

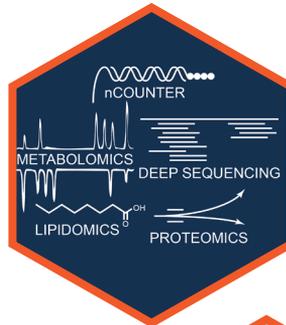
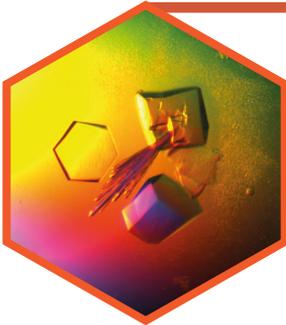
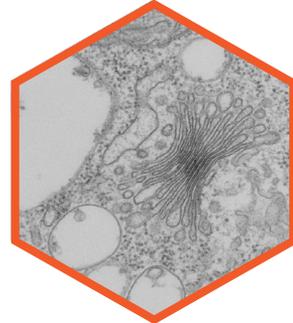


UNIVERSITÄT
HEIDELBERG
ZUKUNFT
SEIT 1386

CellNetworks

High-tech collaborative research





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HIGH-TECH RESEARCH IN THE LIFE SCIENCES

The Cluster of Excellence CellNetworks was founded at Heidelberg University in the context of the Excellence Initiative and developed into a top quality interdisciplinary research network, renowned far beyond the borders of Heidelberg. The Cluster focuses on the behavior and dynamic changes of complex biological networks and develops a systematic understanding of the regulation mechanisms.

CellNetworks unites 110 international renowned researchers in the molecular life sciences, namely biology and medicine, in technology development in physics, chemistry and nanotechnology as well as computer science and scientific computing. This research focus includes four successive and interrelated areas which study many objects of different sizes starting with the molecular components of the cell. Among those, the supra-cellular networks in neurosciences are the largest and most dynamic objects. The research projects depend on a state-of-the-art technology infrastructure, which is the reason for this booklet.

The CellNetworks research groups belong to six faculties of Heidelberg University and five non-university institutions, including the German Cancer Research Center (DKFZ), the European Molecular Biology Laboratory (EMBL), the Heidelberg Institute for Theoretical Studies (HITS), as well as the Max Planck Institute for medical research (MPIImf) and the Central Institute of Mental Health (ZI) in Mannheim. These groups do joint research and contribute to the excellent position of the Heidelberg life sciences in Germany, and to taking the research forward.



Cluster of Excellence: The funding line of the Excellence Initiative known as Cluster of Excellence focuses on scientific research on a broad topic at one location, and receives approx. EUR 6.5 million in funds per year. The aim is not just to explore one area of a discipline. Outstanding scientists from different fields join together and investigate one of the greatest research issues of our time. Universities specifically want this to impact on their organizational structure. CellNetworks is located in the BioQuant Center (see picture). Even after DFG funding ends, it will continue as a central facility of Heidelberg University, working on research projects and offering technical services.

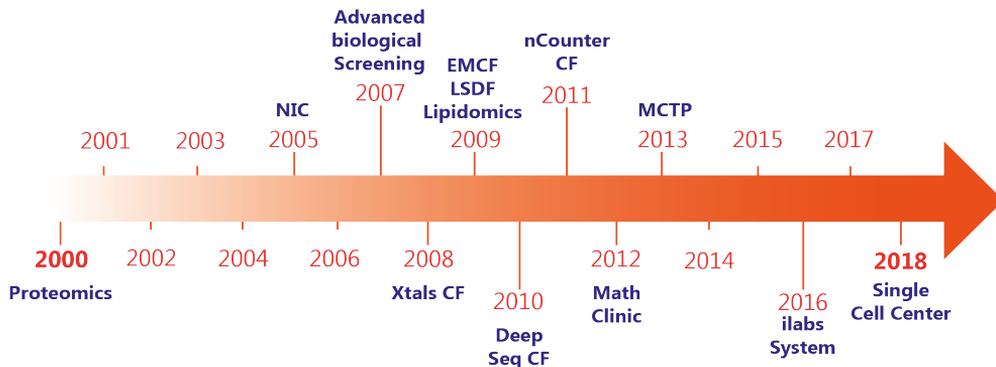
CORE FACILITIES

Before CellNetworks was established, there were only few core facilities and shared infrastructure on the Heidelberg life-science campus. This went ahead without much organization, and access to expensive equipment and high-end technology was dependent on individual collaboration agreements.

