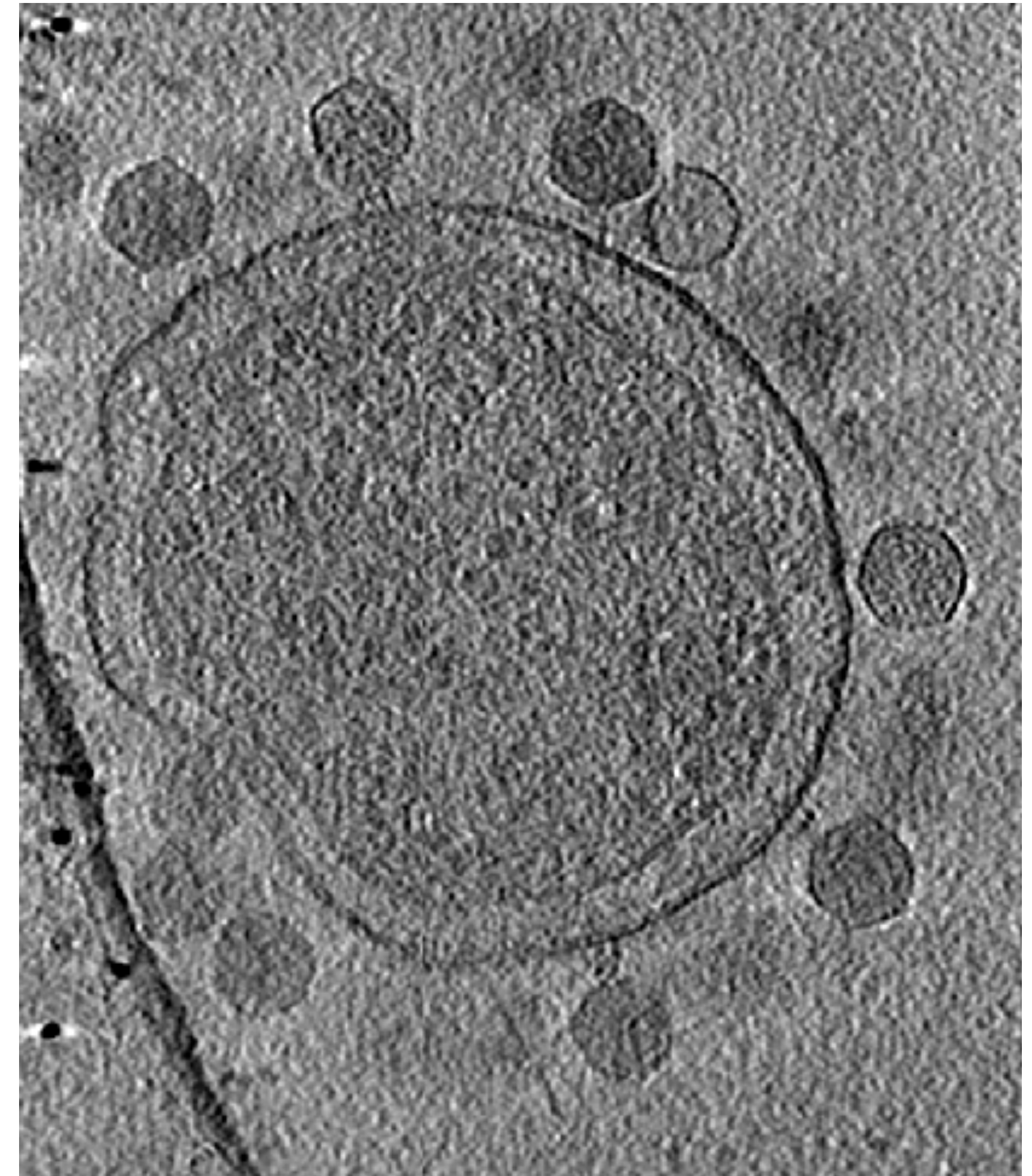


# CryoET data processing in EMAN2

Muyuan Chen  
2023-05

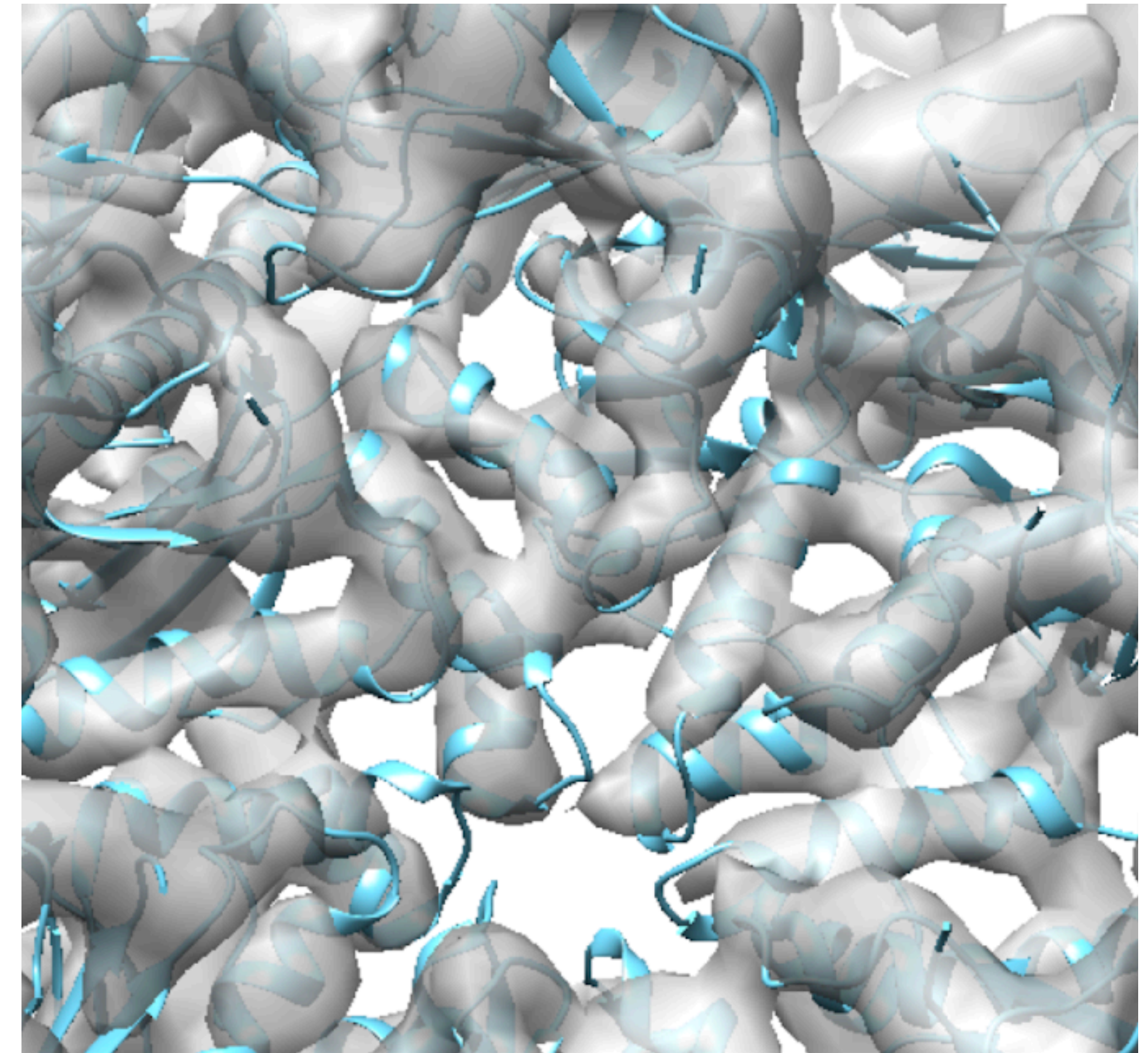
# What's included

- Reconstruction of cellular tomogram
  - P22 phages infecting bacteria
- CTF estimation and correction
- Manual and automatic particle picking



