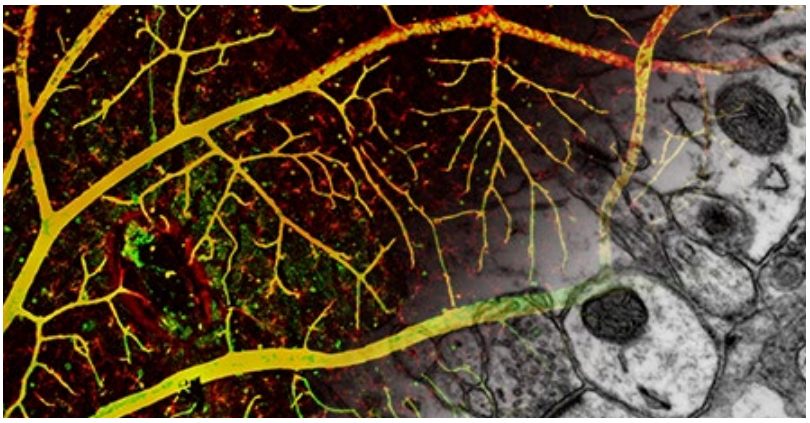
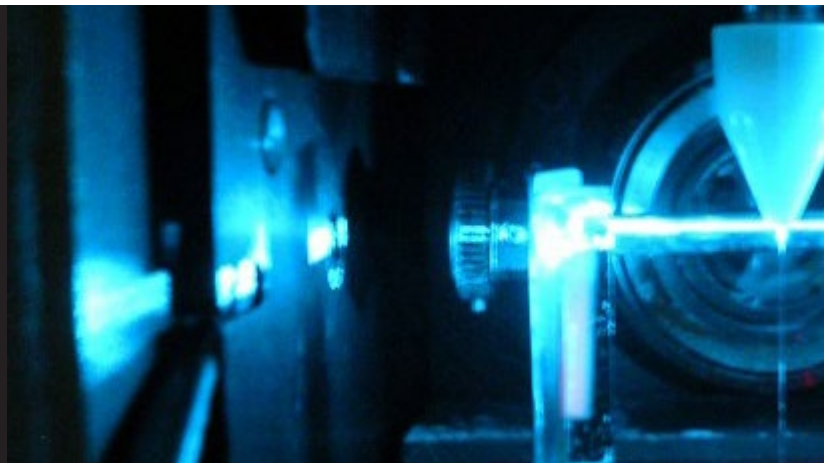
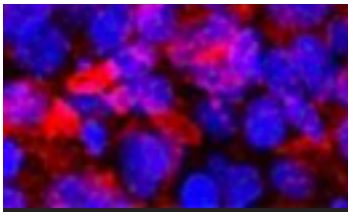
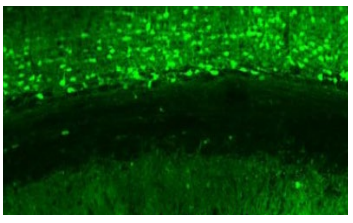
Bonn Technology Campus

Life Sciences





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Handbook

May 2024

UNIVERSITÄT BONN
BTC LIFE SCIENCES
UNIVERSITÄT BONN ukb universitäts klinikumbonn
MEDIZINISCHE FAKULTÄT

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UNIVERSITÄT BONN

BTC LIFE SCIENCES

CORE FACILITIES

UNIVERSITÄT BONN ukb universitätsklinikumbonn

MEDIZINISCHE FAKULTÄT

What is a Core Facility...

Many, if not most of the research in life science depends on the availability of and access to resources, like advanced technologies, databases, sophisticated instrumentation, and the expertise for proper operation. The interdisciplinary approach to address current topics in life science needs interaction, that should not be hampered by technical, scientific nor institutional boundaries. The complexity of operation has therefore promoted the aggregation of these technologies into core facilities, that are at the heart of a Life Science Technology Campus here in Bonn.

Core Facilities provide all researchers access to state of the art instrumentation and assure an easy and structured way to do so. However, cutting edge instrumentation does not guarantee high quality research. Adequate quality controls, system performance tracking, experience with the experimental methods as well as assistance in data interpretation are therefore indispensable components of a Core Facility. Consulting and training is important for regular as well as novice users and the expertise of the resource staff is essential for that.

Shared Resources usually have a professional management, user guide lines, access policies and a cost recovery model to ensure they continue to meet the needs of their users.

