User Regulations
Central Research Facility Structural Biochemistry

Services

The Central Research Facility Structural Biochemistry (ZFE Structural Biochemistry) operates as a service laboratory primarily for research groups at the Hannover Medical School (MHH). It follows the recommendations of the European Science Foundation for the operation of equipment centers (Basic Requirements for Research Infrastructures in Europe).

The ZFE Structural Biochemistry at Hannover Medical School provides support for the following research activities:

- Initial optimization of protein samples for crystallization
- High-throughput screening of protein crystallization conditions
- For high-throughput crystallization experiments, we use SwissciTM 96-well 2drop crystallization plates (UVP). These plates provide sufficient precision of geometric parameters for nanodispensing and sufficient transparency in the visible and UV regions for imaging
- Support for crystal optimization
- Plate incubation and control of crystal growth
- Crystal handling and preparation for cryocrystallographic data acquisition
- Diffraction data acquisition with sealed-tube and rotating-anode X-ray sources
- Advice on data acquisition strategies
- Initial characterization of crystal cell parameters and the Bravais lattice
- Access to our 3D graphics workstations and computing environment for full data processing, structure determination, and analysis
- Determination of oligomerization states of proteins and characterization of hydrodynamic properties and macromolecular interactions
- Finally, we assist our users in requesting beam time at synchrotron facilities and provide support for remote and on-site access at DESY, XFEL, ESRF, and Soleil beamlines

Technical equipment

The ZFE Structural Biochemistry is equipped with state-of-the-art instrumentation that allows sensitive and highly specific analyses. In addition, the ZFE has equipment for sample preparation and can advise and assist users in the production of proteins and protein complexes.

Instrumentation

- D8VENTURE single crystal sealed tube X-ray system (Bruker). The instrument can be used for testing diffraction properties and acquiring complete data sets of frozen crystals at cryogenic temperatures.
- D8VENTURE X-ray system for *in situ* plate screening (Bruker). This instrument can be used to test the diffraction properties of crystals and characterize crystal symmetry and unit cell parameters directly in crystallization plates.
- Fully automated high-throughput ultraviolet and visibility crystal imaging and protein crystal monitoring system Minstrel HT UV (Rigaku). The system supports both 96-well and 24-well high throughput linbro plate formats. It can be used to monitor and control crystallization experiments.
- The PHOENIX (Art Robbins) high-throughput crystallization robot is equipped with a non-contact on-the-fly nanodispenser. The robot is capable of placing seated droplets in 96-well plates with a sample volume of only 100 nanoliters per well. It can perform an initial screening of more than 1000 crystallization conditions within 2 hours.
- Analytical ultracentrifuge Optima AUC with interference and absorption optics and analytical ultracentrifuge Beckman Coulter ProteomeLab XL-I equipped with an Aviv fluorescence detection system. Both systems can be used to determine the oligomerization state of proteins and to characterize macromolecular interactions and hydrodynamic properties.
- StepOneTM Real-Time PCR System (Applied Biosystems) can be used to find the best buffer conditions for the crystallization of your protein.
- Viscotek Dynamic Light Scattering System can be used to obtain a homogeneous oligomeric state for your protein sample by optimizing protein buffer conditions.
- The laboratory and cold rooms are equipped with high-quality optical microscopes for crystal handling, cryogenic tools, liquid nitrogen tanks, and dewars for crystal freezing and safe storage.
- Vibration-free crystallization incubators for crystal optimization can be used to incubate crystallization plates in the temperature range of 4°C to 20°C.
- 3D graphics stations equipped with stereo visualization hardware and access to the multiprocessor Linux MPI cluster HALIME. These systems can be used for data processing, structure determination, and analysis.

Usage

Users should provide liquid protein or protein complex samples with a protein concentration of 10 mg/ml or higher and purity of 95% or higher (to be verified by SDS gel and UV/Vis spectra). To remove possible aggregation products, the sample should be clarified by centrifugation (run for 30 minutes at a speed of 13,000 rpm).

For successful crystallization, it is essential that the protein or protein complex has a homogeneous oligomerization state. To maximize the chances of success for your project, it is recommended that the aggregation state of the protein or protein complex be checked in advance using one of the following techniques:

- Gel filtration
- Dynamic light scattering
- Analytical ultracentrifugation

Direct operation of the equipment by users is generally not intended. In justified exceptional cases, users can be trained. In this case, however, it must be ensured that the actual benefit is greater than the effort due to the training period. In any case, trained users must coordinate the type of samples, the planned measuring methods, and the measuring time with the laboratory management beforehand.