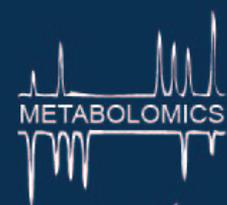
CellNetworks has laid particular emphasis on the development of core facilities, in order to expose young researchers and junior groups to them and enable training in state-of-the-art and high-end technologies. All core facilities are facing a very high demand, which shows the great success of this idea. Where applicable, electronic booking systems have been introduced, and all core facilities have approved access regulations and regular training activities.

Access to the CellNetworks core facilities is open to all researchers in the life sciences, independent of their institutional affiliation. The services are offered on the basis of user fees or within the framework of scientific collaboration.

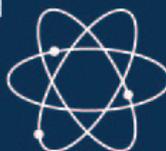
CellNetworks has been instrumental in implementing nine core facilities with support from its central technology platform. In addition, joint infrastructure for computational sciences was installed including a computing cluster and methods support as well as the Large Scale Data Facility (LSDF) with a storage capacity of 6 petabyte.



CORE FACILITIES SYMPOSIUM



CRYSTALLISATION



DEEP SEQUENCING



ELECTRON MICROSCOPY

RNAi SCREENING



EXZELLENZCLUSTER

CellNetworks



NEUROBEHAVIOUR



NIKON IMAGING CENTER

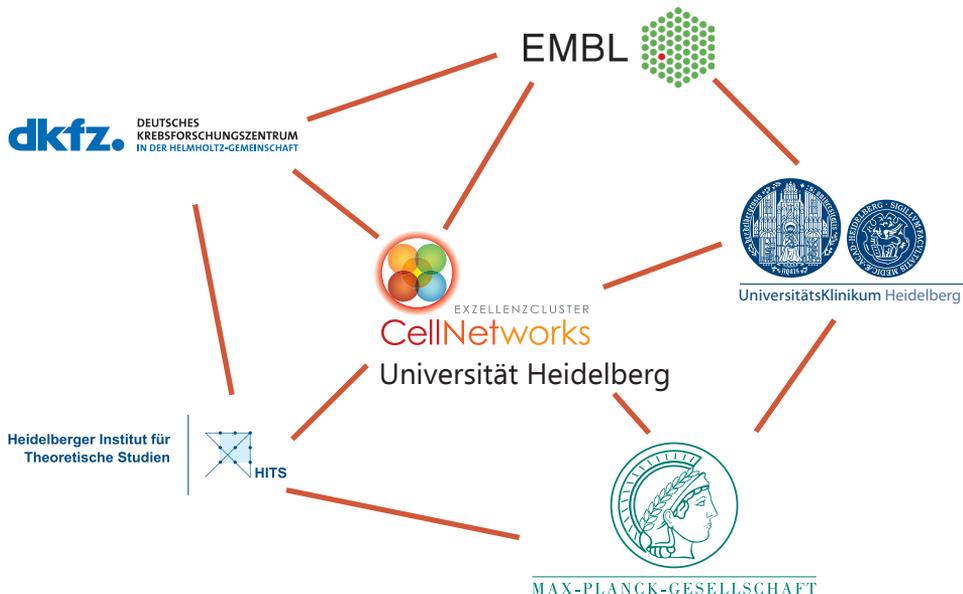
November 08, 12:00

BIOQUANT 041

REACHING THE TOP TOGETHER

Building Networks – Celebrating Success

With more than 110 excellent research groups from institutes of the Heidelberg molecular life sciences, CellNetworks forms a framework for interdisciplinarity and interchange in the life sciences in Heidelberg. The fast pace of the technological and methodological development continuously influences research in the molecular life sciences. The group leaders of the CellNetworks research alliance have identified these developments and fostered the forward-looking establishment of core technology and methods platforms, in order to continue working together in the spirit of the German Excellence Initiative. Also, the boundaries between the different research organizations have been loosened up, creating synergies that drive the development of interdisciplinary research in Heidelberg. This promotes interaction and networking that would not have been possible without the umbrella of CellNetworks.