Core Facilities Business and Operations Coordinator

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... and what is it good for

- Core Facilities provide all researchers access to state of the art instrumentation and methods and assure an easy and structured way to do so. However, cutting edge instrumentation does not guarantee high quality research. Adequate quality controls, system performance tracking, experience with the methods as well as assistance in experimental setup and data interpretation are indispensable components of a Core Facility.
- It is therefore not all about the number of lasers that you have on the machines or the number of base pairs that you can sequence at a given time. It is about people who work in the Facility. What you could or what you should expect from a Facility is people, or, better, experts, that you can talk to and that will listen to you. People that will help you from your idea through your experiments all the way to your publication or next grant proposal.
- They will take care that you're not starting your project with an error that they have seen many others make before, and they will stay at your side to help with time management. They care about the instrumentation and will provide you with all the tools that you need to do your experiments, so that you can focus on your research. And it doesn't matter if you are a PhD student or a PI with a European Consolidator Grant.
- Despite the fact that Core Facilities are already established within the faculty, there is a lack of awareness regarding the full potential of currently available resources. The intention of this handbook is to increase the visibility of resources and promote the communication among Core Facilities and their prospective users.
- Enough said about the concept of the Core Facilities at the medical faculty. Enjoy reading about the methods and instrumentation in the Core Facilities and may good ideas come along.

KWI Koordinationsstelle wissenschaftliche Infrastruktur

BTC LIFE SCIENCES

Bioinformatics

Venusberg-Campus

Expertise

The Core Unit for Bioinformatics Data Analysis (CUBA) provides quantitative and computational analyses, training and consultancy. Increasingly complex and large data sets are characteristic for molecular biology and medical research driven by technology advancements. These high-volume data sets require quality control to filter artefacts, statistical rigor to minimize false positive findings and intelligent experimental design to maximize insights. Data processing pipelines, e.g. for transcriptomic data, are provided as well as guidance on available analysis tools and databases. Analyses are primarily based on freely available open source software essential for reproducible and independent research.

CUBA benefits from shared computing infrastructure and exchange of expertise due to its embedding and liaison with the Institut für Medizinische Biometrie, Informatik und Epidemiologie (IMBIE) and the Institute for Genomic Statistics and Bioinformatics (IGSB). It operates in collaboration with other facilities like the NGS and mass spectrometry facility. Altogether, this facilitates integrative bioinformatics approaches and offers a systems biology perspective. Moreover, data of different type and technology not only represent the same biological sample but also share characteristics like high dimensionality. Thus, common approaches for clustering, structure preserving visualizations and dimensionality reduction can be applied and synergies across different projects emerge.

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Services

- Our expertise ranges from experimental design and study planning to data processing, bioinformatics, statistical analysis and visualisation. We offer bioinformatics services in
  - Statistical analysis and machine learning
  - Consulting on experimental design and methods
  - Single cell RNA-seq and RNA-seq (mRNA; miRNA, etc.)
  - Exome and genome sequencing
  - Variant calling and Burden tests
  - Somatic mutation calling
  - Pathway enrichment
  - ATAC-seq and ChIP-seq
  - Mass-Spec based proteomics (LFQ, TMT, DIA, SILAC)
  - Metabolomic and Lipidomics, MS analysis of pull-down proteins
  - Flow cytometry (FACS data)
  - Methylation and copy number variation analysis
  - Metagenomics

  In addition, CUBA offers trainings in programming and bioinformatics analysis.

- We apply a variety of tools with an emphasis on publicly available software like Bioconductor and nf-core. Our own analysis pipelines are developed using R and Python programming languages and executed in a High Performance Computing (HPC) environment. Moving beyond standard analysis, e.g. for transcriptome and proteome data, we are aiming on more integrative multi-omics approaches, network and single-cell analyses.

CORE BIOINFORMATICS

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Cell Programming

Venusberg-Campus

Expertise

The Cell Programming Core Facility exploits the scientific know-how of the Institute of Reconstructive Neurobiology in cellular (re)programming, genome engineering and stem cell differentiation to support the establishment of cellular disease models on the basis of patient-specific stem cells. We expect that models, which are based on authentic human cells, will provide new insights into the molecular pathogenesis of diseases and promote the development of pharmaceutical and cell-based therapies.

Services

- *Generation and provision of human iPS cell lines*
  As starting material for iPS cell derivation we accept skin fibroblasts or peripheral blood mononuclear cells (PBMCs). Donor cells are reprogrammed using the latest Sendai virus-based reprogramming vectors that guarantee transient introduction of transgenes to avoid the stable integration of reprogramming factors. Depending on the recipients' demands, selected clones are subjected to standardized quality control regimens (ICC and gene expression profiling for pluripotency analysis, assessment of transgene removal, STR analysis, SNP genotyping).

