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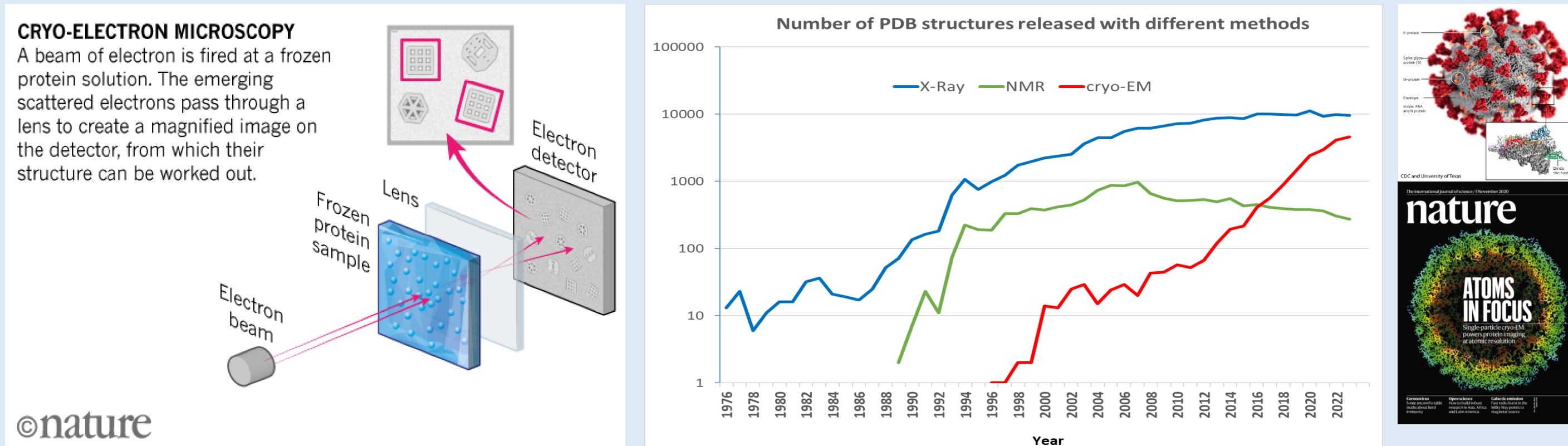
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What is cryo-EM?

Cryo-electron microscopy (cryo-EM) allows for structural determination of various biological compounds (e.g. proteins) as well as small chemical compounds. Over the recent years it has revolutionised the field of structural biology and was awarded the Nobel Prize in 2017.



Who we are?

Our Core Facility is one of the two cryo-EM facilities in Poland. It is localised at the Centre of New Technologies, University of Warsaw at the Ochota Campus. We are equipped with the state-of-the-art 200kV Glacios microscope with Falcon3EC and Ceta-D cameras (for imaging and electron diffraction, respectively) and some additional auxiliary equipment for plunge freezing and grid preparation for both imaging and diffraction experiments.



What we can offer?

200kV Glacios cryo-TEM at CeNT UW

Imaging

- Single Particle Analysis (SPA)
- Cryo-tomography (CryoET)

Diffraction

- Microcrystal electron diffraction (MicroED)

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Our Glacios microscope can yield high resolution structures by Single Particle Analysis

0.59 Å/px

0.59 Å/px

0.95 Å/px

3D Variability analysis
~200k particles

Reference based motion correction
~203k particles

~227k particles

Human apoferritin at 1.92 Å

PDB: 8S32
GroEL with GroTAC peptide at 2.45 Å

AbiK polymerase at 2.27 Å
published structure from [3]

Microcrystal electron diffraction (micro-ED)

Micron-Sized Crystal

Continuous Rotation

3-D Electron Diffraction Collection

Structural Determination

3-D Reconstruction and Merging

L-alanine 0.56 Å

α -glycine 0.56 Å

Urea 0.56 Å

- Only few crystals needed
- Low dose imaging ($<1.0 - 4 \text{ e}/\text{Å}^2$)
- Data collection in minutes
- Provides high resolution

Cryo-electron tomography (cryo-ET)

180 nm

Cryo-ET at 200kV provides molecular resolution atlases of intact UZOS mammalian cells [5]

Interactions of amyloid- β oligomer with lipid membranes
(data published in [4])

Our IT infrastructure for storing and processing cryo-EM data

Existing infrastructure

- 200 Nvidia GPUs !!!
- 1 PB storage (90% in use)
- 2400 cores/ 4800 threads data management system

Over 70 user accounts

IT infrastructure for data processing

Operator Workstation

Processing Workstation

GPU
200 Nvidia Tesla

Funk
2400 Xeon cores

Hot Storage

Extension of DataStorage
2 PB 20 GB/s

Users using internet

Open access policy

We welcome users from both academia and industry. Recent users include:

- Internal (from UW): Centre of New Technologies, Biological and Chemical Research Centre, Department of Chemistry
- External (outside UW): IIMCB, Warsaw, University of Gdansk, Institute of Physical Chemistry, PAS, IBB PAS
- Commercial: Cellis Sp. z o.o, Pikralida Sp. z o.o, CelonPharma Sp. z o.o.

Recent publications of our users

- [1]. Kumar, A., Jha, K. K., Olech, B., Goral, T., Malinska, M., Woźniak, K. & Dominiak, P. M. (2024). TAAM refinement on high-resolution experimental and simulated 3D ED/MicroED data for organic molecules. *Acta Cryst. C80*, 264-277.
- [2]. Izert-Nowakowska M., Klimecka M., Antosiewicz A., Wróblewski K., Bandyra K., Góral T.K., Kmiecik K., Serwa R.A., Górna M.W. (2024). Depletion of essential GroEL protein in Escherichia coli using Clp-Interacting Peptidic Protein Erasers (CLIPPERS). *bioRxiv* 2024.02.29.582761
- [3]. Figiel M., Gapińska M., Czarnocki-Cieciura M., Zajko W., Sroka M., Skowronek K., Nowotny M. (2022). Mechanism of protein-primed template-independent DNA synthesis by Abi polymerases. *Nucleic Acids Res. Sep 23;50(17):10026-10040.*
- [4]. Tian Y, Liang R, Kumar A, Szwedziak P, Viles JH. 3D-visualization of amyloid- β oligomer interactions with lipid membranes by cryo-electron tomography. (2021). *Chem Sci. Mar 31;12(20):6896-6907.*
- [5]. Szwedziak P. (2024). In situ structural analysis of mammalian cells using a 200kV electron cryomicroscope – implications for research infrastructure. *bioRxiv* 2024.12.06.627167