

Updates from the Centre of Molecular Structure

CF Protein Production

The Protein Production core facility provides services covering plasmid DNA constructs preparation, protein expression in *E. coli* expression systems and recombinant protein purification (affinity chromatography, ion-exchange chromatography, gel permeation chromatography, etc.). Our services also include preparation of DNA templates (in form of DNA string), small scale expression and solubility tests, production of labelled proteins in minimal media, optimization of expression and purification protocols, protein identity and purity testing and determination of protein concentration or preparation of competent cells. Customization of our standardized protocols or preparations according to your established protocols are welcome. For more information do not hesitate and contact miroslava.alblova@ibt.cas.cz. You can also directly submit your project at <https://www.ciisb.org/open-access/proposal-submission>.



CF Crystallization of Proteins and Nucleic Acids

The Crystallization CF is already routinely using the SONICC instrument (Formulatrix) in many projects. SONICC is based on the Second Harmonic Generation (SHG) and Ultraviolet Two-Photon Excited Fluorescence (UV-TPEF) in a completely automated imager to quickly image high throughput crystallization plates and positively identify protein crystals. SONICC is capable of detecting even extremely small micro and nanocrystals. This is a unique installation in our country, offered under standard screening conditions.

CF Diffraction techniques

The core facility provides services in X-ray diffraction and scattering techniques. The diffractometer D8 Venture is used to collect high resolution diffraction data mainly from protein crystals, to test diffraction quality and identify diffracting crystals in crystallization plates. Special dehydration experiments using HClab can be designed in pursue of higher diffraction quality. The latest addition is the X-ray fluorescence detector, which enables element identification. SAXSpoint 2.0 brings modern approaches to X-ray solution scattering experiments, including SEC-SAXS. This technique enables in solution size, shape and low-resolution structure determination.

CF Structural Mass Spectrometry

A new quadrupole time of flight mass spectrometer timsTOF SCP from Bruker Daltonics is now installed in the Structural Mass Spectrometry core facility of CMS. The instrument provides extremely high speed and sensitivity to tackle proteomes of single cells or post translational modifications in a few cells. The trapped ion mobility spectrometry (TIMS) device accumulates and concentrates ions of a given mass and mobility, enabling a unique increase in sensitivity and speed. The robustness and high throughput sample analysis is achieved by an Evosep One HPLC system using special tips as disposable trap columns. Besides single cell proteomics, the new mass spectrometer allows high sensitivity peptides and proteins identification and quantification.

CF Biophysical Techniques

The newly installed **Refeyn Two MP** mass photometer measures the mass of unlabeled single biomolecules in solution based on light scattering.



The instrument operates in a wide range of native buffer solutions with minimal sample consumption and can be used to study protein interactions, oligomerization and macromolecular assembly. Another new arrival – a **MicroCal PEAQ-ITC** is a highly sensitive, low volume isothermal titration calorimeter for the label-free in solution study of biomolecular interactions.





The system directly measures heat released or absorbed during biochemical binding events, from which it calculates binding affinity (KD), stoichiometry (n), enthalpy (ΔH), and entropy (ΔS) in a single experiment and can analyze weak to high affinity binders.

[Access to use the Centre of Molecular Structure](#)

CMS is a member of several research infrastructures and projects which enable our users to select different ways of accessing our services based on various criteria such as funding, project duration, or area of research. This initial selection of the best way of accessing CMS can be challenging so on the following page we would like to summarize the different modes and give you a brief overview of the differences.

If you have any questions regarding which mode of access to use, please feel free to contact us at lubica.skultetyova@ibt.cas.cz or jan.dohnalek@ibt.cas.cz

We are looking forward to meeting you in CMS,

Miroslava Alblová (Protein Production), **Tatsiana Charnavets** (Biophysical Techniques), **Olga Dzmitruk** (Biophysical Techniques), **Tereza Nepokojová** (Protein Production), **Jiří Pavlíček** (Crystallization of Proteins and Nucleic Acids), **Petr Pompach** (Structural Mass Spectrometry), **Pavla Vaňková** (Structural Mass Spectrometry), **Jan Stránský** (Diffraction Techniques), **Michal Strnad** (IT), **Lubica Škultétyová** (technician), **Magdalena Schneiderová** (admin), **Jan Dohnálek** (CMS Head)

You can realize your projects at CMS via an online application at ciisb.org/open-access/proposal-submission.

Access to the CMS techniques can be granted via the funding scheme of Instruct-ERIC as well (instruct-eric.org/submit-proposal).

Commercial subjects are also welcome to use the CMS facilities. For a listing of the offered services see ibt.cas.cz/cs/servisni-pracoviste/centrum-molekularni-struktury/#companies

Find out more information at ciisb.org, ibt.cas.cz/core-facility/CMS/, instruct-eric.org/centre/biocev/, biocev.eu/en/services/centre-of-molecular-structure.3
or contact lubica.skultetyova@ibt.cas.cz, jan.dohnalek@ibt.cas.cz

CIISB – Czech Infrastructure for Integrative Structural Biology

- Proposal submission: <https://www.ciisb.org/open-access/proposal-submission>
- Who can apply: all researchers from research institutes and universities
- Financing: access is paid by user, prices are partially covered by MEYS funding
- CMS core facilities: all facilities
- Duration of access: accepted projects are valid for 1 year; it depends on the user and facility availability how many times or how often access will be used



Instruct-ERIC – The European Research Infrastructure Consortium for Structural Biology Research

- Proposal submission: <https://instruct-eric.org/submit-proposal/?t=instructeric>
- Who can apply: all researchers
- Financing: access for users from Instruct-ERIC member countries is free of charge; travel costs are also reimbursed
- CMS core facilities: all facilities
- Duration of access: access is funded based on project needs, typically in units of days
- Instruct also announces calls for transnational 3-6 month internships where travel costs are reimbursed and additional funding for consumables can be obtained



MOSBRI – Molecular-Scale Biophysics Research Infrastructure

- Proposal submission: <https://www.mosbri.eu/apply-for-tna/>
- Who can apply: researchers from EU and associated countries applying to an abroad facility
- Financing: access is free of charge for user; user receives reimbursements for travel costs
- CMS core facilities: Biophysical Techniques; Crystallization of Proteins and Nucleic Acids; Diffraction Techniques; Optical Tweezers
- Duration of access: access is funded based on project needs, typically in units of days/weeks



ISIDORe – European large-scale research infrastructure for epidemic-prone pathogens

- Proposal submission: <https://isidore-project.eu/calls/>
- Who can apply: researchers from EU and associated countries applying to an abroad facility; projects focused on infectious diseases
- Financing: access is free of charge for user
- CMS core facilities: all facilities
- Duration of access: access is funded based on project needs, typically in units of days