- *Genome editing*
  We also offer genome editing services for the generation of isogenic iPS cell lines with KO alleles, introduced and repaired point mutations, respectively, as well as the targeted introduction of transgene expression cassettes into the genomic 'safe harbor' locus AAVS1.

- *Neural differentiation of iPS cells*
  The Cell Programming Core Facility has in-depth expertise in the differentiation of iPS cells into neural precursors as well as terminally differentiated neural cells. Currently, we provide the generation and provision of stable neural precursor cells (NPCs), cortical NPCs and NGN2-induced excitatory forebrain neurons, all of which are available in cryopreserved formats. Please contact us for availability of other neural cell types.

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BTC LIFE SCIENCES

Flow Cytometry

Venusberg-Campus

Expertise

The Flow Cytometry Core Facility covers a wide range of flow cytometric methods and applications. The FCCF provides access to High-end, state-of-the-art flow cytometers for multiparametric single cell analysis and sorting. A motivated team of well-trained experts with many years of experience in the field of flow cytometry guarantees best support for every scientist in this field.

The demand for a multiplexed analysis between 10 and 18 colors simultaneously is no longer extraordinary, and strategies for the isolation of rare cell populations are frequently asked for. Beside these obvious applications of flow cytometry, the “flow cytometry” platform contributed to the analysis and separation of micro vesicles, operating the cytometers at their physical detection limit, and encouraged the interaction of researchers from different disciplines.

Furthermore, the flow cytometry platform offers educational activities as stand-alone opportunities or as part of the existing graduate and professional programs, provides technical training, and conducts research that enables development of the next generation of state-of-the-art flow cytometry technology.

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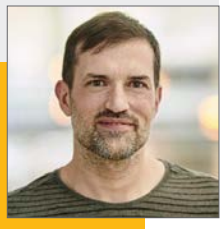

Instrumentation

- *Analysis*
  Researchers are trained by Core Facility personnel to perform their experiments without assistance of an operator. The Core Facility takes care of eight analyzers from standard three laser, eight color systems to seven laser, spectral instruments, that are able to detect more than 40 parameters simultaneously. Users receive detailed advice and support on the choice of dyes and equipment that are best suited to answer their scientific questions. Systems available include: three *BD FACSCantoII*, one *Miltenyi MACSQuant*, two *BD LSRFortessa* and two *SONY ID7000*.

- *Cellsorting* is mainly performed by experienced operators from the Core Facility. Two high-end, high-speed Cellsorters are available: *BD FACSAria Fusion* (biosafety level S2 approval), *BD FACSAria III*. A spectral cell sorter has already been granted and will arrive soon.
  For operator free cell sorting, the core facility staff offer training for the *Sony MA900* cell sorter, which is housed in a biosafety cabinet.

- *Imaging Flow Cytometry* combines the speed, sensitivity, and phenotyping abilities of flow cytometry with the detailed imagery and functional insights of microscopy. Researchers receive support in experiment design and instrument handling by the Core Facility staff: *Amnis ImageStreamX MarkII*.

- *Multiplexed, bead-based analysis* of cytokines, hormones or many other soluble biomolecules can be analyzed on a Flow Cytometer specially designed for this application: *Luminex FlexMap 3D*.

FLOW CYTOMETRY CORE FACILITY

BTC LIFE SCIENCES

Gene Editing

Campus Poppelsdorf + Venusberg-Campus

Expertise

The ability to generate genetically modified mouse models significantly contributes to the molecular understanding of human health and disease. The Gene-Editing Core Facility supports researchers to do so by using state-of-the-art gene-editing technologies utilizing CRISPR/Cas9-mediated genome engineering, a technique successfully established on campus since 2015. The application of this versatile tool accelerates the generation and establishment of mouse models and is considered to be the gold-standard for the generation of gene knockouts, conditional mice as well as insertions of small tags or point mutations.

These models can be often generated without elaborate and time-consuming cloning of targeting vectors and subsequent recombination in murine embryonic stem cells. Thus, the Core Facility aims to utilize CRISPR/Cas9-mediated approaches for the generation of genetically modified mice whenever possible and is actively working on improvements and refinements of the editing technologies, considering latest publications and methodologies in the field.

The University of Bonn has two large facilities for breeding of transgenic mice, HET at Venusberg Campus and LIMES-GRC at Campus Poppelsdorf. As mirco-manipulated embryos are directly introduced into the corresponding clean areas of the two breeding facilities via embryo transfer, the Core Facility Gene-Editing therefore has two sites. Depending on where you plan to house your mice you can directly contact the corresponding core facility.

