Harvard Cryo-EM Center for Structural Biology

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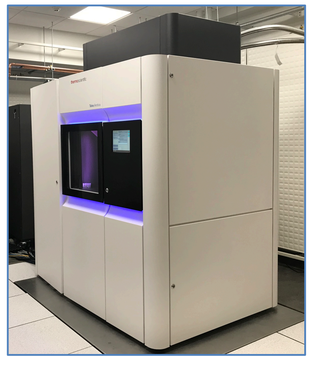
www.cryoem.hms.harvard.edu

Our Mission

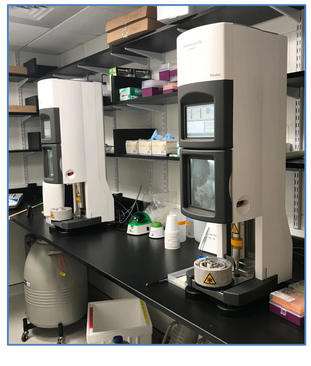
The new center is a joint effort of Harvard Medical School, Dana-Farber Cancer Institute, Boston Children's Hospital, and Massachusetts General Hospital to provide state-of-the-art cryo-EM instrumentation and expertise for the Harvard structural biology community. This user facility will offer consultation and training by staff in specimen preparation, microscope operation, image acquisition, and data analysis.

Microscopes & Equipment

Two Titan Krios, configured identically:
- 300 kV with X-FEG beam source
- 3 condenser lens system to ensure parallel beam for high resolution imaging of biological specimens
- Cryo-autoloader, up to 12 grids per load
- Volta phase plate
- Gatan BioQuantum energy filter with K3 direct electron detector
- For high-throughput, high-resolution, single-particle data collection, and cryo-tomography data acquisition

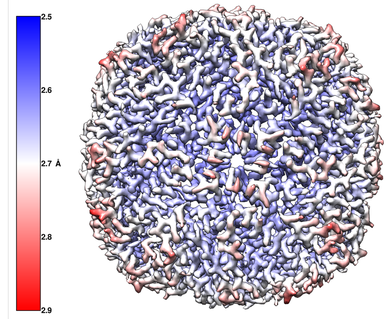


One Talos Arctica:
- 200 kV with X-FEG beam source
- Cryo-autoloader, up to 12 grids per load
- Gatan K2 direct electron detector, to be upgraded to K3
- Volta phase plate
- For high-throughput, single-particle data collection, and for high-throughput cryo-grid screening

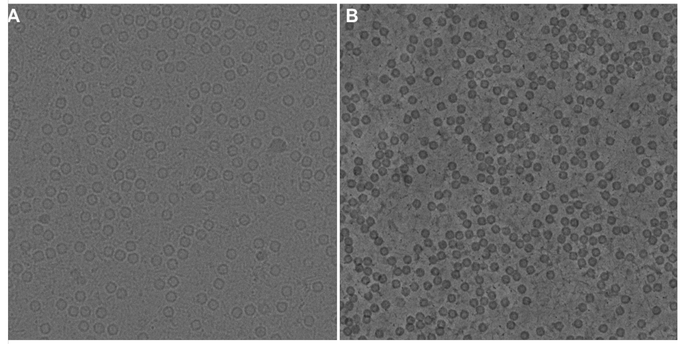


Two Mark IV Vitrobots:
- Automated vitrification device for plunge-freezing of aqueous samples
- Controlled environment for reproducible results
- Touch-screen interface and user-defined settings allows for parameter flexibility

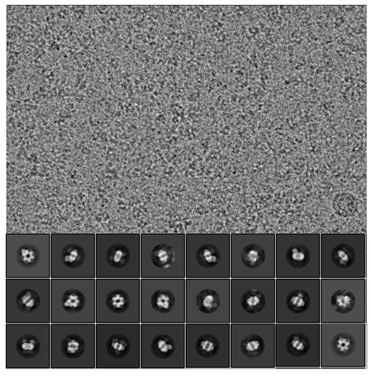
Examples of Data Collected on the Talos Arctica with K2 Direct Detector



Apoferritin at an average resolution of 2.6Å. RELION-3 was used to process 48,749 particles from 926 images stacks. Apoferritin will be used as a standard sample to test quality of microscope alignments, micrograph collection, and data processing.



Illustrating the impact of a Volta phase plate on particle contrast. Motion-corrected image stacks of apoferritin A) without Volta phase plate and B) with insertion of Volta phase plate.



Motion-corrected image stack and 2D class averages of CaMKII, a 600kDa protein kinase complex. *-courtesy of Luke Chao, MGH*

Computational Infrastructure

On-the-fly inline pre-processing:
- Motion correction and CTF estimation standard
- Automated particle picking and 2D classification being tested

Hardware:
- ~40 GPUs, 100+ CPU cores and 400 TB storage in first phase
- Expansion planned to double resources over 3 year period

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