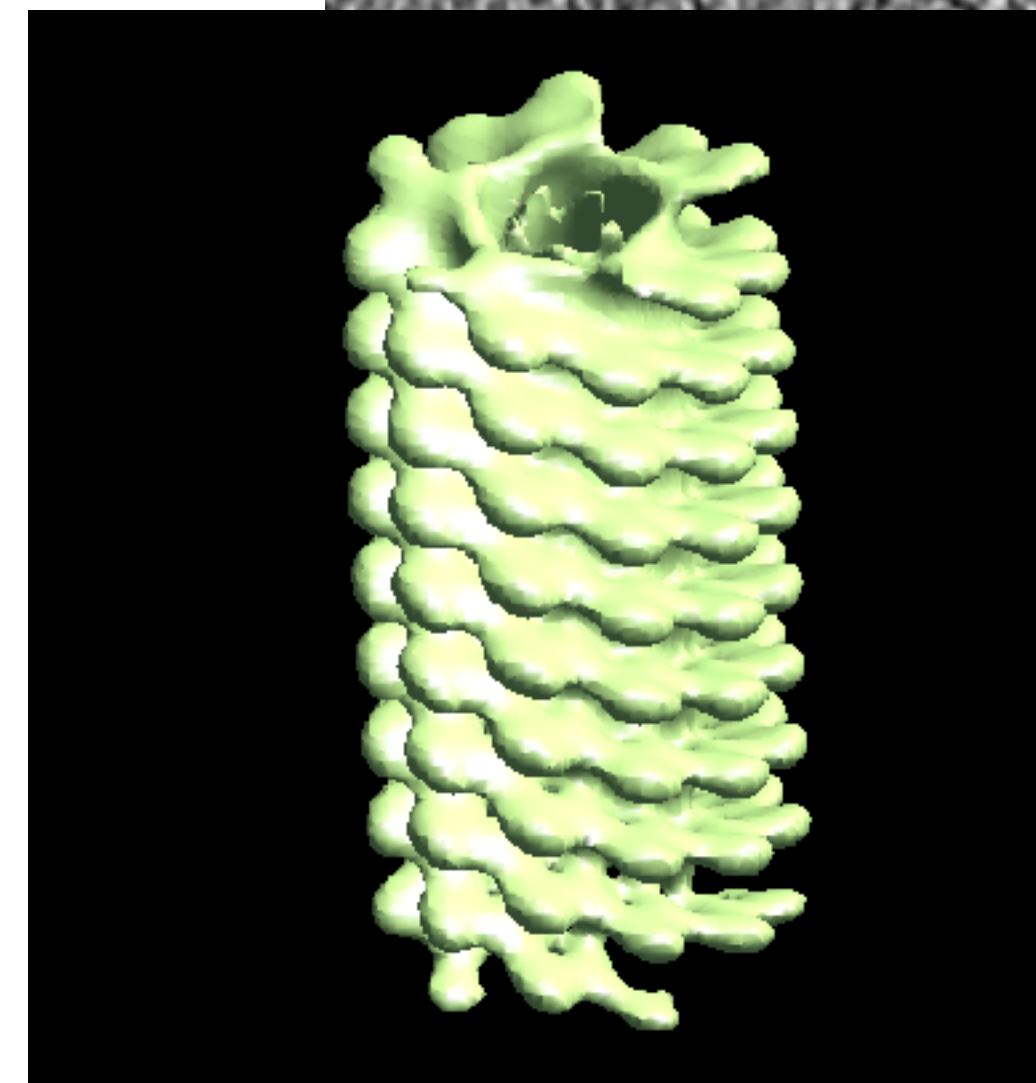