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Services

- *Generation of CRISPR/Cas9 gene-edited mouse models*
  The Gene-Editing Core Facility develops and employs customized gene-editing strategies for the generation of genetically modified mouse models. Ubiquitous gene knockouts are generated using a combination of two different guide RNAs in combination with non-homologous end-joining (NHEJ) repair to induce genomic deletions of a few base pairs (bp) up to several hundred kbp to disrupt a genes reading frame or to delete larger regions. Precise point mutations or small tags are introduced using the CRISPR/Cas9 system in combination with homology directed repair (HDR) using short single stranded oligonucleotides (ssODNs) acting as repair template. The components are delivered into fertilized oocytes via electroporation allowing for a fast and high-throughput manipulation of oocytes for an efficient and cost-effective generation of gene-edited mice. For conditional strategies we aim to use the Easi-CRISPR approach using 1-2 kbp ssODNs. These constructs are delivered to fertilized oocytes via pronuclear or intracytoplasmatic injection using an inverted DIC (differential interference contrast) microscope equipped with micromanipulators, Piezo-element and an EppendorfTM Femtojet injection device. Micromanipulated embryos are transferred into pseudo-pregnant foster mice by oviduct transfer of 2-cell stage embryos to finally obtain gene-edited founder mice.

- *Blastocyst injections*
  For knock-ins of larger sequences (>1.5 kbp), the CRISPR/Cas9 system is not efficient enough yet and requires „classical“ embryonic stem cell (ES cell) based approaches. If provided with a targeting construct, the Core Facility will perform the ES cell targeting in proven germ-line competent ES cells followed by blastocyst injection. Blastocysts are transferred into pseudopregnant foster mice to generate chimeras. For design and procurement of larger targeting constructs, the Core Facility can also assist you.

Human 3T MRI

Venusberg-Campus

Expertise

Magnetic resonance imaging is a non-invasive imaging procedure that has become an indispensable part of modern medical research. The advantage of this method is that tissue types of varying density can be displayed in MRI images with different contrasts. This is particularly beneficial in neurological imaging of the brain and is the basis for neurocognitive research.

Via the BOLD effect it is possible to observe neuronal activity in the brain (functional imaging, fMRI). Other techniques include resting state MRI or diffusion tensor imaging (DTI).

The Core Facility "Human 3T MRI" provides access to a modern MRI scanner (Siemens Magnetom Trio) for research purposes.

The MRI Core Facility supports scientists in the implementation of their research project, for example in measurement planning, the creation and optimization of measurement protocols or troubleshooting, but also in the development and programming of paradigms. To enable their users to carry out the investigations independently, the MRI Core Facility offers training courses. The goal is to ensure the highest quality in data recording and the safe execution of the investigations. CF-MRI offers support in accessing and pre-processing the data.

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Instrumentation

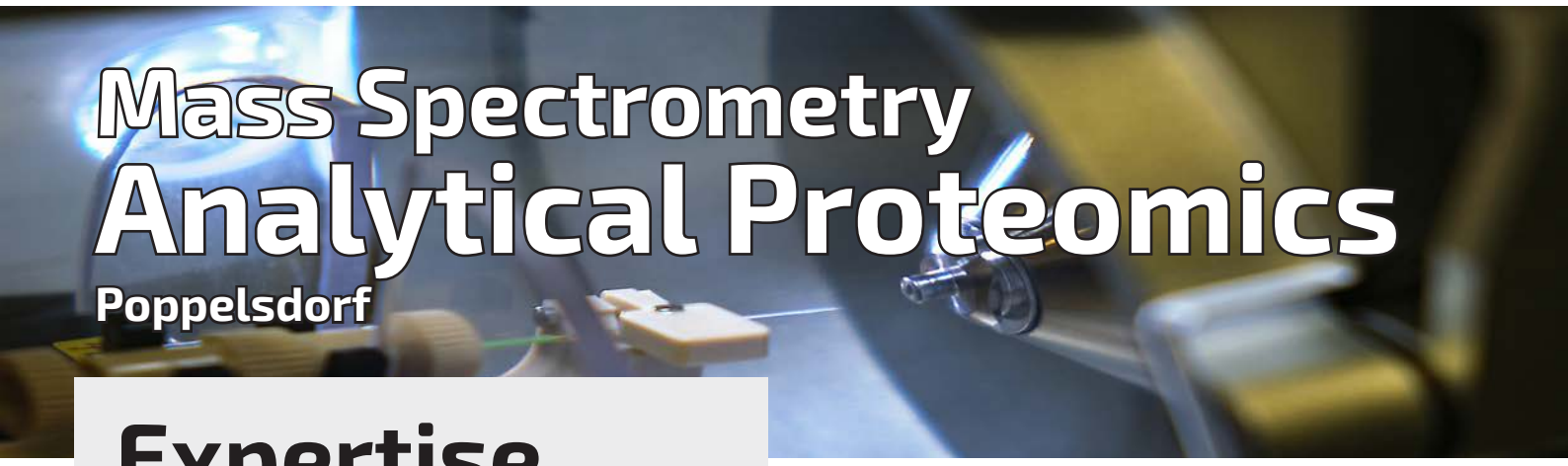
- *Scanner*
  The scanner is equipped with a Spine Matrix Coil and two Body Matrix coils, the standard 12-channel head coil and a 32-channel head coil. Furthermore, a transmit/receive coil (TX/RX) can be used for spectroscopy.
  The scanner holds sequences to cover a wide range of examinations. Besides the usual sequences for brain imaging (FLAIR, STIR, T2-weighted, T1-MPRAGE), protocols for DTI and functional MRI (EPI) are available. The Core Facility supports its users in setting up the measurement protocols and adjusting the measurement parameters.