Winners of the prestigious ERC grants in Heidelberg

THE NIKON IMAGING CENTER

State-of-the-art microscopy – open for everyone

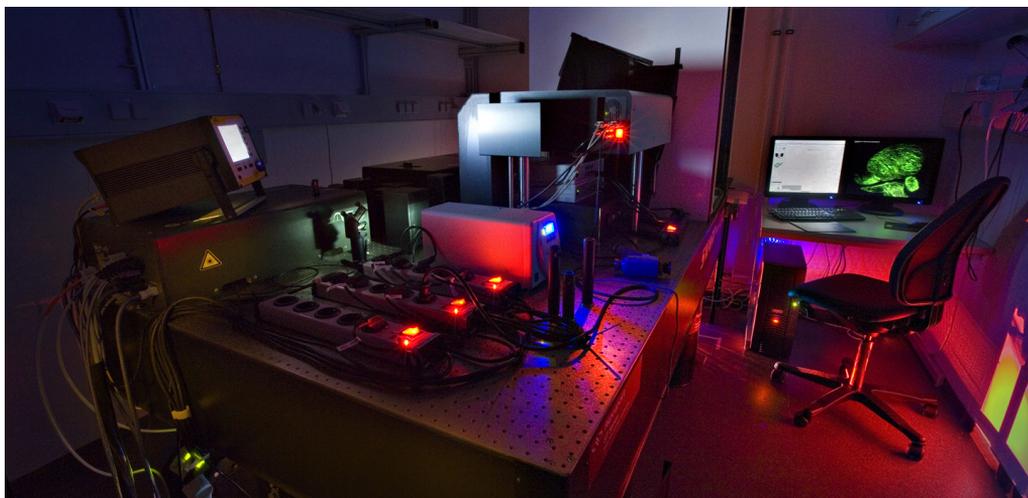
The founding of the Nikon Imaging Center at Heidelberg University (NIC) in 2005 was a first step towards open access to core infrastructure on campus. Developed in partnership with Nikon, the NIC at Heidelberg University is one of eight Nikon Imaging Centers worldwide to provide state-of-the-art instrumentation and services for advanced light microscopic imaging. The NIC is open for all researchers on the life science campus at Heidelberg University.

The microscopic instruments offered by the NIC cover a wide range of state-of-the-art confocal, automated wide field and screening microscopes, as well as a two-photon live imaging microscope for intravital imaging. CellNetworks significantly contributed to the acquisition of new instruments during its two funding periods, adding important technologies to the NIC.

Two-photon laser scanning microscopy

One example for the fascinating research, which is only possible due to the support of the NIC, is the LaVision Biotec TriM Scope, a two-photon live imaging microscope that was acquired with funding from CellNetworks back in 2008. At this time, the LaVision Biotec TriM Scope at the NIC was the first two-photon microscope that provided open access to all scientists on the campus. As opposed to conventional fluorescence light microscopes, two-photon microscopy allows imaging of living tissue up to about one millimeter in depth without side effects such as scattering or the destruction of tissue. In contrast to one photon excitation, 2-photon uses near-infrared laser light delivered in short pulses of high intensity, which can then also excite fluorescent dyes. Due to the localized excitation of 2-photon microscopy, out of focus signal and bleaching is strongly suppressed. These effects lead to an increased penetration depth. The scientists at the NIC understood the potential of two-photon microscopy early on and wanted to make it available to developmental biologists with the possibility to study development of organisms at deeper cell levels than what was possible with traditional light microscopes.

The technical breakthrough with LaVision Biotec TriM Scope was a four-day two-photon live imaging of the brain development in a zebrafish. During his PhD project, Dr. Carlo Beretta was interested in the temporal-spatial control of bilateral habenulae formation nerve axon growth, which presumably develops synchronously and has gained only little attention. Under the supervision of Prof. Dr. Matthias Carl at the Interdisciplinary

