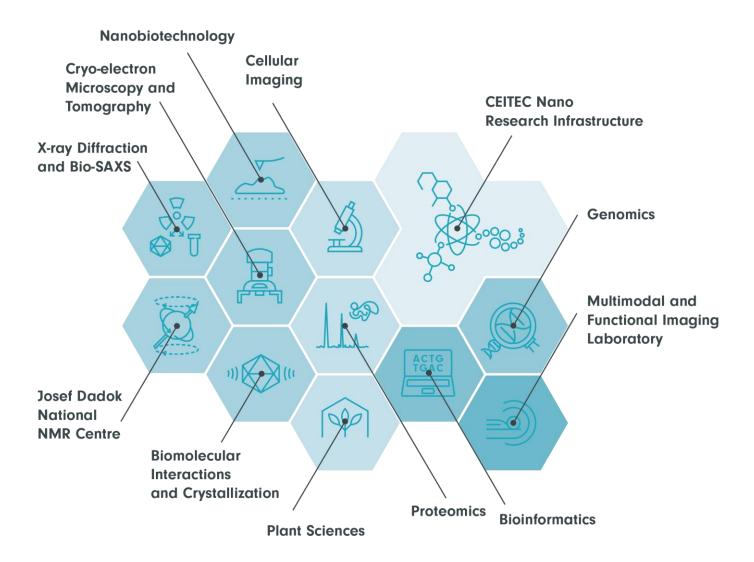


CEITEC MU Core Facilities

The Core Facilities of CEITEC Masaryk University are scientifical-technological units equipped with **state-of-the-art instrumentation** that is available to researchers from a range of fields, especially in **life sciences**. The aim is to provide the infrastructure for academic, as well as commercial users from the Czech Republic and abroad to allow them to effectively carry out their scientific projects, with **support from experts**.





Bioinformatics Core Facility

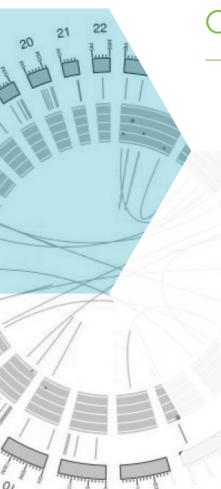
The Bioinformatics Core Facility at CEITEC provides expert bioinformatics analysis and consulting to support research activities. We develop and apply computational tools and methods to biological or biomedical research data including acquisition, storage, organization, analysis, or visualization of the data. The facility maintains standardized data processing pipelines for the high-throughput data analyses (e.g., expression analysis, variant calling, protein-DNA/RNA interactions). We establish best practices for high-throughput data analysis in a production environment and develop custom solutions to assist research with data analysis and biological interpretation. We are also able to provide long-term support for extensive and complex experiments. The core serves as a central point of contact and venue for collaboration with bioinformatics and computational biology specialists. As part of our educational responsibilities, we provide training and consultations in bioinformatics, biostatistics, and experimental design. We organize and collaborate on workshops and bioinformatics courses. The facility offers services to researchers both within and outside CEITEC on both grant-funded and chargeback-based projects for analysis of large-scale biological datasets produced by high-throughput experiments.



Our facility offers high-throughput data analysis services to support the research activities. The facility maintains and implements standardized data processing pipelines for the large-scale biological data analysis. Our custom-made workflow management system allows us to provide reproducible and scalable data analyses with a quick turnout. Detailed downstream analysis of the results and assistance with the results interpretation can be provided upon individual requests. If your experiment requires a specialized and tailored custom pipeline, we can help with the implementation and development.

We will meet with you to discuss your needs free of charge. We are able to help you in all the stages of your project: before grant/project submission, after your project was approved before you start the analysis of your data or even if you have already started analyzing your data and need help to troubleshoot any ongoing procedure.

We can provide training for the usage of our standard pipelines in both Linux environment as well as the friendly graphical interface of our Galaxy server. We closely collaborate with Pls, researchers and graduate students on their projects and help them to get the most out of their data.