User groups and fees

The ZFE Structural Biochemistry is available to the following groups in graded priority and at different fees:

(1) research groups of MHH, LUH, TiHo, HZI, and research associations (e.g., SFB) with the participation of MHH

(2) Users from commercial companies

For users of group 1, no fees are charged for scientific advice and equipment sharing. The costs for consumables will be charged.

For users of group 2, individual offers will be made covering the entire effort of the measurements (full cost calculation).

Data protection information according to EU-DSGVO

When samples are sent to the ZFE Structural Biochemistry of MHH in the context of scientific collaborations or service measurements, data about you (name, official address, e-mail address, telephone number) and the type of samples are collected, recorded, stored, processed and the analysis results received are transmitted to you by e-mail (encrypted using Cryptshare).

For data protection reasons, this data processing is only possible if you, as the sender, have given your consent to this.

Processing purposes

It is also necessary to process your data for administrative purposes, for example, for billing the requested analyses, for reasons of controlling and auditing, for asserting, exercising as well as defending legal claims, etc.

Source of data

As a matter of principle, we collect the relevant data from you.

Access to your data

Only the staff of the ZFE Structural Biochemistry responsible for data processing and the administrative staff of the MHH involved in invoicing have access to your personal data.

Legal basis for data processing

The basis for allowing MHH to process your data in accordance with data protection law results from the fact that you have requested the analysis of samples sent in.

Archiving

The documentation on the samples is kept in the ZFE Structural Biochemistry for 10 years. Likewise, all electronic data, including raw and result data, are stored for 10 years. These data are available to users and can be transferred in whole or in part at any time.

Responsible body for data processing

The responsible body for data processing is the Director of the Institute of Biophysical Chemistry at Hannover Medical School. Contact via:
Hannover Medical School Institute of Biophysical Chemistry - OE 4350 Email: BiophysikalischeChemie.sekretariat@mh-hannover.de
Carl-Neuberg-Straße 1, 30625 Hannover Phone: +49 (0) 511 532-3701

Rights of individuals with regard to the processing of their personal data

Based on the EU Data Protection Regulation (DS-GVO), you are entitled to the following data subject rights, which you can assert against MHH:

- You have the right to information about the personal data stored concerning you (Art. 15 DS-GVO). If you discover that incorrect data concerning you is being processed, you may request correction or purpose-specific addition (Art. 16 DS-GVO).
- In case you notice that inaccurate data concerning your person is being processed, you may request correction or purpose-specific addition (Art. 16 DS-GVO).
- You have the right to request the deletion of your data if specific grounds for deletion exist. This is particularly the case if they are no longer necessary for the purpose for which they were originally collected or processed (Art. 17 DS-GVO).
- You have the right to restrict the processing of your data, which means that your data will not be deleted but will be marked to restrict its further processing or use (Art. 18 DS-GVO).
- You have a right to data portability (Art. 20 DS-GVO).
- In principle, you have a general right to object also to lawful data processing that is in the public interest, carried out in the exercise of official authority or based on the legitimate interest of a body (Art. 21 DS-GVO).

Complaint to the supervisory authority about data protection violations

You have the right to complain to the supervisory authority if you believe that the processing of your personal data is not lawful. The address of the supervisory authority responsible for the MHH is:

The State Commissioner for Data Protection of Lower Saxony; Prinzenstraße 5; 30159 Hannover. The contact to the MHH - Data Protection Officer is as follows:

> The Data Protection Officer - OE 0007 E-mail: Datenschutz@mh-hannover.de Carl-Neuberg-Strasse 1, 30625 Hannover Tel. +49 (0) 511 532 - 2555. Mobile +49 (0) 1761 532 - 2555

Intellectual property and publication of results

The users are the sole owners (IP) of the measurement results. Users from academia can use the information and intellectual property of ZFE Structural Biochemistry, which can be summarized under the term foreground IP, for teaching and research. The involvement of the Structural Biochemistry ZFE in the generation of data must be taken into account when publishing them. If the extent of involvement justifies co-authorship by members of the laboratory (e.g., development of methods, participation in experimental design, extensive analyses, etc.), they must be involved in the preparation of the manuscript. Any other form of participation must be listed in the Acknowledgement, e.g., with the wording: "We acknowledge the support of the Research Core Unit Structural Biochemistry at Hannover Medical School. "

Prof. Dr. Dietmar J. Manstein Hannover, den 5.08.2022