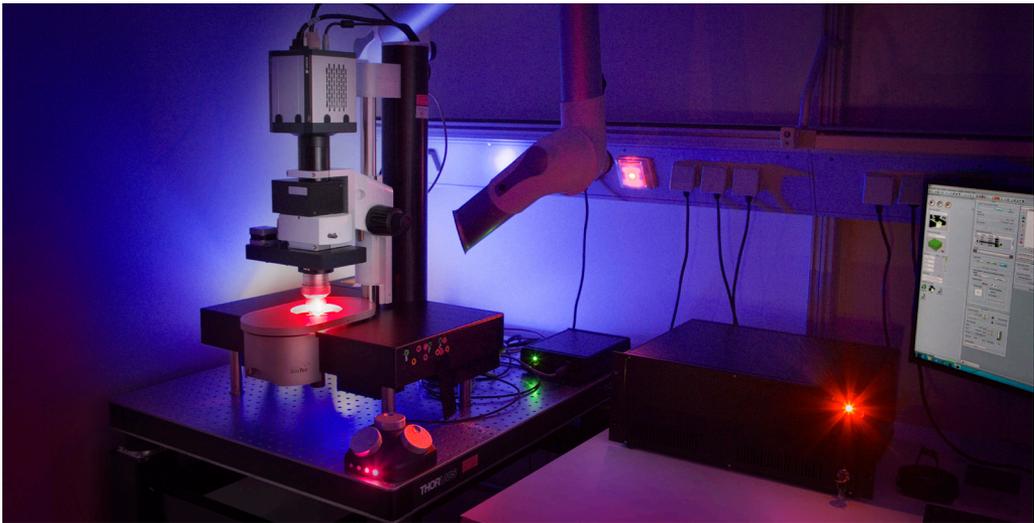


Center for Neurosciences at Heidelberg University, he teamed up with two-photon specialist Dr. Nicolas Dross at the NIC to study the brain cell assembly and axon growth in a volume that spanned the whole developing zebrafish brain (1/3 mm in depth). Dr. Beretta and Dr. Dross for the first time were able to visualize in vivo that the formation of the habenular neural network depends on an intersecting commissural network in the diencephalon of the zebrafish. The results of his research were published in *Current Biology* in 2017.

Lightsheet fluorescence microscopy

The NIC continuously expands and renews its equipment with the latest technologies available. Recently, it implemented the UltraMicroscope II, a second generation bidirectional triple light sheet microscope which generates 6 focused light sheets to excite samples from the side while the fluorescence light is detected by a camera perpendicular to the illumination plane. Moving the sample through the light sheet generates a 3D image. This technology can be used for large samples such as the brain of a mouse. In addition, selective excitation reduces bleaching and photo toxicity significantly. The UltraMicroscope II has been co-financed by CellNetworks and the DFG Collaborative Research Center "Functional Ensembles". Collaboration agreements among many re-

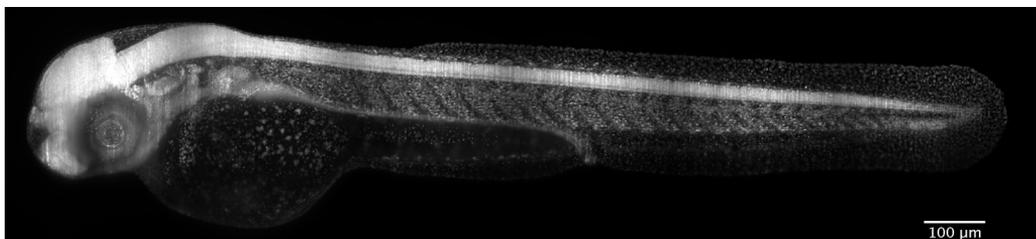
searchers facilitate the funding of fantastic technologies. With this the NIC shows once again how strong collaboration allows a better use of resources.



Open SPIM in South Africa

The OpenSPIM project developed an Open Access platform, which allows for the use and improvement of light-sheet microscopy. SPIM stands for “Selective Plane Illumination Microscopy”, a technology which enables the imaging of a fluorescing sample in three dimensions over time while being minimally invasive. The technology achieves that by focusing a thin laser light-sheet on the sample, taking two-dimensional images of the illuminated slice with a perpendicularly positioned detector. Moving the sample orthogonal to the light sheet between consecutive images results in three-dimensional stacks generates a three-dimensional image of the probe.