— Our facility provides following data analysis solutions for:

- Gene expression studies (RNA-Seq,smallRNA-Seq)
- DNA variation single-nucleotide variant identification (SNP/InDel), structural variant (SV) and copy-number variation (CNV) analysis
- Protein-DNA/RNA interactions (ChIP-Seq, CLIP-Seq)
- Genome and transcriptome assembly
- Customized and project-tailored workflows and pipelines

— In addition, we provide following services:

- Downstream bioinformatics support, statistical analysis and creation of publication-ready visualizations
- Teaching, training and consultation in high-throughput bioinformatics, experimental design and statistics
- Access to bioinformatics software and computational resources



02 Overview of visualisations used for somatic and copy number variant effect estimation.

03 Circo plot of chromosomal rearrangements identified in sequenced tumor sample.

Contact

CEITEC Masaryk University

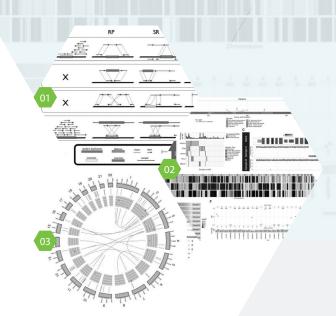
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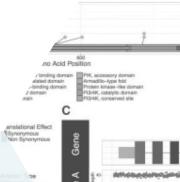
www.ceitec.eu/bioinformatics













Core Facility Biomolecular Interactions and Crystallization

The core facility provides services leading to biophysical and structural characterization of biomolecules and to study (bio)molecular interactions. It is equipped with the instrumentation to screen for crystallization conditions of biomolecules and their complexes, for basic biophysical characterization of the molecules (analytical ultracentrifugation, dynamic light scattering, CD spectroscopy, differential scanning calorimetry, differential scanning fluorimetry), and to study thermodynamics and/or kinetics of interactions (isothermal titration calorimetry, surface plasmon resonance, microscale thermophoresis, analytical ultracentrifugation).

Case Studies

Bees in danger – Know the enemy
 Detailed 3D-structure of bee virus

Researchers from the CEITEC Structural virology group investigated the structure of Israeli acute bee paralysis virus. Using a single batch of the isolated virus and screening of 1800 different crystallization conditions in CF BIC facility, they were able to produce two different forms of crystals – one containing the full viral particle and one composed of capsid protomers. Solving of both structures depicted uniqueness of this virus among the structural family and pointed out the key features for potential antivirotic compound design.

 Entrap pathogens into self-assembled net Clustering of lectins from pathogens by multivalent inhibitors

The Glycobiochemistry Research group from CEITEC in collaboration with Debrecen University in Hungary and help of CF BIC studied multivalent inhibitors of lectins – proteins that enable binding of pathogens to the host tissues. Combining ITC and SPR, they analysed the binding properties of inhibitors and lectins. Using analytical ultracentrifugation, they clearly proved the ability of inhibitors to crosslink, cluster and aggregate these proteins. Increased avidity through multivalency makes these inhibitors a promising target for a drug development.

Services Provided

We will help you with setting up experiments involving any SERVICE listed bellow. In addition, measurements using our EQUIPMENT are available within CF BIC.

— Analytical ultracentrifugation services:

Analytical ultracentrifugation can be used for the characterization of (bio)molecules and their interactions in a solution. It can be used to determine the degree of sample heterogeneity, the shape and the molar mass of the particle, and the affinity and stoichiometry of the binding. Two complementary techniques (sedimentation velocity and sedimentation equilibrium) are offered by CF BIC as a service.





— Crystallization services:

Crystallization is the crucial step for X-ray diffraction analysis to obtain the 3D structure of biomacromolecules and their complexes. We offer almost 3000 crystallization conditions in various set-ups, automated plate storage and imaging for regular plate inspection with online access to the data and wide range of optimization approaches (temperature, additives, detergents, heavy atom derivatization, etc).

— Calorimetric services:

Calorimetry allows to obtain a complete thermodynamic profile of interaction in a single experiment. Numerous set-ups can be chosen, including possibility to use automated instrument (Auto-iTC200) or manual VP-ITC.

Equipment

Interaction and stability studies

Biacore T200 (SPR), Auto-iTC200, Monolith NT.115 (MST), VP-DSC, VP-ITC, Prometheus NT.48 (DSF), ProteomeLab XL-I analytical ultracentrifuge, CD Jasco J-815, Delsa Max Core and Wyatt DLS Plate reader

01 Crystallization robotics

high speed set-up of crystallization plates due to combination of 96-head pipetting and non-contact nanodispensing of volumes down to 100 nl.

02 Surface Plasmon Resonance

monitoring of interaction in real time with one binding partner immobilized on the surface of sensor chip and the other one in solution.