- *Paradigms*
  The Core Facility provides a workstation for the presentation of paradigms (stimulation in functional MRI). Various software packages like "Presentation" (Neurobehavioral Systems), „matlab toolbox" or „psychopy" are available to the user. In addition, the Core Facility also provides the "ScenarioDesigner", a python-based program developed by the Core Facility itself. It enables the particularly simple programming of paradigms. The Core Facility supports users in the creation of ScenarioDesigner programs.

- *Visual System*
  The "Visual System" from NNL (Nordic Neuro Lab) consisting of video goggles and response buttons is available. The video goggles create the impression of a large image (like a cinema screen) and shield lateral influences. This allows the respondent to immerse himself more intensively in the scene and is less distracted. A correction of defective vision is directly integrated into the goggles.

- *LCD Monitor*
  Alternatively, the paradigms can be displayed on an LCD screen placed at the head-side magnetic tunnel entrance. The subjects see the image through a mirror attached to the head coil. A set of lenses is available to correct defective vision.

CORE FACILITIES HUMANES 3T MRT BTC LIFE SCIENCES



Mass Spectrometry
Analytical Proteomics
Poppelsdorf

Expertise

The Core Facility Analytical Proteomics offers services for a broad range of protein analyses. We apply a variety of mass spectrometric approaches to identify proteins after proteolytic digestion (from polyacrylamide gels or in solution), analyze post translational modifications, and measure intact protein masses.

Modern mass spectrometers with high resolution and sensitivity allow analysis of complex samples such as cell lysates. These machines are also used for quantitative analyses with or without stable isotope labeling strategies like SILAC and TMT. Targeted quantification can be done for example if good antibodies are not available (multiplexed “next-generation Western Blot”).

The data we provide can be very informative but also challenging, in particular the quantitative characterization of proteomes. Therefore, early consultation with us is essential to improve the chances for a successful mass spectrometric analysis. We need to discuss the strategy, scope, and pitfalls of the experiments.

We collaborate closely with the Core Facility Translational Proteomics and the Core Unit Bioinformatics in order to assess the data quality and apply statistical methods. Together, we will help you in finding biological knowledge in your proteomics datasets.

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Instrumentation

- *Thermo Orbitrap Lumos with ETD*
  The Orbitrap Lumos is a modern spectrometer that is extremely versatile: Classical measurements can be done with high sensitivity; label-based quantification is improved. It is also capable of better intact protein analyses, targeted measurements for selected proteins and the modern quantitative approach of Data Independent Acquisitions.

- *Hybrid instrument Thermo Orbitrap Velos*
  The Orbitrap Velos has two detectors: a fast low-resolution linear ion trap and a high resolution, high accuracy Orbitrap detector which can be used in parallel. The instrument is used for proteome analyses of medium complexity.

- *nanoLC systems*
  Three ultra-high performance liquid chromatographs for nanoflow (~300 nl/min) are used for coupling with mass spectrometers. These systems perform chromatographic separations very reproducibly and assure a stable delivery of analytes to the mass spectrometers. An Advion Triversa Nanomate nanospray robot can be used for automated delivery of small sample amounts for direct infusion.

