

WRAIR

Walter Reed Army
Institute of Research

WRAIR CRYO-ELECTRON MICROSCOPY SERVICES

Cryo-electron microscopy (cryo-EM) is an emerging method for imaging high-resolution 3-D structures of biomolecules when X-ray crystallography may not be feasible. The Walter Reed Army Institute of Research's cryo-electron microscope, housed at the Institute's labs in Silver Spring, Md., is a unique, powerful asset for pathogen research and countermeasure development.

WRAIR's proven cryo-EM infrastructure, protocols and staff of scientists are available to support outside research projects within the U.S. Department of Defense, as well as for academic and industry clients.

Methods

Cryo-EM involves flash-freezing fragile biological samples in vitreous ice to preserve native conformations and allow for imaging in the high vacuum of a transmission electron microscope. This allows for any biological samples less than 0.5 micron in diameter to be preserved and imaged at high resolution. In particular, WRAIR specializes in sample preparation and data acquisition for high-resolution structure determination of purified proteins and protein-drug complexes by single-tilt single particle averaging (SPA) methods. Additionally, staff can collect high quality negative-stain EM data to guide early sample optimization alongside or prior to cryo- sample preparation.

Semi-automated data collection allows for rapid collection of small datasets or collections of large datasets on the order of one million particle images. Semi-automated online or "live" data processing allows staff to rapidly assess results and data quality, and to optimize data collection strategy or sample preparation. Post-processing by staff on high performance computing cluster can provide publication-quality 3D maps and atomic models. Staff is able to aid in structure interpretation or figure generation.

- Cryo-electron microscopy from frozen samples to determine molecule structures at atomic-level resolution
 - Single Particle Averaging (SPA)
- In-house sample optimization for rapid iteration times
 - Live data processing
 - Negative-stain Electron Microscopy
 - Leica EM GP2 Plunge Freezer
 - Protein purification and expression (bacterial and mammalian)
- GPU-accelerated image processing

This informational flyer was developed by HJF. The views expressed are those of the authors and should not be construed to represent the positions of the U.S. Army, the Department of Defense or HJF. August 2023

CRYO-EM BY THE NUMBERS



12-24
Samples run per day



1 million
2D images of each sample



<7 days
For 3D image results

Working with WRAIR

WRAIR scientists work to remain on the cutting edge of cryo-EM methods and practices, and they're experienced in applying the technology to biomedical research and product development. Staff will be available to:

- Consult on project feasibility and expected results
- Advise on sample preparation
- Provide Sample Optimization
- Collect data
- Process images and 3D structure model building
- Assist in interpreting results and figure generation
- Regular data collection allotments available

TECHNICAL SPECIFICATIONS

Microscope: JEOL Cryo-ARM 200 + Gatan K3 Direct Electron Detector

- Up to 1.2Å resolution
- 3 x 4 grid autoloader allows for rapid iteration times
- High nitrogen loading station for ultra-low ice contamination
- Energy filtered 200 kV for high contrast
- Gatan K3 provides industry-leading data acquisition in speed, size, and quality
- Current collection speed of ~230 micrographs/hr (40 square microns/hr)

Compute:

- 12 GPU, 96 CPU, 350 TB GPU-accelerated HPC high-bandwidth cluster
- 2 GPU-accelerated visualization terminals for live data analysis
- Automatic drift-correction

Sample Preparation:

- LEICA EM GP2 plunge freezer
 - High nitrogen vapor for ease of use and ultra-low ice contamination
 - Required Sample volumes as low as 1.5 µl
- Full complement of grid varieties
- 4 AKTA FPLC's for protein purification
- 3 Mammalian Shakers

For more information, contact
usarmy.detrick.medcom-wrair.mbx.cryoem@health.mil

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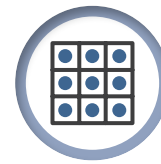
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