The particular aspect of the OpenSPIM project is that it is also conducive to teaching light-sheet microscopy. In the framework of the EMBO course on “Imaging Infection and Immunity” the lessons on the microscope were carried out in an exceptional and elaborate way. The course, which has already been organized four times by CellNetworks member Freddy Frischknecht, Musa Mhlanga and Jost Enninga, was carried out at the CSIR in Pretoria, South Africa. For this reason, the OpenSPIM somehow had to be transported to South Africa. Pete Pitone, who had attended the entire course, took on this task. But how can you move an instrument that looks like a bomb? The answer is easy: in a suitcase! No sooner said than done! The team managed to move the OpenSPIM 10,000 km to South Africa to build the system there. And it was worth the effort! The course, attended by high school students from the African Leadership Academy (ALA), was a great success. The students were interested and described setting up the microscope as “absolutely easy-peasy [...] just like Lego”. Also the feedback from the students was overwhelmingly positive. The African students seemed to highly appreciate the effort of the team in making such great technology accessible and in fact showed again how networks, internationality, exchange and open access enrich the life sciences.



ELECTRON MICROSCOPY

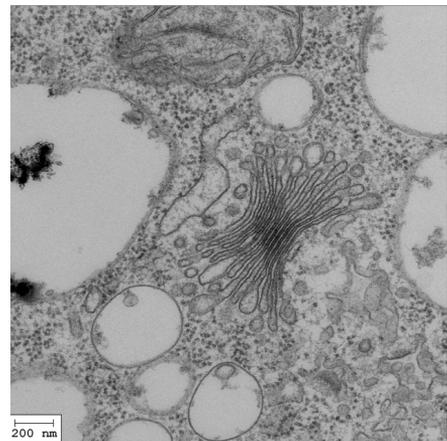
The Electron Microscopy Core Facility (EMCF) provides technical and scientific support for transmission and scanning electron microscopy to all members of Heidelberg University and to external users. Key to successful electron microscopy is long-standing expertise in sample preparation, the adaptation of protocols, along with imaging, which is guaranteed by the experts working at the EMCF. The EMCF's aim is not just to provide technical resources but to combine them with their expert knowledge in cell biology. Therefore the EMCF also connects its customers to other, more specialized EM groups on campus, which provide additional expertise. Various techniques are used for sample preparation to image biological material at high resolution: This has often allowed for the linking of structure and function with each other and has helped to answer numerous biological questions in the past. With the help of electron microscopy the subcellular structures can be identified directly and thereby help to supplement and confirm light microscopical studies. This additional data provide information which is otherwise very hard to get.

The Electron Microscopy Core Facility – ultra-structural research in the process of change



The development of electron microscopy technologies is an example of how technological development goes hand in hand with progress in research. The wish to reach more detailed insights in cell processes has driven the need to gain insight into cellular structures at a very high resolution. Meanwhile it is a major aim in life sciences to visualize structures on the atomic level to create a better understanding of cellular processes. Such demand has fueled technological advancement in electron microscopy. The progress, in turn, leads to a continuous necessity for investment in expensive instruments as the microscopes have to be constantly upgraded to keep up with research needs. In particular for electron microscopy, the desire to obtain super-resolution with the help of short wavelength electron beams, the size of the

microscopes, as well as the cost of acquiring and setting up the instruments, are beyond the scope of the traditional department structure of a historically growing university. Heidelberg University recognized the need to establish a different kind of research structure at an early stage, and this led to the foundation of the Electron Microscopy Core Facility in 2009. The investment in a Krios 300kV and a Fei F20 200kV Electron Microscope attracted many users on the campus due to its versatility and gave them the opportunity to use electron microscopy on a level which goes far beyond the internal instrumentation offerings. With this, even skeptics were convinced that centralizing expensive equipment and specialists from various fields of study at one spot were the right way to go, in the long run. The University rectorate supported the facility by new appointments in this research area and provided more spacious premises for sample preparation in building 345 at the Theoretikum. This has generated an increased use of the equipment, a better exchange of knowhow and enhanced awareness of the core facility on the campus. A good example is the involvement of the facility within the research program SFB 1129 and the GCIR, where it possesses a strong ultrastructural focus in their research projects. Besides conventional electron microscopy studies, there is also a big demand for correlative microscopy as viruses are so small and therefore make it almost impossible to find single virus particles.



MATH-CLINIC

Following the spirit of time - The growing importance of bioinformatics

As one of CellNetworks youngest Core facilities, the Math-Clinic keeps up with the times in life sciences and provides computational support to CellNetworks members for quantification and analysis tasks. The support is intended work in the same way as going to hospital: you go there with a problem, are referred to an expert and receive case-specific treatment. Driven by new technologies, such as high-throughput and high-content approaches in screening, sequencing and imaging, the life sciences are becoming increasingly quantitative. The analysis of complex data sets requires expertise in state-of-the-art image processing, statistical data analysis and mathematical modelling.

