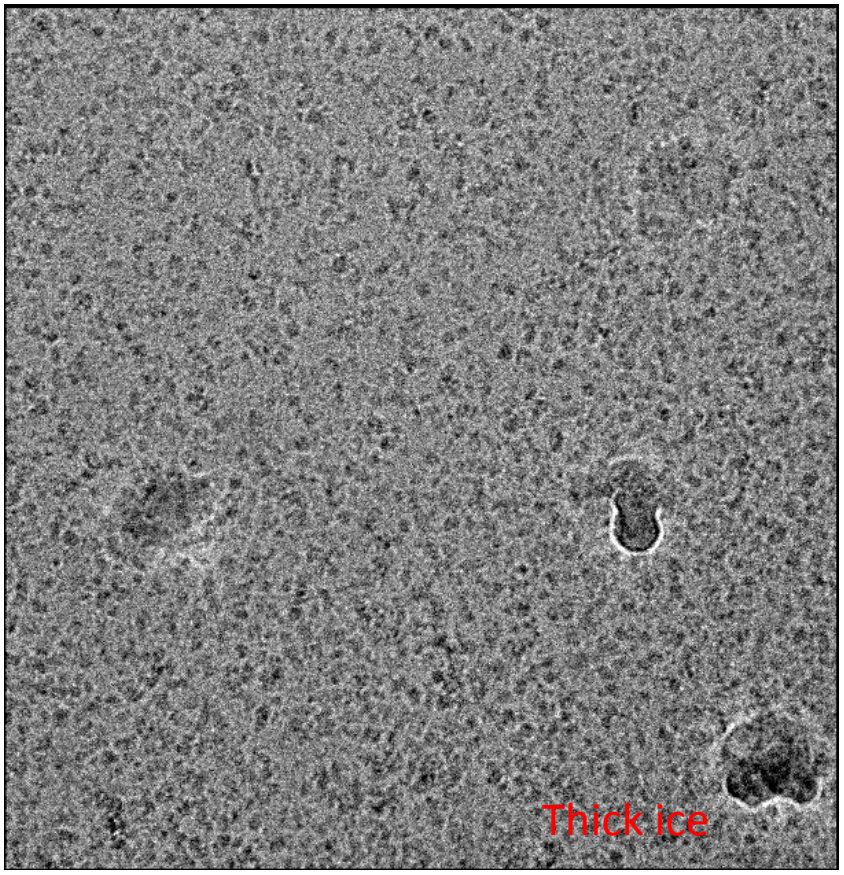
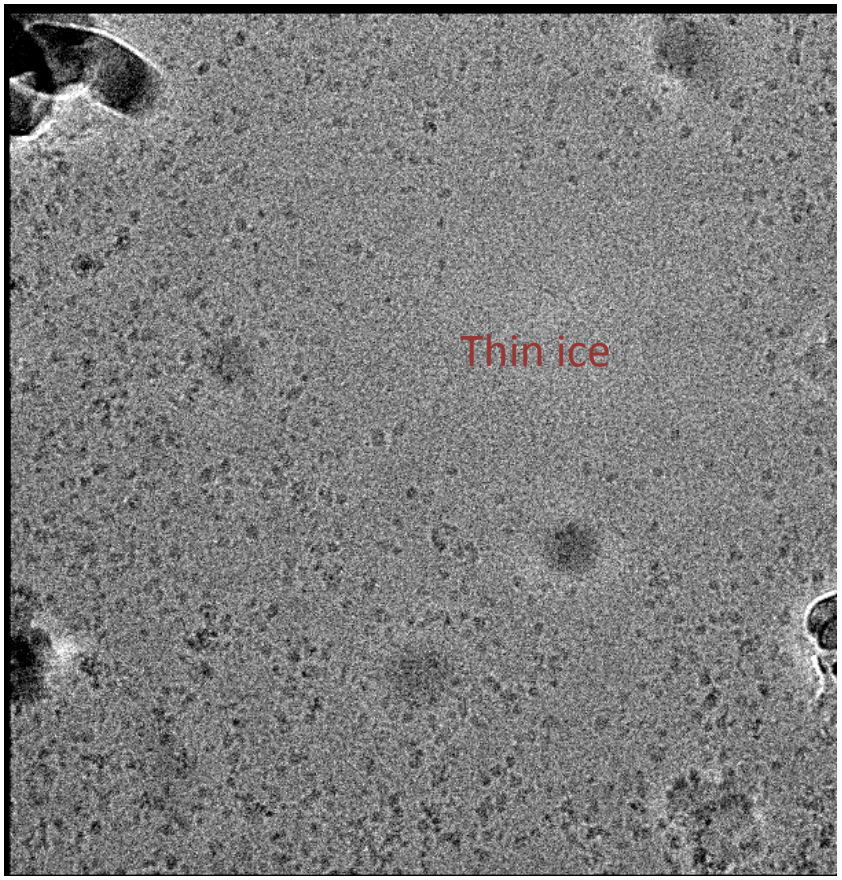
Li Lab 100kD TM protein