03 Microscale Thermophoresis

measuring of changes in mobility of molecules in microscopic temperature gradient, induced by the ligand binding.

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Crystallization techniques

Mosquito, Phoenix, Dragonfly, automatic inspection and storage Minstrel HT UV + Gallery HT (4°C and 20°C), Centeo TG40















Core Facility Cellular Imaging

Core Facility Cellular Imaging (CELLIM) provides services in the area of light microscopy and offers comprehensive expertize related to sample preparation, image acquisition and data analysis. We also provide access to widefiled and confocal microscopes and individual training of users in operation of microscopes, image acquisition and data analysis.

Case Studies

Live cell imaging is quickly becoming standard technique for addressing variety of questions in cell and molecular biology. Although this technique is well established for most of the regular tissue culture cells and lineages, challenges are still remaining in application of live cell imaging for studies on primary cells or even tissues or organoids. By organizing workshop focused on methods used in imaging of live specimen we would like to convey recently accumulated knowledge in the field to researchers and students, and help them to improve their experiments.





- Access to widefiled and confocal microscopes
- Access to image analysis tools
- Project design and assistance in planning of experiments
- Training of users in sample preparation, image acquisition and data analysis

Equipment

— Equipment currently available

- Variety of laser scanning confocal microscopes inverted and upright, with different combinations of lasers and detectors, including Airyscan Fast module
- Lightsheet microscope
- Wide-field fluorescence microscopes
- Histological microscopes
- Stereomicroscope with fluorescence
- Computer workstations with image analysis software IMARIS, ZEN, FIJI,
 Cell Profiler, Image

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Core Facility Cryo-electron Microscopy and Tomography

Electron cryo-microscopy is a method for imaging frozen-hydrated biological specimens at cryogenic temperatures by electron microscopy. Specimen is retained in near-native state without a need of additional chemical fixation or staining allowing structural studies of cellular structures, protein or protein-RNA/DNA complexes, and viruses at molecular resolution. Thus, electron cryo-microscopy is becoming an invalueable tool for both structural and cellular biology research.

Expertise

Single particle electron cryo-microscopy

Single particle electron cryo-microscopy enables determination of near-atomic resolution structures of purified mono-dispersed protein or protein-RNA/DNA complexes or viruses. A set of micrographs containing 2D projections of different but structurally similar entities is acquired in automated manner and subsequently used for reconstruction of three-dimensional model. The technique is applicable to proteins and their complexes large than ~200 kDa in size. Utilizing phase plate technology, structures of <100 kDa complexes can be obtained from single particle data.



Electron cryo-tomography is the only method to address structural characterization of pleiomoprhic objects in close-native state. Specimen is rotated and imaged in electron microscope and the data are back projected to create a three-dimensional model of studied object. The method thus enables structural studies of protein complexes, virus, and organelles within the context of the cell under the near-native conditions.

Focused ion beam micro-machining

Electron cryo-tomography studies of proteins or viruses within the context of the cell are often hampered by cell dimensions which prohibits electron penetration especially in the case of large eukaryotic cells. Focused ion beam micro-machining is employed to perform precise ablation of parts of cellular content to produce a thin cellular cross-section which is suitable for the purposes of structural biology studies *in situ* by electron cryo-tomography.





- specimen vitrification
- TEM/cryo-TEM imaging
- SEM imaging
- automated single particle electron cryomicroscopy data collection
- electron cryo-tomography
- focused ion beam micro-machining of vitrified biological specimen

Equipment

- Titan Krios cryo-TEM
- Talos Arctica cryo-TEM
- Tecnai F20 cryo-TEM
- Versa 3D cryo-FIB/SEM
- Vitrobot IV

01 Titan Krios

high-end transmission electron microscope equipped with phase plate, Falcon3 and post-GIF K2 direct electron detectors

02 Talos Arctica

high-end tranmission electron microscope equipped with Falcon3 direct electron detector

03 Tecnai F20

transmission electron microscope for cryo-electron microscopy

04 Versa 3D

FIB/SEM microscope with Quorum PP3010T preparation system

05 Vitrobot IV

vitrification robot

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Core Facility Genomics

Core Facility Genomics (CFG) offers genomic analysis service and access to up-to-date genomic instrumentation. Main technologies available at the facility are massively parallel sequencing (Illumina), single molecule nanopore sequencing, microarrays and high-throughput & digital PCR. Through cooperation with CEITEC Center of Molecular Medicine it is possible to access other instrumentation – cell sorter, flow cytometers or Laser Capture Microdissection.