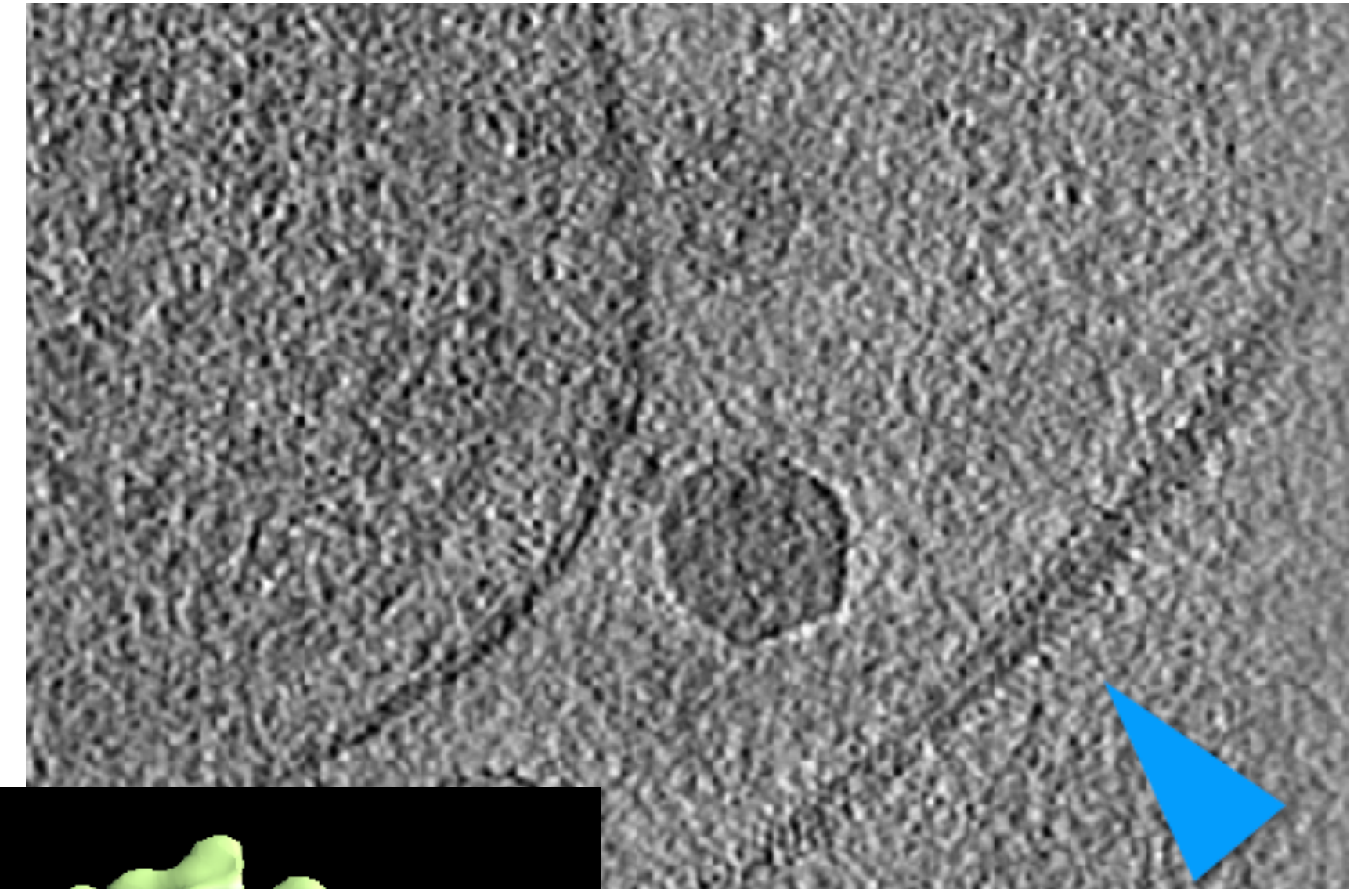
# What's included

