

Details

Sample Preparation and Characterization Core Facility (SPC)

The SPC core facility at EMBL Hamburg offers a pipeline from the lab bench to the beam lines', helping you to optimize and prepare samples for structural studies. Our high-throughput crystallization laboratory offers initial crystallization screens as well as customized screens for optimization of initial hits, both suitable for soluble and membrane proteins. Online observation of the plates is possible via the Crystallization Information Management System (CRIMS), which makes results available to users in real-time, along with all experimental parameters of the crystallization condition. Integration of crystallization and synchrotron data collection facilities can be implemented through automated crystal harvesting and processing. In addition, we offer assistance to perform SAXS batch measurements with near-real time outputs of macromolecular structural parameters and low-resolution solution-state structures. The biophysical platform of the SPC includes cutting-edge technologies to measure interactions and to precisely determine the stability, shape and size of different biomolecules and biomolecular assemblies identifying the most suitable biophysical techniques to answer the biological questions the researchers are trying to tackle.

Address: Notkestraße 85, Gebäude 25a
22607 Hamburg
Hamburg
Deutschland
[To website](#)

Host Institution

European Molecular Biology Laboratory (EMBL)

Notkestraße 85, Gebäude 25a
22607 Hamburg
Hamburg
Deutschland
<http://www.embl-hamburg.de/services/spc/index.html>

Centre for Structural Systems Biology (CSSB)

Notkestraße 85, Gebäude 15
22607 Hamburg
Hamburg
Deutschland
https://www.cssb-hamburg.de/facilities/index_eng.html

Scientific Domain

Primary Subjects:

- Biology

Secondary Subjects:

- Chemistry
- Physics

Category

Systems Biology/Computational Biology Facilities

Scientific Services

EMBL Hamburg has established a fully automated platform for the high-throughput crystallization of biological macromolecules in order to address a common bottleneck in x-ray crystallography. The SPC crystallisation platform offers a wide range of crystallisation screening conditions and flexible methods have been developed to adapt each step to individual project requirements. The services are available to the general user community. Our crystallisation platform supports both nanodrop crystallisation and lipidic cubic phase (LCP) crystallisation. All plates can be imaged in one of our Rockimaker 1000 imagers (4° or 19 °C) and images accessed off-site through CRIMS. The facility is well supported with two Mosquito-LCP at room temperature. Custom screens can be formulated using automated dispensing robots. Moreover, our Molecular Biophysics platform offers one of the most-well

equipped biophysical laboratories in Europe. We support users with the design, execution and data analysis of biophysical experiments aimed at the characterization of proteins, protein complexes and interactions between proteins and other types of molecules. The characterization of these structures are analysed by studying parameters such as stability, shape, folding state, aggregation tendency, homogeneity and oligomeric states. The interactions in which they are involved can be followed by measuring biophysical criteria like; specificity, kinetics, affinity, and thermodynamics.

Scientific Equipment

- Mosquito LCP crystallization robots and online follow
- CrystalDirect Automatic crystal harvester
- Scorpion Screen Formulator and Biomek automated
- Microcal VP-ITC and PEAQ-ITC
- Microscale Thermophoresis Labelled and Label Free
- nano Differential Scattering Fluorescence (nDSF)
- Circular Dichroism spectrophotometer
- Bruker Vertex 70 Fourier-transform infrared spectrophotometer
- MALDI-TOF with High Mass detector
- Biolayer Interferometry Octet RED96
- SX-20 Stopped-Flow spectrophotometer
- Dynamic Light Scattering (DLS)
- SPR T200 (Biacore)
- SAXS-batch mode
- Molecular Dynamics simulations

Keywords

- Structural Biology
- Molecular Biophysics
- Crystallization
- Stability
- Homogeneity
- Thermodynamics
- Kinetics
- Structure and Function
- Protein interactions
- Scattering
- Binding
- Complexes
- Aggregation
- Protein Folding and Unfolding
- Data Analysis

Networks

iNEXT- Discovery

<https://inext-discovery.eu/network/inext-d/home>

Instruct-ERIC

<https://instruct-eric.eu/>

Association of Resources for Biophysical Research in Europe (ARBRE-MOBIEU)

<https://arbre-mobie.eu/>

Users per annum

Internal Users: 57 (2019)

External Users in total: 177 (2019)

External Users: 112 (2019)

External Users in the EU: 67 (2019)

External Users outside of EU: 55 (2019)