Case Studies

— Parasitology – Worms, are you there?

Screening for specific nematoda parasites in primates. Researchers from Veterinary university Brno (Dept. of Parasitology) and Czech Academy of Science (Institute of Vertebrate Biology) collected in central Africa gorilla, bonobo and human fecal samples. In cooperation with CF Genomics they employed NGS based metagenomic method for analysis of several DNA markers. This method involves PCR amplification of marker sequences (16S for bacteria, 18S, ITS and Cytochrome C oxidase for eukaryota), sample barcoding (up to 384 samples) and sequencing on Illumina MiSeq.

Inherited cancer – Unwanted heritage

Screening for disease associated genes in families with high incidence of early-onset cancer. Researchers from CEITEC Medical genomics are currently running a project that aims to identify possible causative genes in families suspected of hereditary (hematology) cancer. In this case whole exome sequencing of both affected and unaffected family members was selected and found genetic variants are analyzed in conjunction with pedigree.

Cancer cells – Evolution in real time

Ultrasensitive screening for subclonal somatic variants. Researchers from CEITEC Medical genomics in cooperation with CF Genomics established method for detecting subclonal mutations in TP53 gene. Impaired function of the TP53 gene has huge negative impact on the prognosis of Chronic lymphocytic leukemia (CLL). Deep sequencing using massively parallel sequencers is currently the only available method to screen whole gene for mutations present in only a very small fraction of tumor cells. It is important to monitor mutated subclones as they may have different response to therapy and may become refractory to immuno-chemotherapy.





We will help you with experiments involving any SERVICE or METHODOLOGY listed bellow. For NGS we can help you with library preparation and sequencing or for standardized applications like RNA-seq or exome sequencing we can prepare the libraries ourselves. We also offer complementary services to library preparation - sample/library quality control or library size selection. You can also use software and hardware installed in core facility to analyze NGS data.

- NextGen Sequencing on Illumina NextSeq and MiSeq and Oxford Nanopore MinION
- Library QC electrophoresis, qPCR
- Library preparation RNA-seq, whole exome sequencing

01 PCR lab

We have capacity to allow users perform many simultaneous experiments.

02 Illumina MiSeq

One of our sequencers, can be used for almost all NGS experiments, for others we have Illumina NextSeq or Oxford Nanopore MINIon.

03 QuantStudio 12k

We operate several qPCR instruments including ThermoFisher QuantStudio 12k, Roche LightCycler 480 or Qiagen RotorGene Q5.

04 QuantStudio 12k

Most of our instrumentation is 384-well compatible.

Equipment

- Illumina NextSeq and MiSeq
- Pippin Prep, TapeStation
- qPCR Roche, ThermoFisher, Wafergen

Contact

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www.ceitec.eu/genomics-core-facility













Core Facility Josef Dadok National NMR Centre

NMR (Nuclear Magnetic Resonance) spectroscopy is a key technology in chemistry and related disciplines. It allows detailed investigation of molecular structure and dynamics at the atomic level, both in solutions and in the solid state. The high-end instrumentation and a team of experienced researchers ensure expert services, user training, and a cost-effective use of resources both for internal and external users. Benefits include access to state-of-the-art high-field NMR instrumentation and support in processing, analysis and interpretation of the experimental data. The facility also offers training enabling non-specialists to develop the necessary skills. Support from national and European programs is available for academic users to cover the cost of the measurement. To the commercial users, the services are offered for a fee. The Centre is named after Professor Josef Dadok, a pioneer of nuclear magnetic resonance spectroscopy in Czechoslovakia and an important figure in the NMR instrumentation and methodology worldwide.

Case Studies

Josef Dadok National NMR Centre offers analyses using NMR spectroscopy. We are equipped with spectrometers in the range of proton frequencies from 500 MHz to 950 MHz. Spectra of liquid as well as solid-state samples can be measured. Our instrumentation is ideally suited to the studies of structure, dynamics and interactions of biomolecules, i.e. proteins, nucleic acids and carbohydrates. However, the spectrometers are flexible enough to cover most research needs in organic and inorganic chemistry, material science, biochemistry, biology and biophysics. Qualified users can access the instrumentation independently and perform their own measurements.