- Initial model generation
- Subtomogram averaging
  - in situ 7Å from 4 tomograms
- Heterogeneity analysis
  - symmetry breaking
  - multi-model classification
  - continuous movement



# What's included

- Filament refinement
  - Manual filament picking
  - Initial model generation
  - Subtomogram refinement



# Acknowledgement

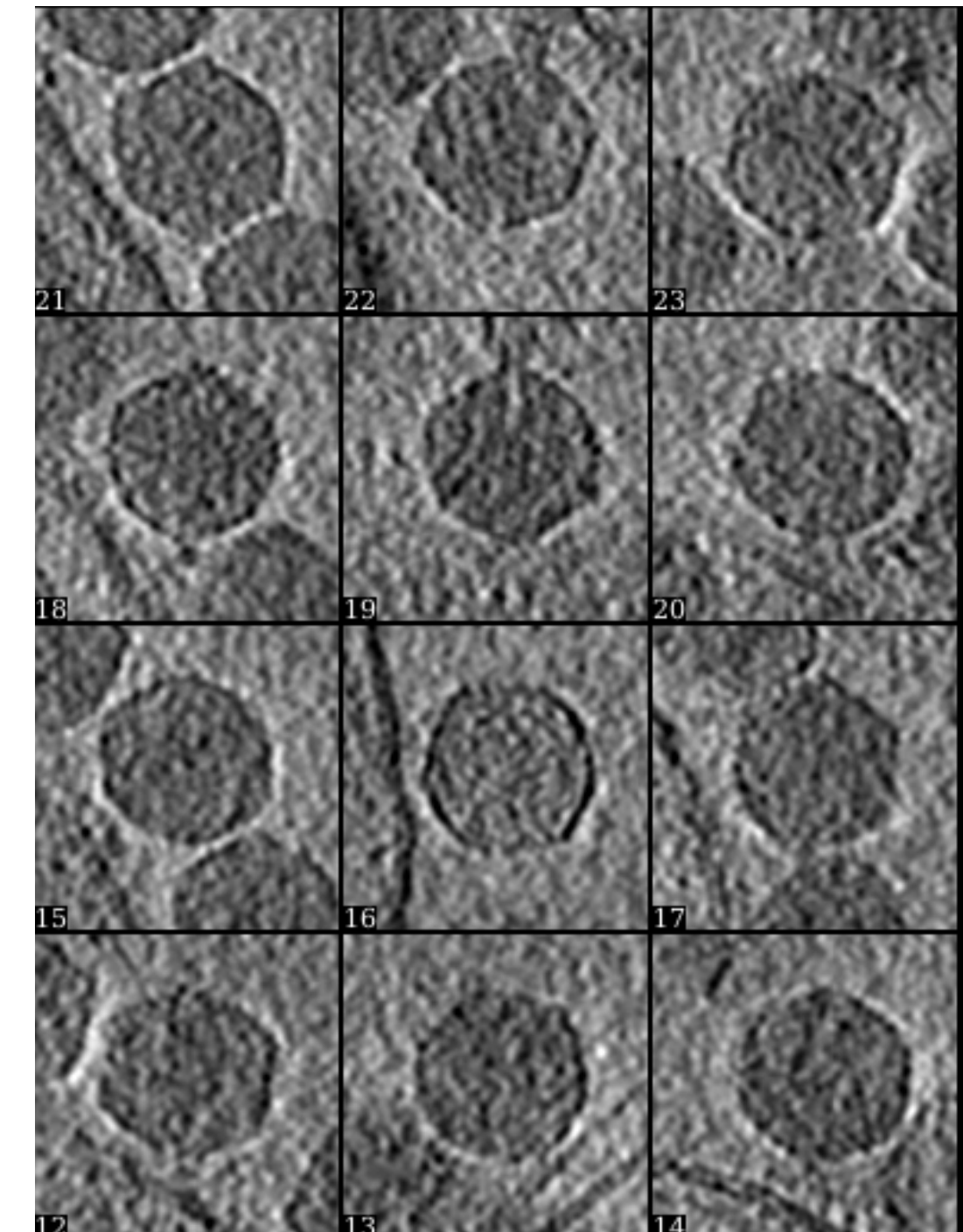
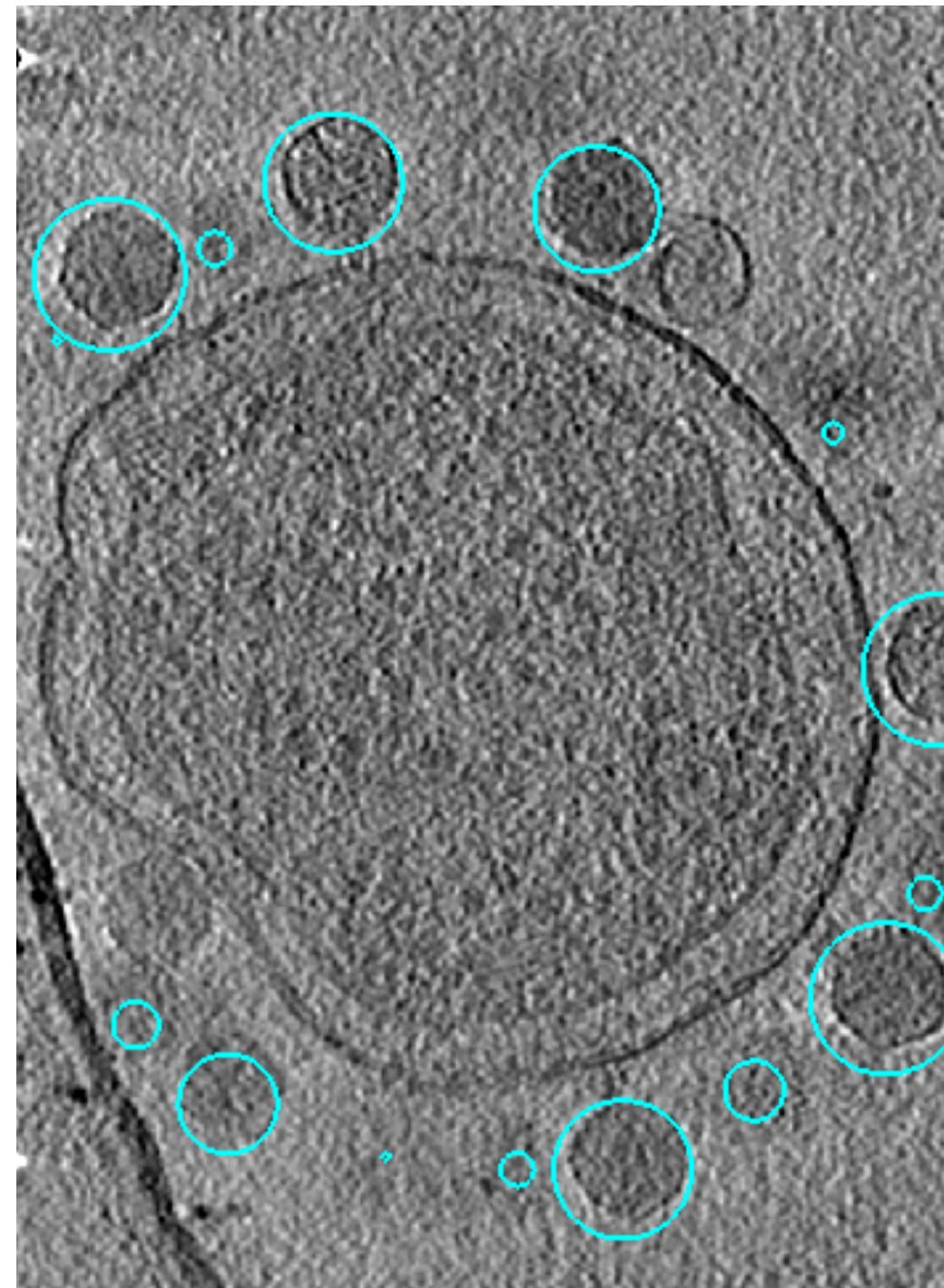
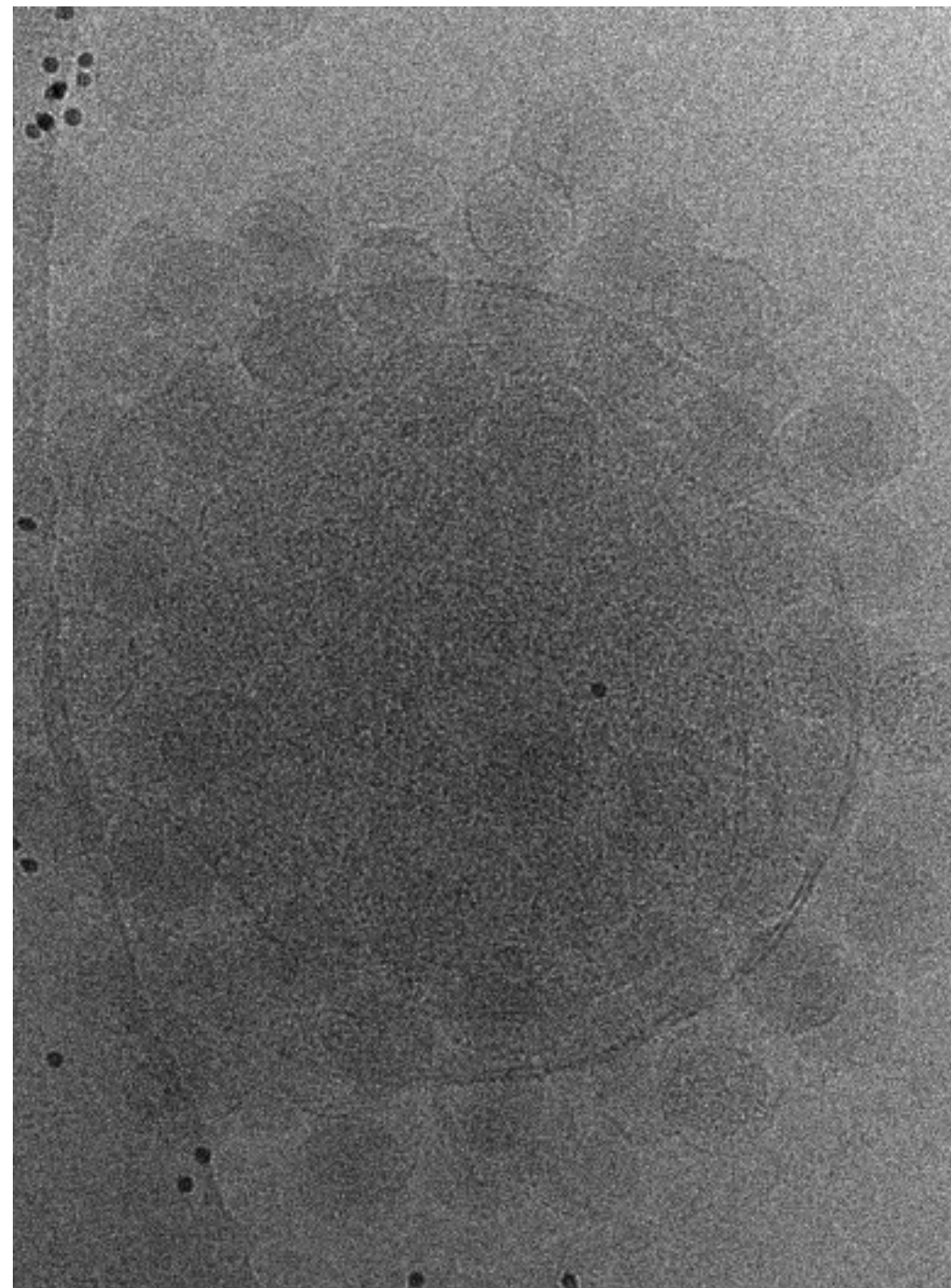


