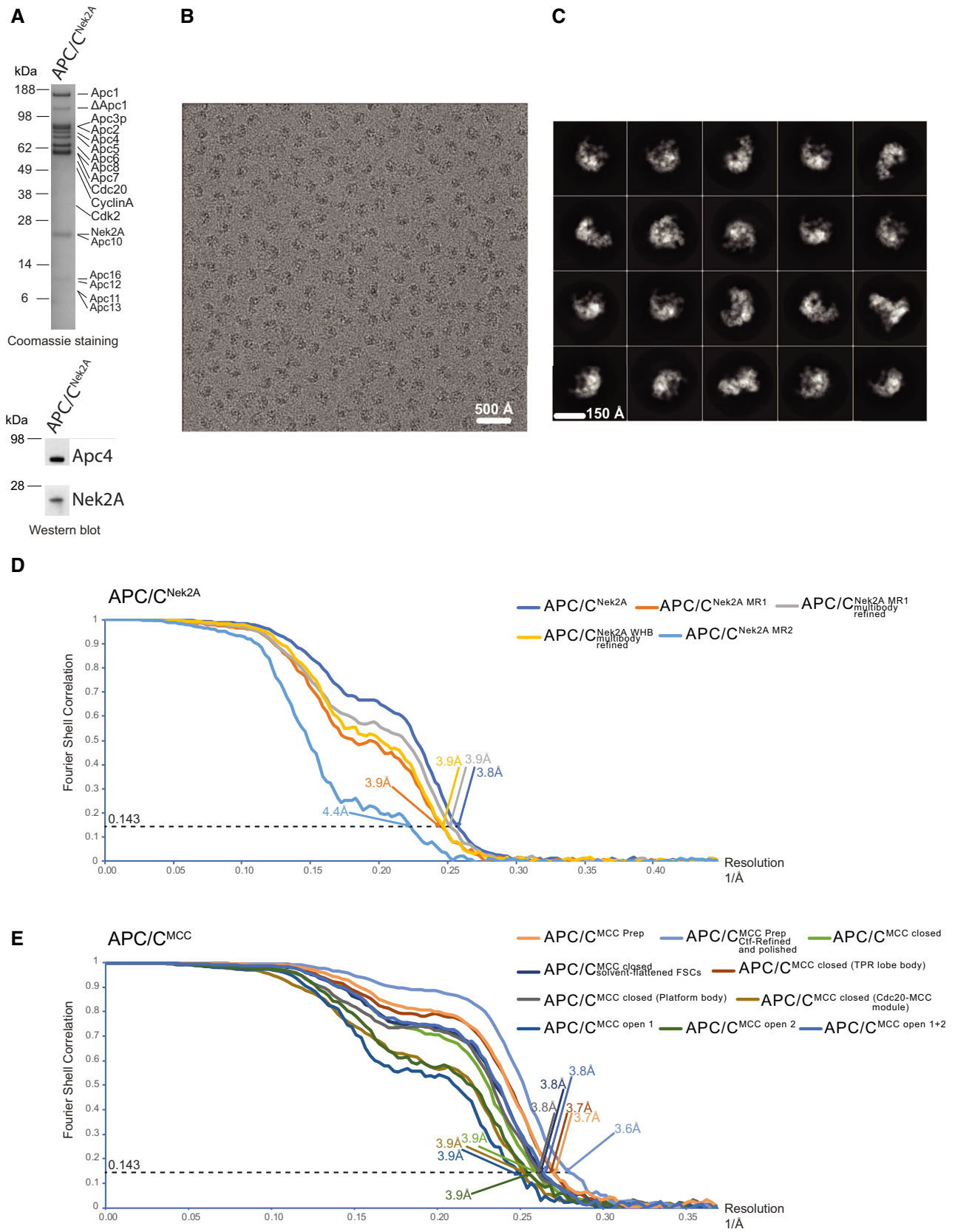
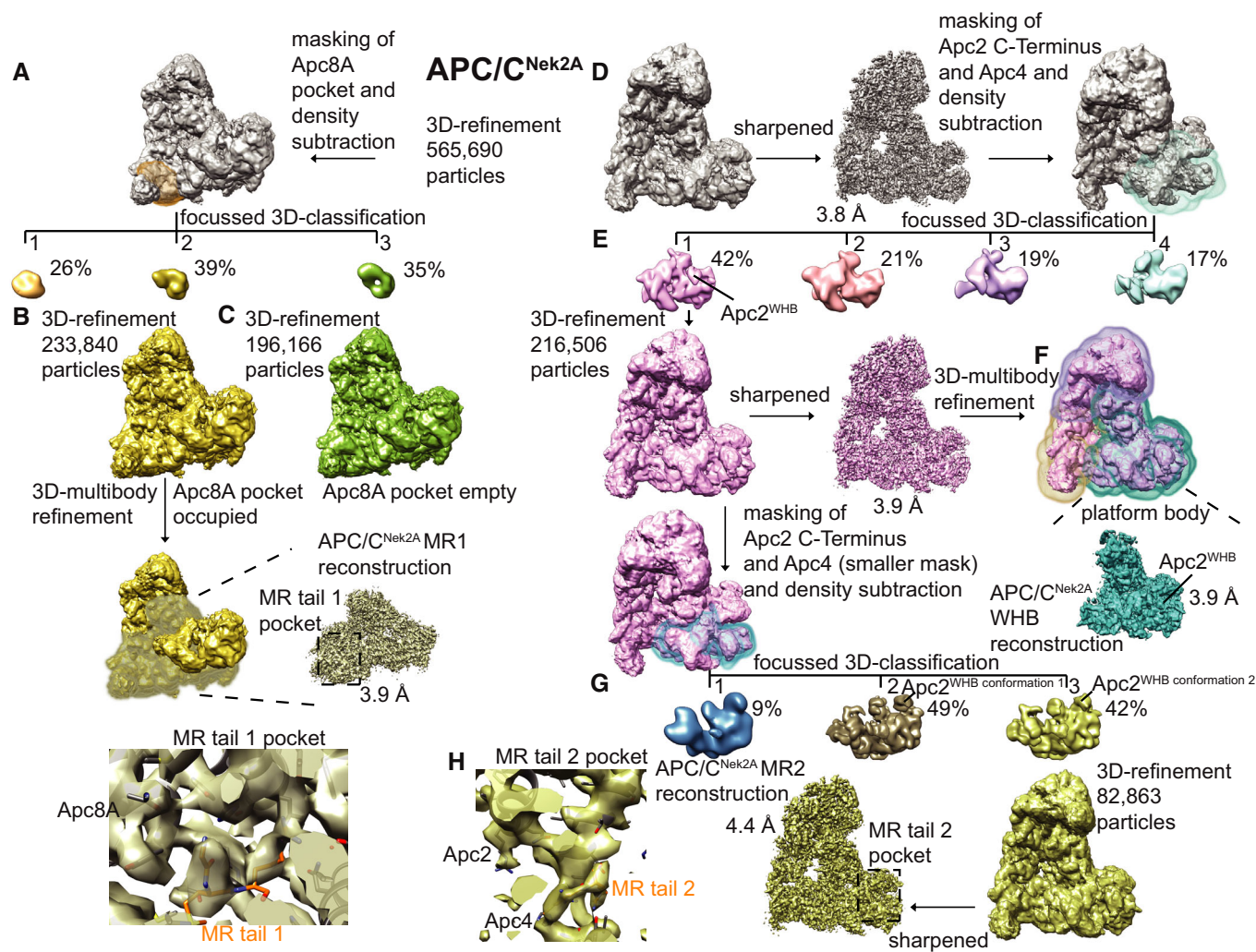