Services Provided

NMR structural analysis in Liquids

Complete 3D structure of compounds can be solved. However, the procedure may be laborious. Ask for details if you are interested.

Biomolecular structure and dynamics by NMR

Proteins of up to 200 amino acids, nucleic acids up to 50 nucleotides can be studied. For solving 3D structures, isotope labeling with ¹⁵N and ¹³C is always needed for proteins and for oligonucleotides larger that approximately 30 nucleotides.

NMR analysis in solid state

The application of solid-state NMR techniques usually arises due to specific interest in the physics of solid state, including packing effects and polymorphic structures. We routinely measure 1D CP MAS spectra of ¹³C, ¹⁵N, ²⁷Al, ²⁹Si, and ³¹P.





Compound identification

The NMR spectrum reflects connection between atoms in the molecule, which makes the method ideally suited for identification of compounds.

Quality control

NMR is a suitable method for detecting impurities such as solvent residues and it is widely used in the pharmaceutical, medical, and food industries for quality control. Our laboratory is equipped for measuring of a wide range of elements.

Equipment

- 950 MHz NMR spectrometer Bruker Avance III HD for high resolution spectroscopy in liquids,
 5 mm triple-resonance (¹H-¹³C-¹⁵N) inverse cryoprobe
- 850 MHz NMR spectrometer Bruker Avance III HD for high resolution spectroscopy in liquids, 5 mm triple-resonance ($^{1}H/^{19}F-^{13}C-^{15}N$) inverse cryoprobe
- 700 MHz NMR spectrometer Bruker Avance III HD for biomolecular applications,
 5 mm triple-resonance (¹H-¹³C-¹⁵N) cryoprobe optimized for ¹³C detection
- 700 MHz NMR spectrometer Bruker Avance III HD for multinuclear applications in liquids and solids
- 600 MHz NMR spectrometer Bruker Avance III HD for high resolution spectroscopy in liquids, quadruple-resonance (¹H-³¹P-¹³C-¹⁵N) inverse cryoprobe
- 500 MHz NMR spectrometer Bruker Avance Neo

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- **01** 850 MHz NMR spectrometer with cryoprobe
- ${\bf 02}$ Operator room with a view of the laboratory with 600 MHz and 700 MHz NMR spectrometers
- **03** Sample ready for NMR measurement













Core Facility Multimodal And Functional Imaging Laboratory

MAFIL is shared CEITEC laboratory providing advanced imaging services for CEITEC research teams as well as external users. Basic techniques provided are human MR imaging and MR spectroscopy in high field (3T) and electrophysiological techniques (high density EEG, simultaneous measurements of electrophysiology and MRI). MAFIL expertise is mainly focused on functional and structural mapping of human brain because this core-facility was designed primarily to support neuroscience research.

Case Studies

 CoBeN – Novel Network-Based Approaches for Studying Cognitive Dysfunction in Behavioural Neurology

The aim is to search for new possibilities of early detection and more accurate diagnostics of neurodegenerative illnesses such as Alzheimer's or Parkinson's diseases and to verify the efficiency of individualized therapy methods. The project is realized in cooperation with our colleagues from Hungary (Szeged university) and USA (Arizona University). The project contain MR measurements including detailed structural images, several fMRI tasks (focused on reading, writing and speaking), resting fMRI measurement and diffusion measurement.

An evaluation of empathy induction within driver-rehabilitation programs

The goal of the project is finding better understanding of the empathy capability of different groups of drivers and to identify the possibilities of modifying social behaviour in the drivers' population with a complicated record of their driving practice. The project utilises the so-called "hyperscanning" - the brain activity is scanned simultaneously in two interacting individuals (the measurements are taken simultaneously at two MR devices). Thus, neurophysiology of socio-emotional behaviour is analysed in real time interactions.

Neurologic and psychological markers of stress/resistance in the survivors of the holocaust and their descendants

This three-generation study is a research project aimed at investigating the psychological, neurobiological and genetic factors of strong stress in the survivors of the Shoah (holocaust) and finding an association between them. Another goal is to reveal mechanisms of trans-generation transfers of biomarkers by which chronic stress affects the lives of the second and third generations compared to control subjects of corresponding age, gender and education.

fMRI neurofeeback for emotion regulation training

The project examines the effects of real-time fMRI neurofeedback (rt-fMRI-NF) in emotion regulation training. rt-fMRI-NF is an innovative method for intentional brain regulation training which has been already successfully used for reduction of many psychiatric and neurological symptoms. rt-fMRI-NF has not been previously used in the Czech Republic. The project includes implementation of the method, optimization of the method by comparison of different methods for real-time BOLD signal extraction and examination of rt-fMRI-NF effectivity for emotion regulation training in patients with various mental disorders which share emotion regulation deficit.