Microscopy

Venusberg-Campus

Expertise

The Microscopy Core Facility provides services for imaging microscopy techniques for live and fixed cells and tissue sections. We also provide scientific and technical assistance for researchers to design experiments and to facilitate image acquisition and analysis. We also offer full service sample preparations and imaging for electron microscopy related projects.

The Core Facility is equipped with five wide-field microscopes, five confocal systems, and an electron microscope. We also have five analysis workstations.

The Core Facility has two sites, one in BMZ II and the other at the Neurocenter, with the instruments evenly distributed between the sites.

The light microscopes can be booked for an hourly fee after sufficient training. We are also happy to perform the measurements for you, if required. The electron microscope is operated by staff members as full service.

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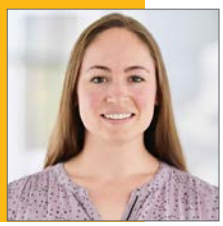

Instrumentation

Wide-field microscopes

- Color- and fluorescence-based automated whole slide scanning
- Automated high-content screening of multi-well plates
- Live-cell imaging
- Dual-camera ratiometric imaging
- STORM super-resolution

Confocal microscopes

- High-resolution live-cell imaging
- Whole-organ / Cleared tissue imaging
- Large-tissue section imaging
- FLIM and FCS measurements
- On-the-fly deconvolution super-resolution
- STED super-resolution

Electron microscopy

- Scanning EM (SEM)
- Scanning transmission EM (STEM)
- FIB-SEM 3D nanotomography
- Sample preparation
- Ultramicrotomy
- Immunogold labeling
- Pre- & post-embedding correlative light and electron microscopy (CLEM)

Image processing and analysis

- Fiji and CellProfiler free software
- Licensed Zeiss, Leica, and Visitron software
- Huygens and AutoQuant deconvolution
- Imaris 4D image visualization and analysis
- Neurolucida analysis software
- Aivia AI-assisted image analysis

MICROSCOPY CORE FACILITY

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Nanobodies

Venusberg-Campus

Expertise

The Core Facility Nanobodies at the University of Bonn offers diverse services based on alpaca or llama variable domains of heavy chain-only antibodies (VHHs), also called nanobodies, and is the first of its kind in Germany.

Nanobodies are highly specific single domain antibodies (ca. 15 kDa) that recognize their targets with affinities comparable to conventional antibodies.
We can identify suitable nanobodies by phage display, produce them in bacteria, or express them in the cytosol of mammalian cells to visualize targets or alter protein function.

The ease of modification by genetic fusion, chemical or enzymatic conjugation makes Nanobodies versatile tools used in the clinic, for diagnostics or for research. They have been used for perturbation studies, microscopy, flow cytometry, mass cytometry, mass spectrometry, or non-invasive imaging methods such as immuno-PET. In structural biology Nanobodies are appreciated as chaperones facilitating protein crystallization.

We offer the customized immunization of alpacas or llamas with provided protein, as well as the identification and validation of specific nanobodies against your desired target. We also produce and (site-specifically) modify nanobodies to adjust them to your needs.

Services

- *Scientific and technical advice for successful generation and usage of nanobodies*
  Contact us and make an appointment. We are happy to help get your nanobody project started!
- *Generation of custom-made nanobodies*
  Immunization of camelids with your antigen of choice and selection of binders by phage display
- *Validation of custom-made nanobodies*
  In vitro by ELISA or ***in situ*** by LUMIER assay
- *Recombinant expression of nanobodies*
  Production at multiple scales in bacteria and in eukaryotic cells (with human/mouse Fc part)
- *Chemical and chemo-enzymatic modification of nanobodies*
  Amine-reactive (NHS ester) or sulfhydryl-reactive (maleimide chemistry) labeling or site-specific Sortase A-mediated labeling by transpeptidation („sortagging“)
- *Custom services involving development, selection or use of nanobodies*

Ask us, we will gladly discuss your specific idea involving nanobodies upon request!