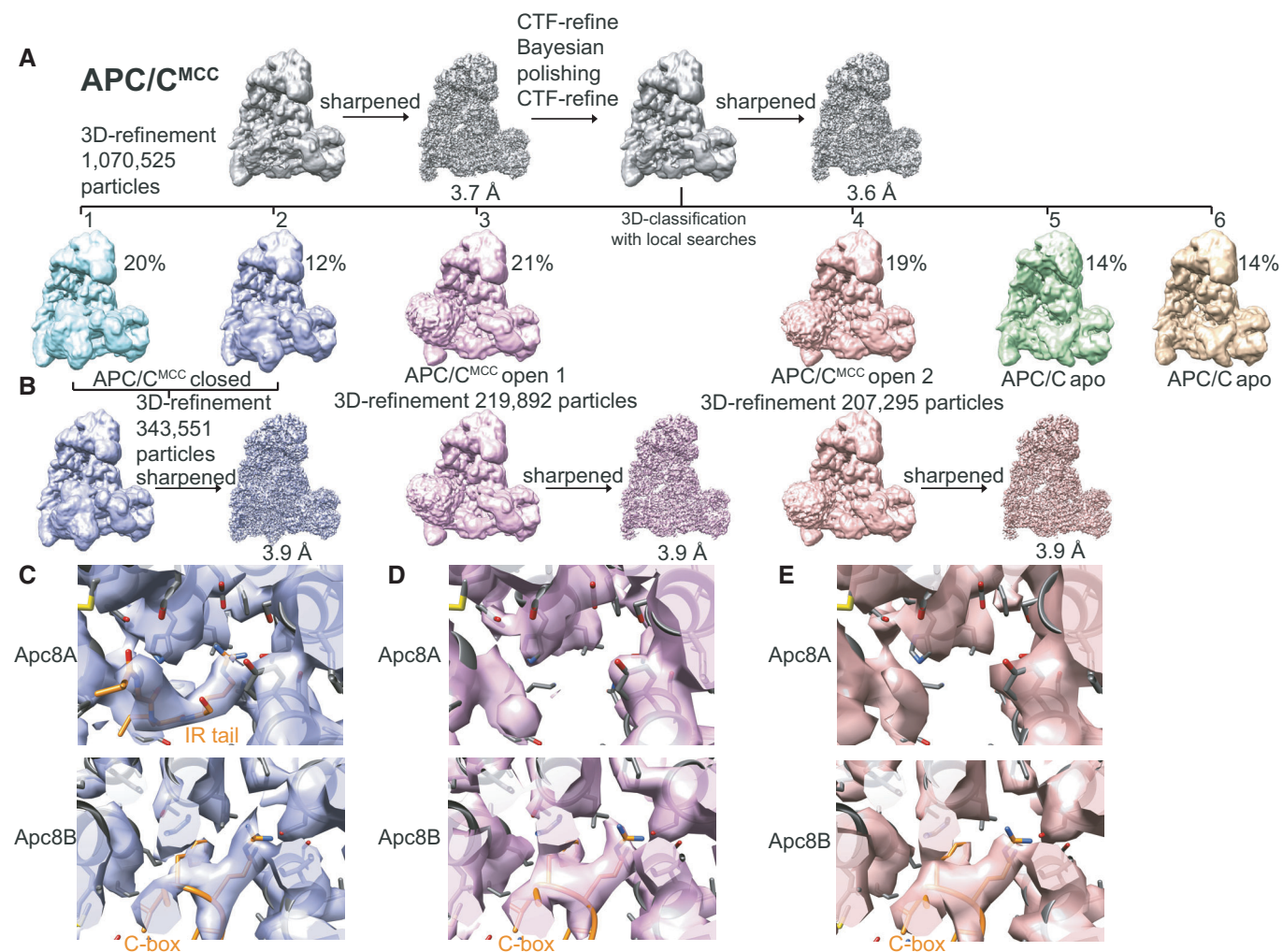