Services and Expertises Provided

- Human MR imaging in high field (3T) with focus on neuroimaging (anatomical, functional, diffusion and perfusion imaging and MR spectroscopy)
- Hyperscanning (two MR scanners used for simultaneous fMRI measurement of two competing or cooperating subjects)
- Neurofeedback (biofeedback based on real-time fMRI processing and evaluation)
- Human electrophysiological studies including neuromodulation
- Simulatneous recording of MR and electrophysiology
- Various types of data processing

Equipment

- Two whole-body human 3T MR scanners (Siemens Prisma 3T)
- 256-channel MR compatible EEG (EGI GES 400 MR) + other MR compatible systems for simultaneous EEG/ExG recordings
- Specialized hardware for stimulation and response recording inside or outside the MRI
- rTMS with frameless stereotaxy for noninvasive brain stimulation + MR compatible tDCS/tACS device
- MR compatible Eye-tracking system

01 MRI scanning room

3T Siemens Prisma MR scanner with participant prepared for functional MRI study.

02 MRI control room

Siemens MR console, stimulation PC and hardware for recording of physiological signals.

03 rTMS lab

Alien technik DuoMag XT-100 system for guided rTMS brain stimuation.

04 EEG lab

High-density EEG cap (256 channels) for EGI GES 400 MR compatible EEG sytem

Contact

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www.ceitec.eu/mafil















Core Facility Nanobiotechnology

Scanning probe microscopies for imaging of biological samples - tissue slices, cells, single biomolecules as nucleic acids and proteins. Studies of affinity interactions at the molecular level. Biomechanical mapping and atomic force spectroscopy. Ink-jet depositions and nanoparticles as labels in bioassays.

Case Studies

Mechanical properties (stiffness, hardness, elasticity) are the basic characteristics of all samples, including living cells, molecules and biomaterials. Change of stiffness is often related to a change of properties. In case of living cells change of mechanical properties may show a significant difference between healthy and abnormal cells – e.g. healthy vs. dystrophic cells, or metastatic and non-metastatic cancer cells. Change of stiffness on a molecular level may bring an interesting information about changes in its conformation, caused for example by interaction with other molecules. We found an interesting connection between our facility (CEITEC MU) equipped with AFM microscopes and advanced microscopy facility in VBCF Vienna, where so called Brillouin microscopes are developed. Both technologies provide information about mechanical properties of samples, certain advantages and disadvantages are associated with both techniques. Correlation of results and trans calibration of instruments would be useful for both research facilities, potential users would benefit from it. Agarose gels of different agarose content (0.25 to 3%) were chosen as a model sample for comparative study of both methodologies. After successful correlation, more complex samples such as 3D biomaterials (hydrogels) or living cells should be studied.

Services Provided

High resolution imaging and nanomechanical mapping (force distance curves) of living cells under nearly physiological conditions (37 °C, 5% CO₂). Biomaterials and other solid surfaces can be characterized, too. Topography images and/or maps of Young's modulus (stiffness maps) will be provided to users as a result of the measurements obtained after mathematical processing of force distance curves.





Equipment

- BioAFM: JPK NanoWizard 3 including ForceRobot head
- Fast speed AFM: Bruker Dimension FastScan
- NTMDT Ntegra Vita, Solver Next

01 BioAFM: JPK NanoWizard 3

Imaging and nanomechanical characterization of bioobjects (biomolecules, bacteria, cells) under nearly physiological conditions (Petri dish heater, CO_2 chamber). Combination with optical/fluorescence/confocal imaging – overlay images. Automatic performance of interaction studies (ForceRobot). Batch processing of force distance curves (force maps) – providing maps of samples surface elasticity (Young's modulus maps).

02 High speed AFM: Bruker Dimension FastScan

High speed, high resolution imaging of individual molecules and nanoobjects – with sub nanometer resolution, rate up to 1 frame per second. Easy to use software environment, user support by ScanAsyst software feature – helps with hardware setting during preparation and measurement. Quantitative imaging provides maps of surface elasticity with high resolution and acquisition rate.

