GW4

Facility for High-Resolution Electron Cryo-Microscopy

- On-demand access
- State-of-the-art equipment
- Technical expertise and service

Single-Particle Analysis
Visualise proteins and macro-molecular complexes at near-atomic resolution.

Cryo-Tomography
Analyse unique sub-cellular structures in nanometre scale.

Arranging Access:
Contact us to discuss project details, requirements, and outlook.
E-mail: GW4-cryoEM@bristol.ac.uk
Twitter: @GW4cryoEM

Equipment

- FEI Talos Arctica equipped with 200 kV X-FEG, Ceta 16M CCD, Gatan K2 DED and Gatan GIF Quantum LS energy filter.
- FEI Vitrobot mark III and Leica GM GP plunge freezing devices.
- ELMO glow discharge system and Leica ACE carbon coater and glow discharger.

Applications of cryo-EM

Antibodies and vaccines:

- Visualise and map interactions between antibodies and antigens.
- Solve and analyse the structure of viruses and virus-like particles.

Drug delivery:

- Image drug-delivery systems such as liposomes and dendrimers in near-physiological conditions.

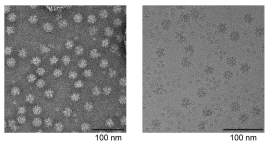
Drug discovery and design:

- Identify the mechanism by which compounds bind their target.
- Solve the structures of difficult-to-crystallise proteins and protein complexes.

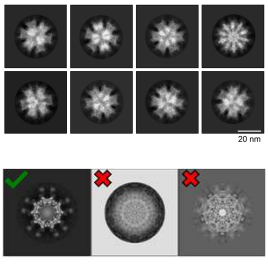
Access and Service

Single Particle Analysis

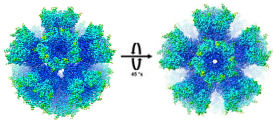
After suitable grid samples have been screened and optimised for ice and particle quality, a dataset of many thousand micrographs is collected.



In the processing pipeline, micrographs are corrected for aberrations and particle images are extracted. Images with the same orientation and conformation are then grouped into 2D classes. The averaging of these 2D classes significantly improves the signal-to-noise ratio of particle images.

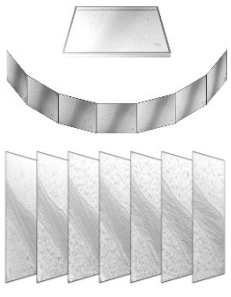


Finally, 3D volumes are reconstructed and refined. At near-atomic resolutions, molecular structures can be elucidated *de novo*.



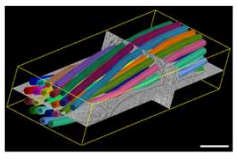
Cryo-Tomography

The sample, usually mixed with fiducial markers to facilitate subsequent computational steps, is captured on EM grids and flash-frozen. Following screening and identification of a suitable specimen, images are recorded as a tilt series, capturing projections of selected areas of interest at various tilt angles.



To analyse the data, tilt images are carefully aligned and then "back-projected" to generate a 3D map of the original object with amplified signal-to-noise ratio.

Finally, unique features can be traced and outlined to elucidate their structure and context. Sub-tomogram averages can be calculated to solve molecular structures in their native environments.



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