Figure EV2.



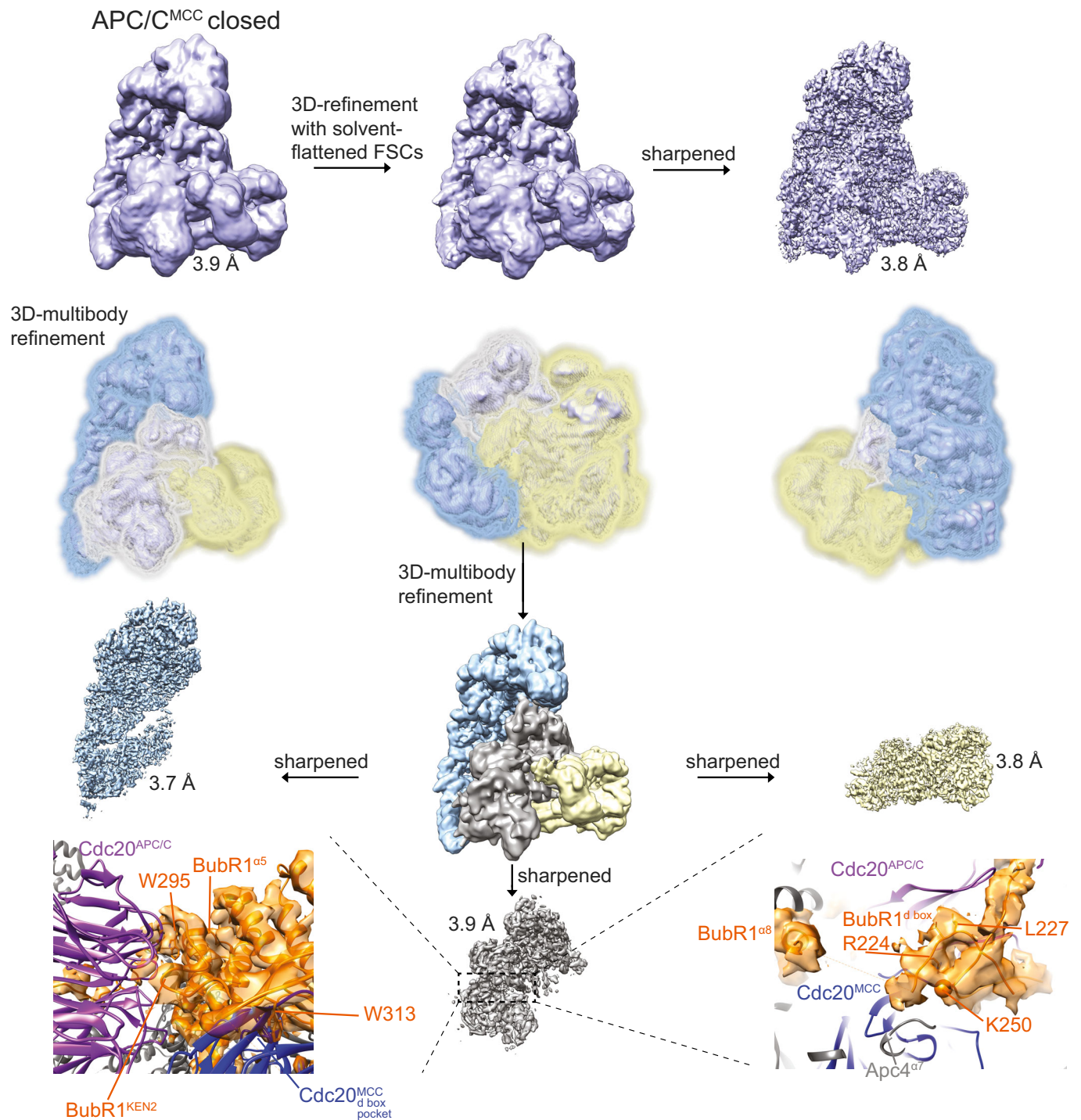
**Figure EV3. 3D reconstruction of APC/C–Nek2A complexes.**