03 NTMDT Solver, Next

Standard AFM microscopes for solid phase imaging under laboratory atmosphere with nanometer resolution. Solver Next – semiautomatic measurements.

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Plant Sciences Core Facility

Plant Sciences Core Facility is an open CEITEC laboratory providing access to the research infrastructure for basic plant growth, environmental simulation and phenotyping analyses. The core facility operates 15 fully controlled walk-in growth chambers (phytotrons) and 10 greenhouses to provide defined environment for controlled plant growing. It serves as a focal point for broad-based cutting-edge biological research.

Case Studies

— Plant Sciences Core Facility is an open CEITEC laboratory providing access to the research infrastructure for basic plant growth, environmental simulation and phenotyping analyses.

— Genome evolution across the plant kingdom

Our growth chambers are used by researchers from the Martin Lysak lab in CEITEC who carrying out research in the field of comparative and evolutionary plant cytogenetics to get new insights into the mechanisms and constraints of chromosome and karyotype evolution in plants, and to amalgamate comparative plant cytogenetics, genomics and phylogenetics.

Telomeres in chromosome stability and plant speciation

The core facility infrastructure help researchers from the Jiri Fajkus and Karel Riha labs of the Mendel Center for Plant Genomics and Proteomics in CEITEC to run projects in the field of telomere biology, chromatin structure and epigenetics. Using unique features of plant systems (namely their high developmental plasticity), and their comparison to yeast or animal models, the aim is to characterise pathways involved in control of chromosome stability and distinguish between specific and general mechanisms involved. Outcomes of the studies (e.g., understanding mechanisms contributing to genome stability, aging or adaptation to changing environmental conditions) can be applied in agriculture, biotechnologies or medicine.

Molecular mechanisms underlying the regulation of plant development by plant hormones

We provide services to researchers investigated hormonal signaling mechanisms in plants: Jan Hejatko lab, Helene Robert Boisivon lab and Tomasz Nodzynski lab of CEITEC MU. Plant hormones, particularly auxins and cytokinins were found to be major regulators of intrinsic developmental programs associated with changes of differentiation status of plant cells and tissues. Identification of basic molecular principles involved in the regulation of plant cell division and differentiation will provide developmental model useful in the comparative biology approaches and identification of corresponding regulatory and developmental events even in non-plant systems.



Services and Methodologies Provided

The Core Facility provides academic community with access to advanced plant growth technologies and highly trained staff. We operate 15 fully controlled walk-in growth chambers (phytotrons) and 10 greenhouses to provide defined environment for controlled plant growing to conduct many types of controlled environment experiments, from the simplest to the most complex. We are able to control: temperature, humidity, light intensity and light quality, day and night length. For optimum plant growth light-emitting diodes (LEDs) as a sole light source are used. Thus provides excellent spectral quality with high irradiance for plant physiology applications. In some chambers the different light wavelengths are possible to combine: UV_{365,385}, blue_{400,450}, green₅₂₅, amber₅₉₀, red₆₆₅ and far-red₇₃₀. We also have chambers where different gas conditions (e.g. ethylene and CO₂) can be adjusted.

Equipment

• Phytotrons (walk-in growth chambers with open shelves or closed cultivation banks)

Greenhouses

• Small growth chambers (Percival, AlgaeTron)

01 Walk-in plant growth chamber (PSI) with open shelves.

02 Greenhouse chamber enable maintaining controlled growing conditions of temperature and humidity.

03 Walk-in plant growth chamber (PSI) with closed cultivation banks serve for precisely controlled plant cultivation and comparison studies.

04 Plants in closed growth bank grown under the high light stress.

Contact

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www.ceitec.eu/plant-sciences













Proteomics Core Facility

The core facility provides the academic and other entities with access to advanced proteomic technologies based on shared resources and the know-how of highly trained staff. Effective utilization of the state-of-the-art mass spectrometric instrumentation promotes understanding proteome complexity according to the demands of research community. Thus, the Core Facility is involved in broad range of projects requiring protein characterisation covering fields of biochemistry, molecular and structural biology, human and veterinary medicine, microbiology, plant, agriculture and food sciences.