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CORE FACILITY NANOBODIES

BTC LIFE SCIENCES

Next Generation Sequencing

Venusberg-Campus

Expertise

Massive parallel sequencing, called Next Generation Sequencing (NGS), is becoming widely applied in many research projects. However, investment in maintenance of NGS systems as well as establishing different applications is expensive and time consuming. The NGS Core Facility at the Institute of Human Genetics is dedicated to provide the research community in Bonn with access to state-of-the art sequencing technologies and to help facilitate cutting-edge omics research. Our service covers all phases of a research project, from experimental design to data generation for the following applications:

- Whole-Genome Sequencing
- Exome Sequencing
- Whole-Transcriptome Sequencing (mRNA-Seq, total RNA-Seq)
- Gene Expression Profiling (3'-mRNA-Seq)
- Single Cell Sequencing (10X Genomics)
- Small RNA sequencing (miRNA-Seq)
- Targeted Sequencing (Amplicon)
- 16S Metagenomics
- ChIP Sequencing
- Proteomics analysis (Olink® Explore)
- Sequencing of final libraries

The facility's modern technical equipment enables sample preparation and sequencing of a few to hundreds of samples and guarantees an ideal balance between data output and costs. Since 2019 the NGS Core Facility is one of the main production sites of the West German Genome Center, one of four DFG-funded NGS Competence Centers in Germany.

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Instrumentation

Sample Preparation & Quality Control
To ensure a high quality of NGS libraries modern technical devices are available for quantification and/ or size selection (Tapestation 4200, Agilent; Qubit/Quant-iT, Thermo Fisher; Fragment Analyzer, Agilent; BluePippin, Sage Science), sample preparation (LE-220 plus, Covaris; Chromium Controller, 10X Genomics), and liquid handling (Biomek i7, Beckman Coulter).

Sequencing Devices
Due to a comprehensive equipment of sequencing devices, the NGS Core Facility is able to offer the most suitable sequencer for each project in terms of required data volume and costs. Currently, most of the short-read sequencing systems from Illumina (NovaSeq 6000, NextSeq 550, MiSeq, MiniSeq and iSeq 100) are available to the scientific community at the Bonn Campus.

Data Analysis
Upon run completion, raw data are converted into standard-format FastQ and provided per download link. Quality control and comprehensive secondary data analysis is ensured through a strong collaboration with the Bioinformatics Core Facility Bonn.

NGS CORE FACILITY

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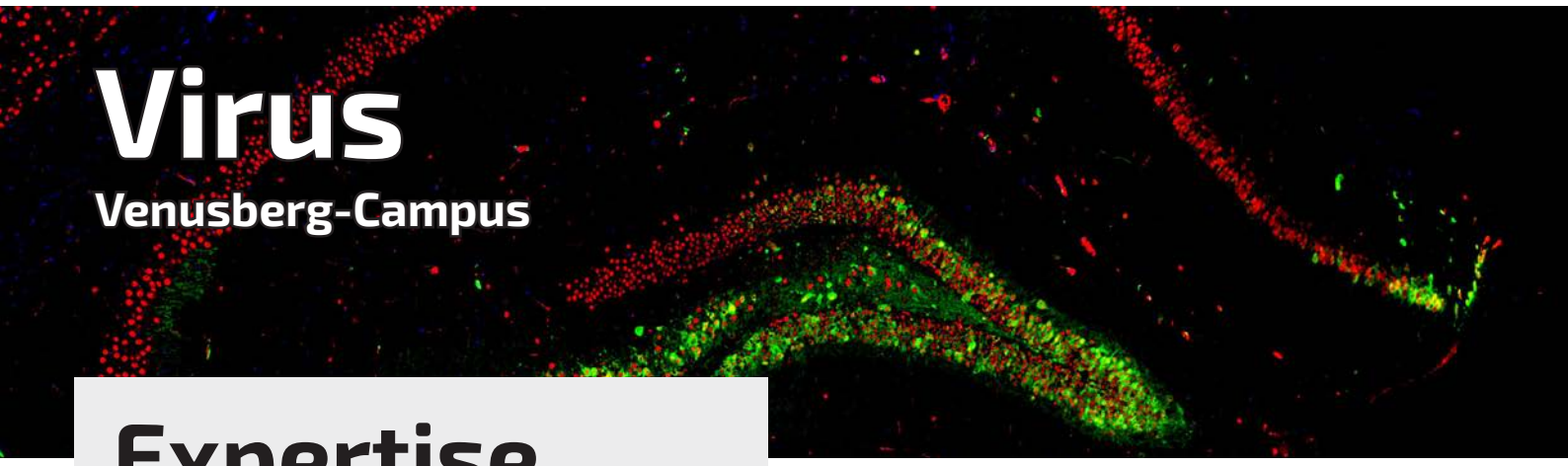
Virus

Venusberg-Campus



Expertise

The Viral Core Facility (VCF) offers the production of adeno-associated viruses (AAV) and the cloning of AAV expression plasmids as a service to scientists. These viruses can be used to study the functions and properties of specific cells by expressing transgenes or downregulating endogenous gene expression.

