Figures:

Figure 1. Structural studies of EAATs in nanodiscs and liposomes. (A) Examples of 2D averages of EAAT1 in nanodisc (top) and the resulting density maps for two structural classes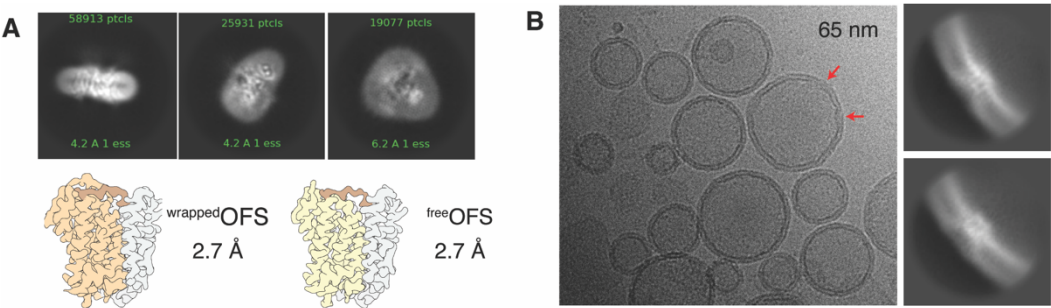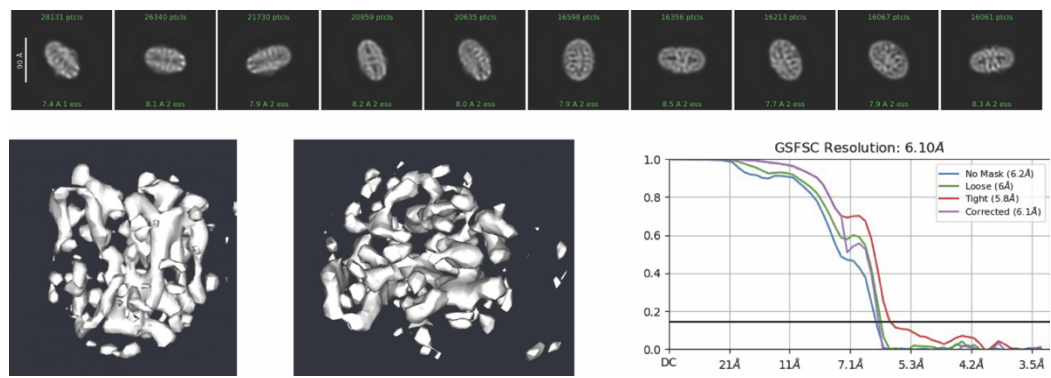 of single protomers of the trimeric transporter, refined to 2.7 Å overall resolution each. (B) Model EAAT homolog, Glt$_{Ph}$, reconstituted into liposomes. Proteoliposomes imaged using in-house Glacios (left) and examples of 2D classes from preliminary data processing (right).

Figure 2. Imaging of human VGLUT in nanodiscs using Krios. (Top) Examples of 2D class averages. (Bottom) 3D volume reconstructions viewed in the membrane plane and perpendicular to the membrane and the SFSC graph, showing ~6 Å overall resolution. Reconstructions were generated using 92,000 selected "best" particles.
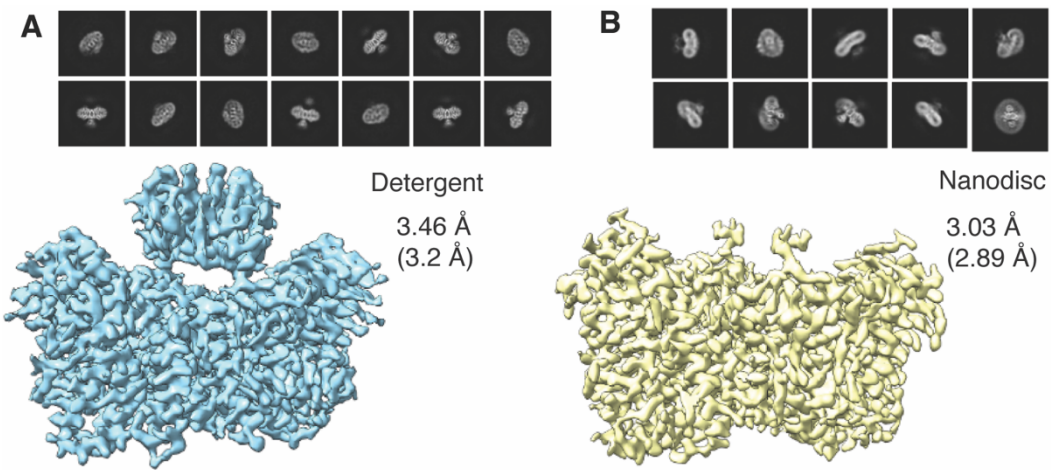

Figure 3. Structural studies of OCA2. Examples of 2D classes and 3D volume reconstructions for OCA2 in detergent (A) and nanodiscs (B). The overall resolutions are shown next to the maps with values in the brackets corresponding to the resolution after symmetrical expansion and local refinement.