Pengbiao

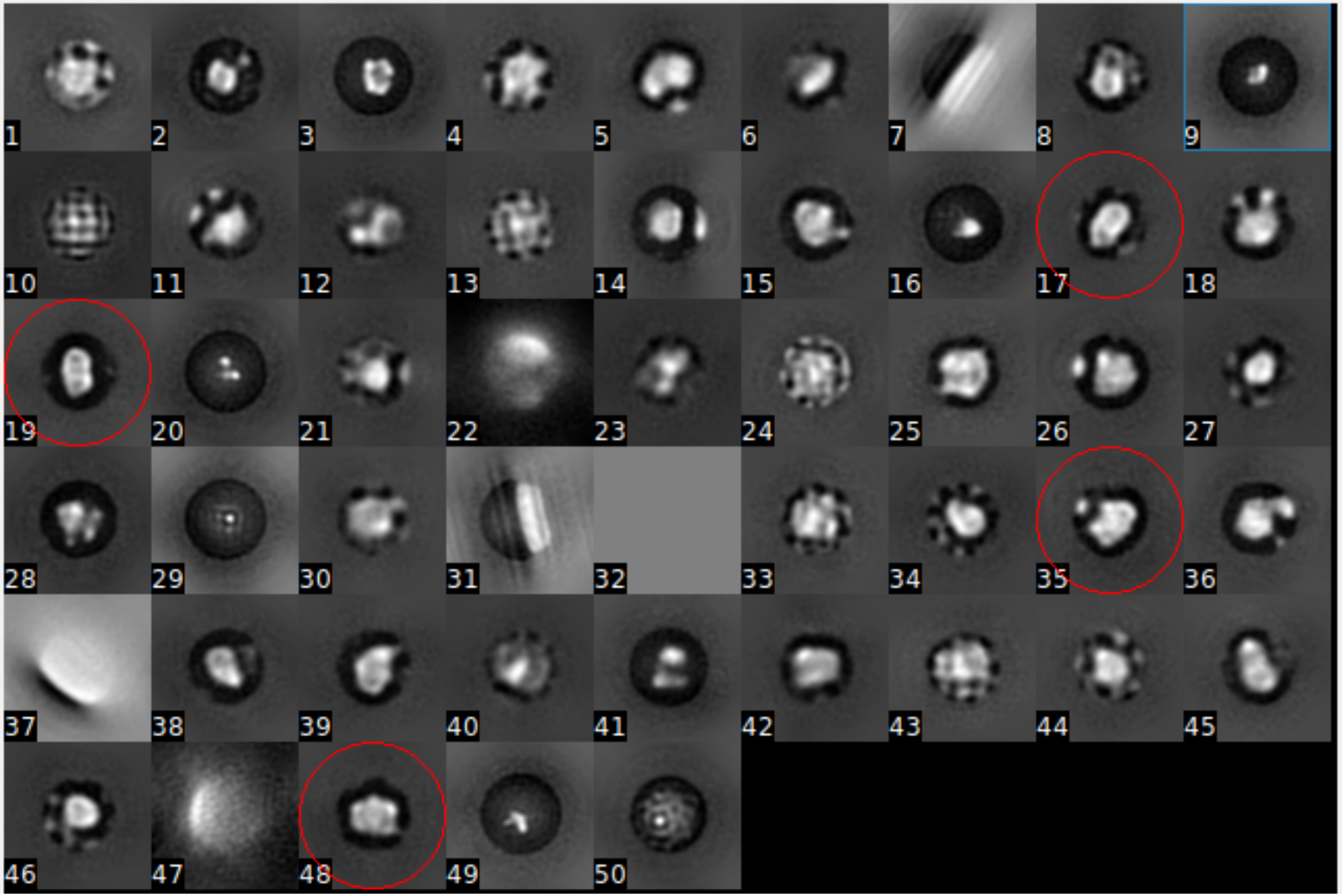


Thick ice



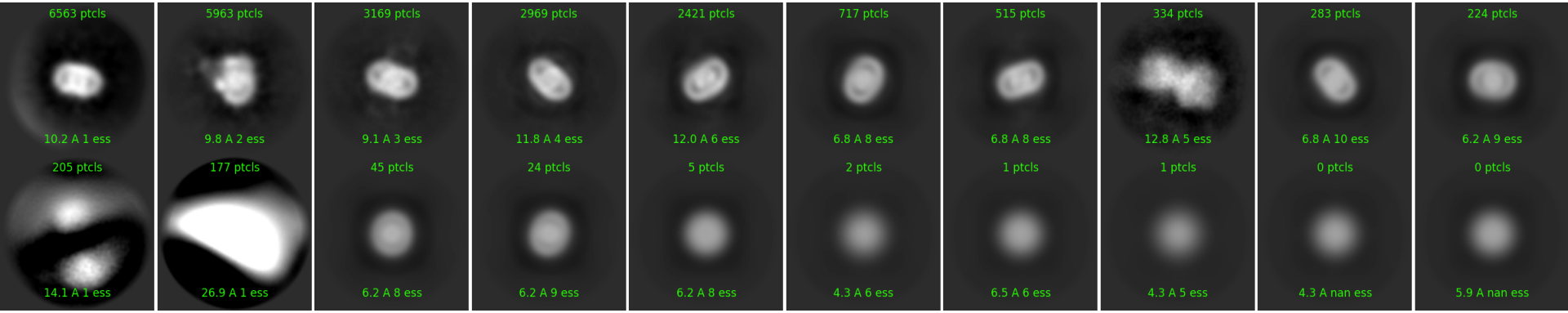
Thin ice

- Particle concentration is very high at thick ice. Particles do no exist in ultra thin ice.
- This representative thick ice is OK with very fewer overlaps. But it should be the up limit.
- We need to find the thin ice area to collect data.

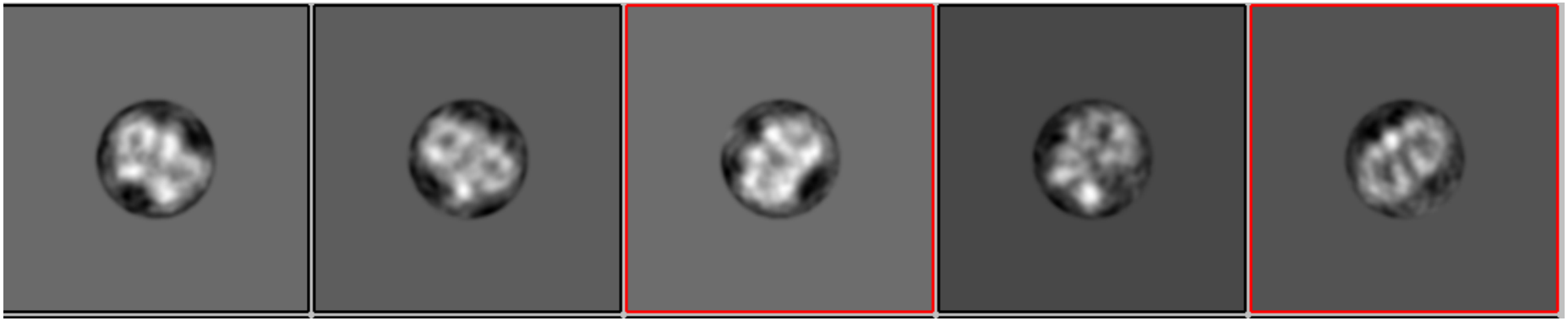


For our local data, only cisTEM works to remove junk particles in first round of 2D. Relion3 and cryosparc do not work. These 4 classes account for 10% of total particles. As biochemistry analyses show this specimen is protein monomer, it is >95% pure, and has no aggregates or breaks. The other classes might contain the misaligned particles due to poor quality data.