AAVs are single-stranded DNA viruses that can infect a wide variety of dividing and quiescent cells and cell types. Due to these properties, they are used as versatile tools for scientific experiments in the laboratory and for gene delivery in humans. With a packaging capacity of about 4.7 kbp, AAVs can deliver not only proteins (e.g. fluorescent proteins, sensors ...) but also constructs to edit the genome (e.g. CRISPR-Cas) or to alter gene expression (e.g. RNA interference). AAVs are not only useful research tools but elicit low immune responses *in vivo* and are not known to cause disease in humans, thereby providing overall high safety.
The selection of an appropriate AAV expression plasmid in combination with a serotype allows the transduction of specific cells *in vitro* and *in vivo*. AAVs are produced in HEK293T cells by transfection of the AAV expression plasmid along with the packaging plasmids required for each serotype. The Viral Core Facility provides support for both AAV expression plasmid design and virus purification.

Services

- *AAV purification*

  Adeno-associated viruses (AAV) of different serotypes can be purified in the Viral Core Facility. Viruses are purified using heparin columns or iodixanol gradients. After purification, viruses are subjected to quality control consisting of three steps:

  - Purity assay: detection of capsid proteins by SDS-PAGE and Coomassie Blue staining
  - Determination of AAV titer by real-time PCR (qPCR)
  - Test of infection efficiency in primary neurons (depending on serotype)

  Stocks of frequently used AAVs are available in the VCF and can be purchased upon request.

  For *in vitro* testing, crude viral AAV extracts (non-purified AAV) can be prepared for all available serotypes.

- *Cloning of AAV expression plasmids*

  For users who wish to design their own plasmids, we offer the cloning of AAV expression plasmids. This allows the custom design of a plasmid including the promoter, gene of interest, and regulatory elements. In addition, project-specific AAV expression plasmids can be generated for knockdown (shRNA), knockout (CRISPR-Cas), or gene editing experiments. All generated plasmids are verified by sequencing or expression assays.

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VIRUS CORE FACILITY

BTC LIFE SCIENCES

Zebrafish

Poppelsdorf

Expertise

Zebrafish *(danio rerio)* and especially zebrafish larvae has become an important vertebrate model organism within the last 30 years. Now they became even more challenging with the invention of the CRISPR/Cas technology in the last few years. There are several reasons to use zebrafish as a vertebrate model: mainly the fast exutero development of the small nearly transparent larvae fish, which makes them very approachable for whole mount (fluorescence) ***in vivo*** microscopy, as well as the fact that they can be raised in large numbers on relatively small amount of space and therefore costs.

Thousands of mutant and transgenic zebrafish (reporter) lines have been established and described already worldwide and are easily available to everyone free of charge (Small handling fees for shipping of the fish-eggs might apply). Furthermore it is easy for everybody to transiently manipulate the larvae fish by injections of RNA, Morpholino® antisense knock-down constructs or overexpressing plasmid DNA which can also be used to raise stable transgenic fishlines via germ line insertion within the next generation.

Services

- As a core facility we offer an all around service for our users:
  - Import and rising of zebrafish lines
  - Generating of new zebrafish lines
  - Keeping and mating of zebrafish lines on behalf of our users
  - Injection of zebrafish eggs or embryos
  - Transplantation of cells into two or three days old zebrafish larvae
  - Support on imaging on our own fluoreszenz, confocal or two photon microscopes
  - Direct transfer of fish samples to electron microscopy core facility (in house)
- Injections and imaging are normally done together by our core facility manager and the user. The close teamwork will help the user a lot in the later interpration and analyses of the fish data as well as planing for the next steps of your experiment.

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ZebrafishCORE

BIC LIFE SCIENCES

Important Announcement

Your Acknowledgement Matters

An acknowledgement in your publication is more than just a nice way to say „Thank you!".

IT HELPS US TO MAINTAIN OPERATIONS

Showing to be part of the scientific community is one of the important measures to maintain funding and investments for core facilities.

IT IS ABOUT PEOPLE IN SCIENCE TOO

The core facility personnel may have contributed significantly to your research project. Authorship may also be appropiate.

DFG
Deutsche Forschungsgemeinschaft

Projektergebnisse, die aus mit DFG-Mitteln finanzierten Projekten resultieren, müssen in geeigneter Art ... einen Hinweis auf die DFG-Förderung (sog. „Funding Acknowledgement") ... enthalten. [DFG-Vordruck 2.00 – 01/21, Verwendungsrichtlinien]

As an example:
„We would like to thank the ... Core Facility of the Medical Faculty at the University of Bonn for providing support and instrumentation funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) – Projektnummer ..."