**NGS Bioinformatics
Networking Meeting**

For experimentalists,
bioinformaticians and
everyone in between.

May 26, 13:00-15:00
BioQuant 041

Organised by Matthew Betts (CellNetworks Math-Clinic), David Ibberson (CellNetworks)

The Math-Clinic is involved in organizing various events and workshops, including the “Unseminars for Bioinformatics” and Bioinformatics Networking meetings (e.g. for Next Generation Sequencing - NGS), and has hosted several bioinformatics training courses for users on all levels. Besides, the Math-Clinic offers a variety of services focusing on microscopy image processing, e.g. segmentation, cell tracking, feature recognition and shape reconstruction. Customers also find support in protein and structural bioinformatics, including sequence analysis, domain composition and interactions.

Collaboration of microscopy and Math-Clinic

Two-photon microscopy (2-PM) allows us to gain fascinating insights into living brains. Therefore, imaging large cortical volumes requires tools for a comprehensive image analysis. One of the ongoing collaborative projects between the Math-Clinic Core Facility and the groups of Prof. Dr. Fred Hamprecht and Prof. Dr. Thomas Kuner is a typical example of how CellNetworks Core Facilities support scientists on campus.

The project aims at understanding structural cortical reorganization and building a bridge between in vivo microscopy and macroscopic structural magnetic resonance imaging. The group led by Prof. Dr. Thomas Kuner monitors the architecture of cells of large cortical volumes in different conditions, e.g. during disease states found to be associated with changes in cortical volume. This change in the cortical volume was observed under the microscope. To address the cellular correlate of such volume changes, the researchers image large cortex volumes using in vivo 2-PM in genetically modified mice expressing a green fluorescent protein in the nuclei of all cells, thereby allowing them to monitor the distances between nuclei and, hence, the local tissue volume over extended time periods. With the help of Dr. Carlo Beretta from the Math-Clinic Core Facility the project has been pushed even further on the bioinformatics level. He developed an image analysis workflow to automatically segment nuclei in large 3D volumes combining deconvolution, machine learning (ilastik software) and ImageJ/Fiji macro language. Now, the 3D segmentation workflow is used to quantify cortical cell density and measure 3D nucleus characteristics. The first author of this study, Livia Asan from the Lab of Prof. Dr. Thomas Kuner, is enthusiastic about the support and consultation offered by the Math-Clinic Core Facility:

“In our research project we collect large amounts of image data to study the architecture of the cerebral cortex. The analysis of these multidimensional data poses a challenge on its own. We profit enormously from the collaboration with the Math-Clinic, whose experts create optimal solutions for automated analysis of our data by combining new top-notch tools that are developed in different facilities in Heidelberg. Not only does our project progress faster, but I personally also learn a lot during the frequent exchanges with the Math-Clinic, advancing my own skills in data analysis.”

ADVANCED BIOLOGICAL SCREENING

The CellNetworks Advanced Biological Screening Facility was established in 2007 at Bio-Quant, and can be regarded as an advancement of a facility of the partner institution EMBL. The facility is well-equipped with state-of-the-art high-tech instruments and the experts working at the Advanced Biological Screening Facility possess long-term experience in the field of RNAi Screenings.

With the help of the Advanced Biological Screening Facility customers can carry out research projects including medium and large scale screens, e.g. genome-wide RNAi. The facility offers the infrastructure and support in screening assay development, automated sample preparation and high-throughput solid phase transfection with siRNAs on well plates or cell arrays. In addition, the facility provides access to automated high-throughput microscopy platforms and helps to set up the conditions suitable for automated data evaluation.

Furthermore, the facility also takes care of the data administration and helps customers with data analysis. In addition, it assists customers in making contact with experts on the campus in order to establish collaboration, which strengthens the research network in the field of biological screening in Heidelberg. In the past, projects starting out as services within the facility developed into solid scientific collaborations that are still very successful. Such examples show the important role of Core Facilities for research in life sciences and the campus.