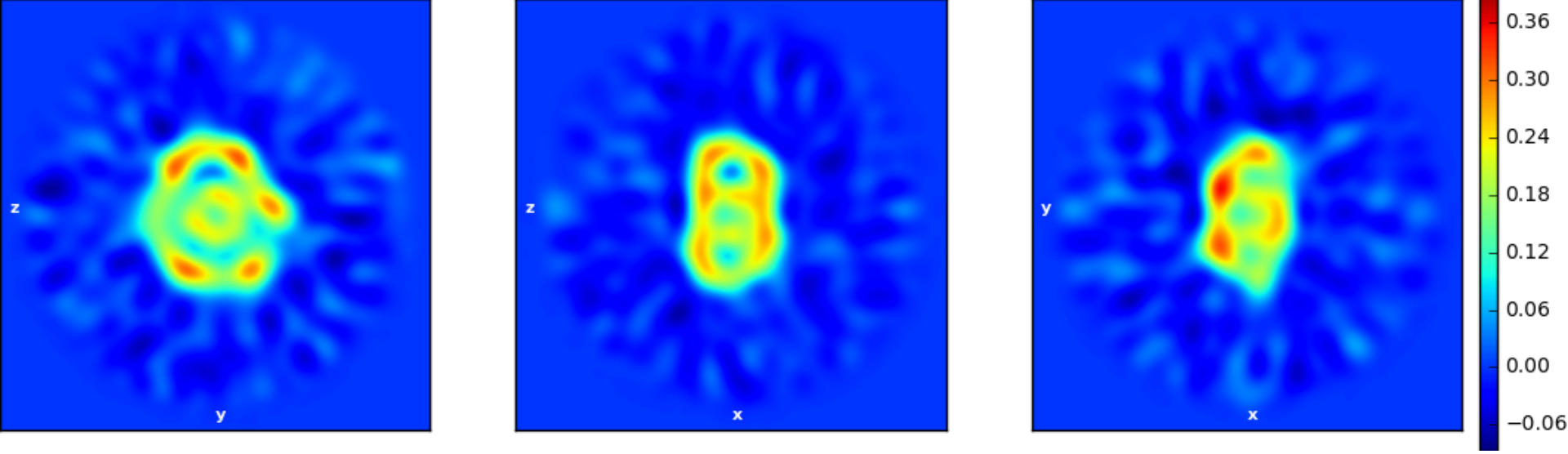
cryosparc



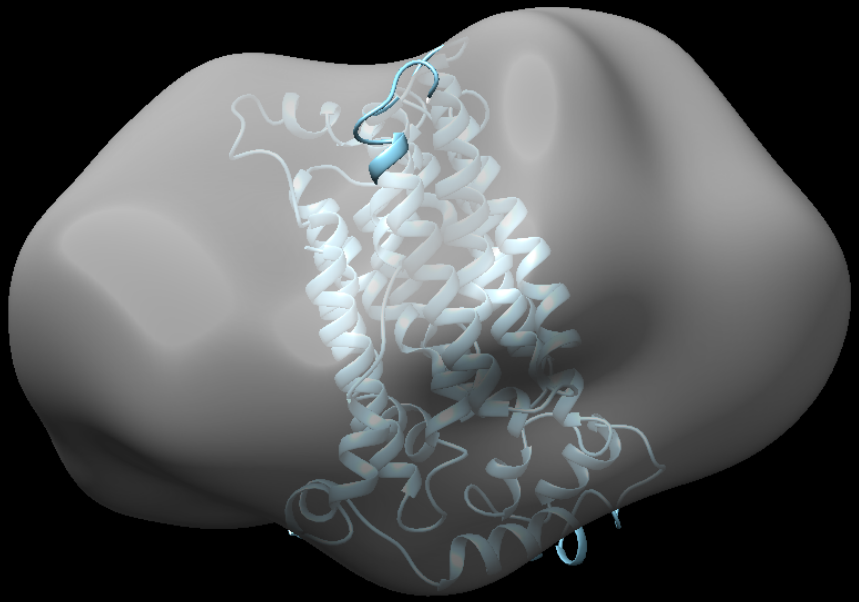
relion

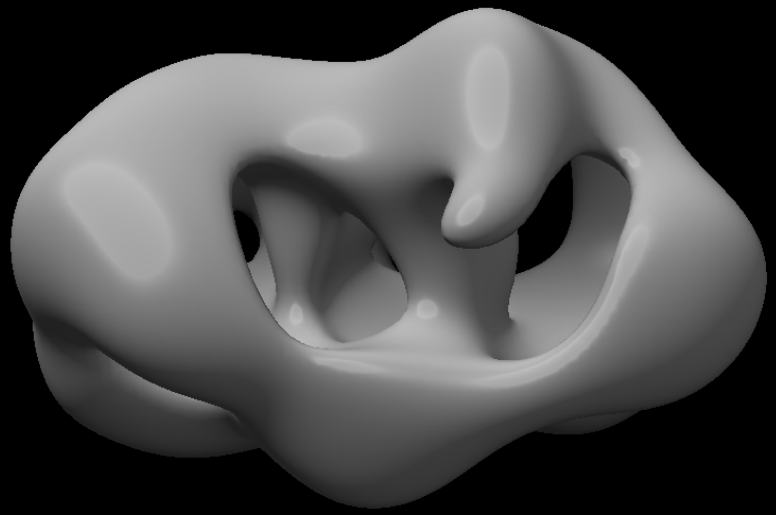


After export the clean particles from cisTEM, I import them to cryosparc and relion again. With clean particles, both software works.



Three views of the model. A clear tunnel is inside the detergent micelle. Generated by cryosparc.
The refinement goes to 13A due to small numbers of particles and poor EM quality





The swiss-model generated resemble homolog model could be fit into the map.
The 3D model has two bundle densities inside.