- A–C Workflow for focussed 3D classification and multi-body refinement for 3D reconstruction and refinement of the cryo-EM density for the MR tail 1 binding site on Apc8A.
- D–H Workflow for focussed 3D classification and multi-body refinement for 3D reconstruction and refinement of the cryo-EM density for the repositioned APC<sup>WHB</sup> domain and for the MR tail 2 binding site on Apc2–Apc4. Classes 2 and 3 shown in (G) differed in the orientation of the APC<sup>WHB</sup> domain, and the occupancy of the MR tail 2 was highest in class 3.



**Figure EV4. 3D reconstruction of the APC/C–MCC complex.**

- A 3D class averages obtained by classification using local searches (see Materials and Methods) are shown for obtaining the APC/C<sup>MCC</sup> reconstructions.
- B Particles from classes 1 and 2 were refined together to obtain the APC/C<sup>MCC</sup> closed reconstruction. Particles from classes 3 and 4 were separately refined to obtain the APC/C<sup>MCC</sup> open 1 and 2 reconstructions, respectively. These latter classes were slightly different in the orientation of the Cdc20–MCC module.
- C Details of the IR tail and C-box binding site of the APC/C<sup>MCC</sup>-closed reconstruction.
- D, E (D). Details of the IR tail and C-box binding site of the APC/C<sup>MCC</sup>-open-1 reconstruction and (E) of the APC/C<sup>MCC</sup>-open-2 reconstruction. Neither of the two APC/C<sup>MCC</sup>-open reconstructions shows clear density for the Cdc20<sup>MCC</sup> IR tail.



**Figure EV5. 3D Multi-body refinement of the APC/C–MCC complex.**

3D multi-body refinement strategy for the APC/C<sup>MCC-closed</sup> reconstruction (see Materials and Methods). Masks defined for the three APC/C<sup>MCC</sup> bodies are shown. Details of new BubR1 regions built guided by the improved APC/C<sup>MCC</sup> cryo-EM map are shown at the bottom. This assignment is consistent with [47–49].