Emotional supporters

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- Many thanks to Jun Liu from Yale for providing the tutorial dataset!
- Initial tests of the workflow is also done by people from Liu's lab, including Huaxin Yu and Chunyan Wang



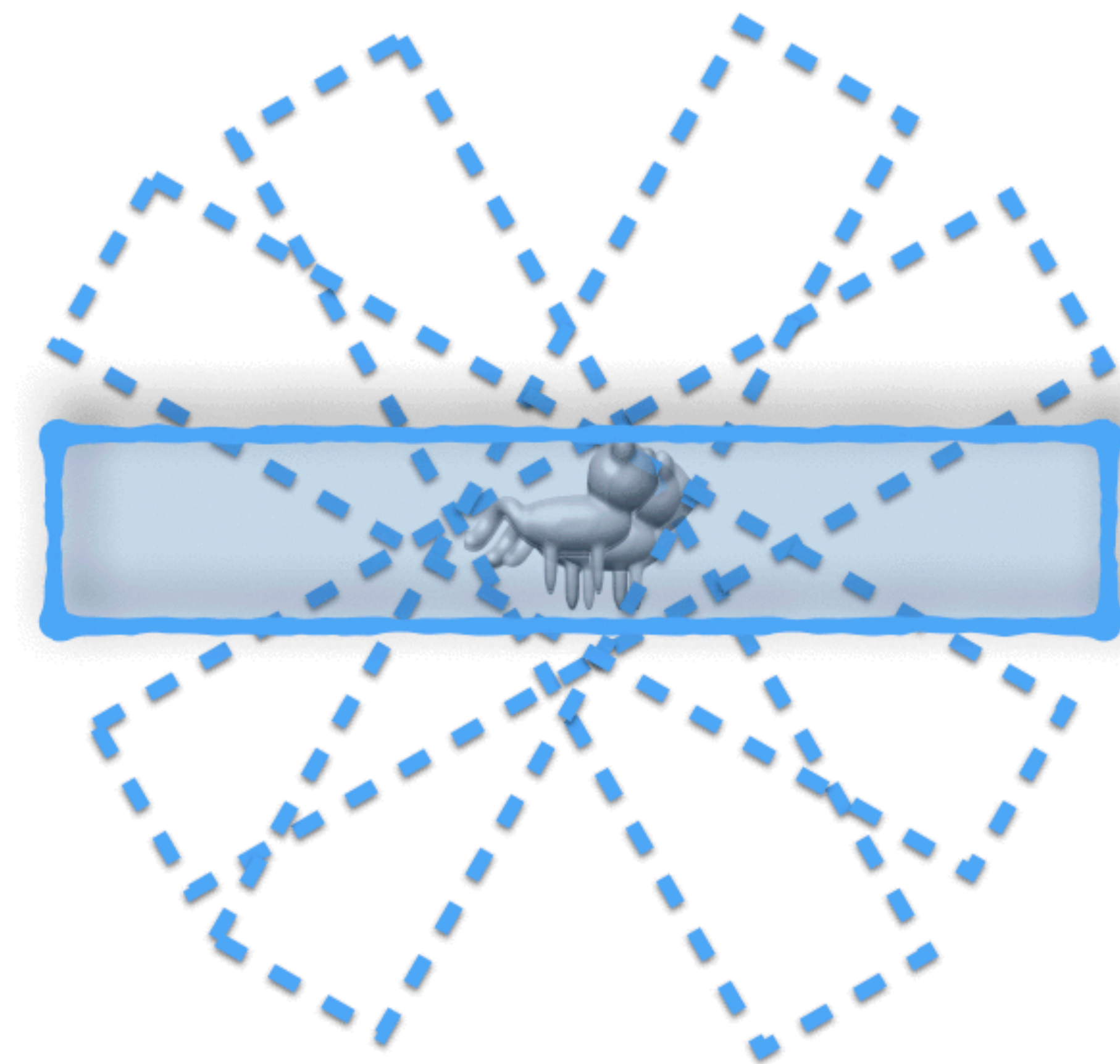
# From tilt series to particles



# Subtomogram vs subtilt alignment



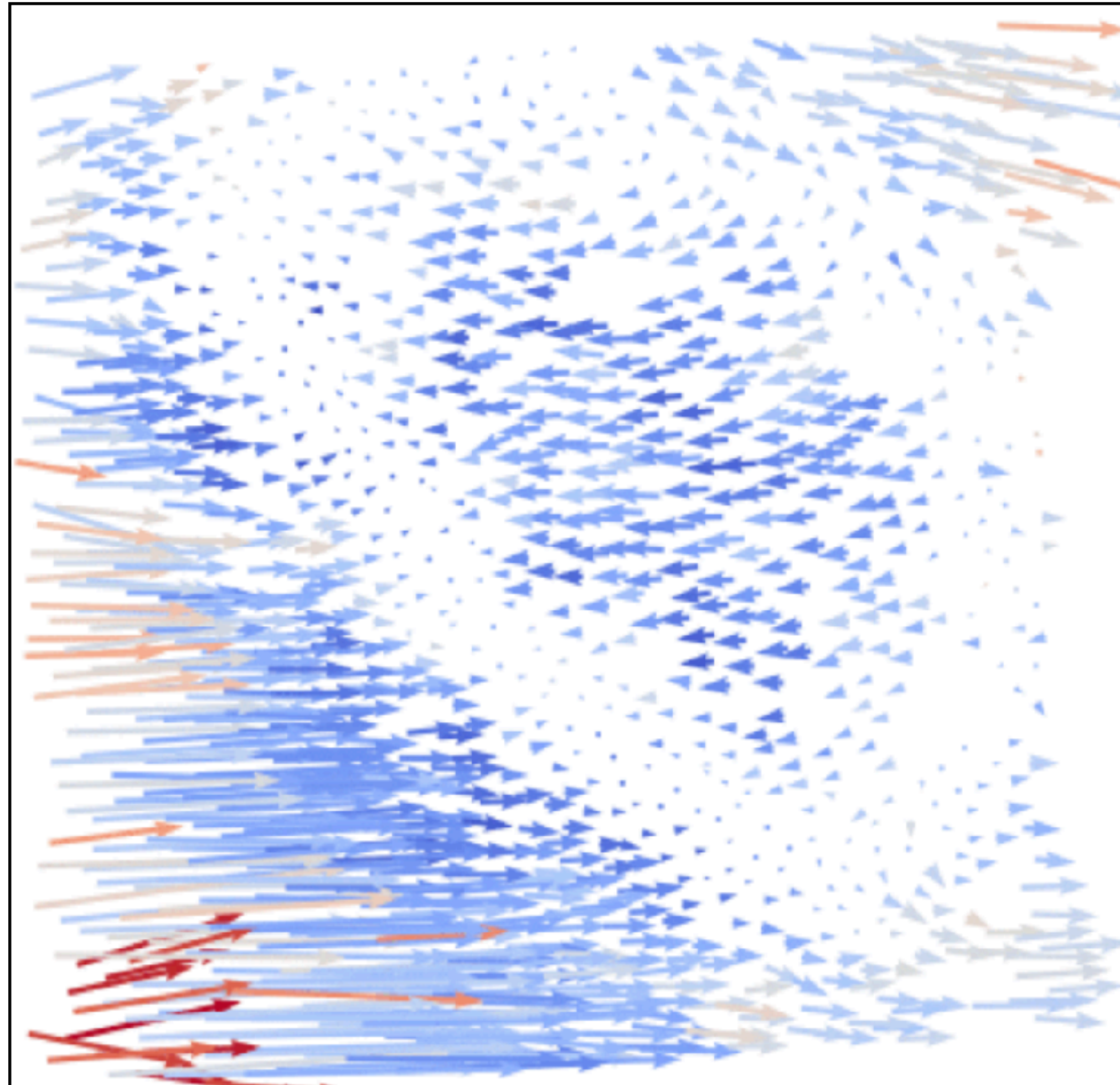
Subtomogram alignment



Subtilt alignment



# Subtilt alignment with multiple particles



- Subtilt movement of nearby particles correlates
- Use information from multiple particles from a local region for better subtilt alignment
- Take subtilt alignment from high SNR particles (virus capsids, ribosomes) to guide the alignment of lower SNR particles (virus tails, smaller proteins in cells)

# Refinement workflow