Case Studies

Deeper insight in Wnt signaling

What signaling is involved in the embryonic development and homeostasis and its deregulation causes serious health disorders. Thus, better understanding of related molecular mechanisms will have impact on treatment of these disorders. Researchers from the Faculty of Science, Masaryk University study What signaling pathways, with special focus on Dishevelled (DVL) proteins, which are important signal integrators in the What pathway. In this study, where our core facility characterized DVL phosphorylation status, they revealed novel function of DVL that creates a mechanistic basis for the novel crosstalk between What signaling pathways and the centrosomal cycle. [Cervenka et al., PNAS, 113 (2016), 9304-9309]

Mystery of plant reproduction

Cell-cell communication plays a crucial role in male–female recognition during plant sexual reproduction. Peptides secreted from the female reproductive tissues guide pollen tubes towards ovules for fertilization. Researchers from the Institute of Experimental Botany, Czech Academy of Sciences in Prague in cooperation with our facility performed genome-wide quantitative analysis of a tobacco pistil-stimulated pollen tube secretome. In this pioneering study, first at this scale, we identified hundreds of novel genome-wide pollen tube-secreted proteins with potential functions in pollen tube guidance towards ovules extending our knowledge about the respective molecular mechanisms. [Hafidh et al., Genome Biology, (2016) 17:81]

- Profiling of barley varieties for beer production

The identity and purity of malting barley varieties is one of key factors in beer production. Our core facility participated in development of MALDI-TOF MS profiling method of barley grains which represents simpler and faster alternative to currently used SDS-PAGE technique for assessment of malting barley varieties. [Šedo et al., Food Chemistry, 206 (2016) 124-130]





We provide general proteomics services based on utilization of mass spectrometry in full service mode. Our expertise covers all steps of proteomic analysis: protein isolation from different types of samples (cells, tissues, membranes, plants, food etc.), variety of sample preparation procedures, enrichment techniques for particular types of PTMs, separation or fractionation of proteins or peptides using electrophoretic or liquid chromatographic techniques, different types of MS analyses and basic data processing which enables understandable reporting of results to users.

We provide consultations (e.g. planning of proteomic experiments) and participate in training of students.

Our services might be divided into four main groups:

- Intact mass analyses
- Protein identification
- Characterization of protein modifications
- Protein quantification



We are comprehensively equipped for processing of protein samples, including instrumentation for sample preparation, electrophoretic and chromatographic separation of proteins and peptides. However, our key instrumentation is mass spectrometers. At present, we operate:

- LC-MS/MS Orbitrap Fusion Lumos
- LC-MS/MS Orbitrap Elite
- LC-MS/MS Impact II
- MALDI-MS/MS Ultraflextreme

Contact

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02 LC-MS/MS - Orbitrap Elite

03 LC-MS/MS - Impact II

04 MALDI-MS/MS - Ultraflextreme















Core Facility

X-Ray Diffraction and Bio-SAXS

X-ray Diffraction and Bio-SAXS Core Facility is equipped with top-class instruments for diffraction experiments with single crystal samples focused on the determination of the 3-D structure of (macro) molecules down to atomic resolution and for small angle X-ray scattering (SAXS) experiments with isotropically scattering samples focused on determination of the shape and size of macromolecules or nanoparticles. The range of applicable molecular mass for diffraction methods: from 100 up to 1000000, where the lower value covers molecules significant for nanotechnology, materials science or pharmacology and the upper limit covers biomacromolecules such as nucleic acids, proteins and their complexes. The range of applicable particle sizes for SAXS: from 2 to 100 nm.

Case Studies

- The diffraction of X-rays in single crystal samples is the most important and if an appropriate crystalline sample is available also the fastest methodology currently available for the determination of the atomic structures of molecules and/or macromolecules and their complexes. The range of applicable molecular mass for diffraction methods: from a few hundreds up to million, where the lower value covers molecules significant for nanotechnology, materials science or pharmacology and the upper limit covers biomacromolecules such as nucleic acids, proteins and their complexes.
- On the other hand, SAXS is a technique capable of determining structural characteristics such as mono dispersity or aggregation, oligomeric state, low resolution three-dimensional shape or even quaternary structure not from a crystal but from a solution of (bio) macromolecules. Range of applicable (nano) particle sizes for SAXS: from 2 to 100 nm.





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 - diffraction experiments with single crystal samples focused on the determination of the 3-D structure of (macro) molecules down to atomic resolution
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02 universal, dual wavelength (Mo-K₂ and Cu-K₂) diffractometer

03 SAXS camera for small angle X-ray scattering from solutions of biological macromolecules

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