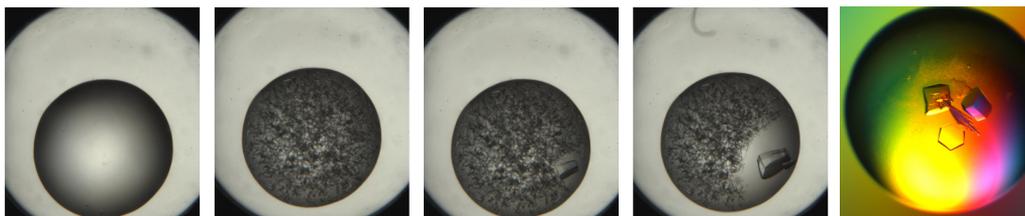


<http://www.bioquant.uni-heidelberg.de/technology-platforms/viroquant-cellnetworks-rnai-screening-facility/screening-core-facility.html>

PROTEIN CRYSTALLISATION

Protein crystals – tiny, beautiful and packed with information

Detailed knowledge about the spatial structure of a specific protein is highly important for many recent studies in the molecular life sciences. To get deeper insight into the protein structures on an atomic level, protein crystallization has been established as the most effective technique. Even though the protein monocrystals needed for this process are usually only a fraction of a millimeter in length, they are hard to obtain. The target protein needs to match high requirements in quality, amount, and purity. In addition, several hundreds to thousand mixtures of target protein and special crystallization cocktails have to be tested for a successful crystallization. In case of successful growth of crystals, the customers or their collaboration partners measure diffraction data sets which, in best case, can be used to calculate the three-dimensional protein structure. For this purpose high-quality X-ray is the method of choice and can only be conducted at a Synchrotron, such as the ESRF in Grenoble and the DESY in Hamburg.



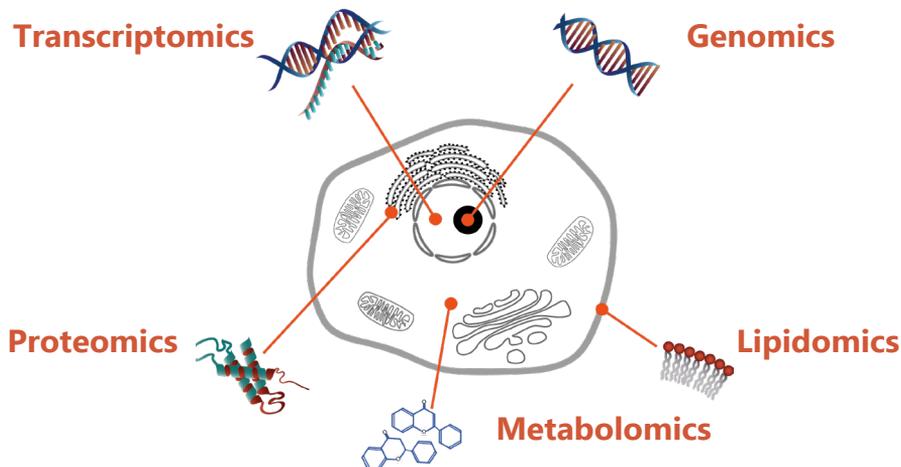
Images showing the process of crystallisation

Recognizing the need and the potential of a service unit for protein crystallization on the Heidelberg University Campus, CellNetworks member Prof. Dr. Irmgard Sinning from the Biochemistry Center established the Core Facility for CellNetworks in 2008. Pipetting robots specifically developed to produce hundreds of crystallization reactions on the nano-liter scale allow the preparation within a very short time. Since 2008, a fully automated system operates day and night to monitor and optically document the crystallization experiments continuously. The mission of the crystallization platform is to provide high-quality service to experts in structural biology and scientists with a different research focus. 10 years into its existence, the core facility is in very high demand by researchers on campus.

<http://xtals.bzh.uni-heidelberg.de>

OMICS

Omics technologies are used to characterize and quantify all sorts of biological molecules and to explore their roles, relationships and actions in the cells of an organism or tissue. These technologies include methods for the global analysis of proteins (proteomics), metabolites (metabolomics), lipids (lipidomics), RNA molecules (transcriptomics) in cells, as well as genomes (genomics). State-of-the-art, high-resolution mass spectrometry allows the identification and quantification of metabolites, proteins and their post-translational modifications. In order to meet the growing Mass Spectrometry demands of the members of CellNetworks concerning specification, resolution and throughput, three core facilities have been set up and expanded at the Heidelberg University - at the Biochemistry Center, BZH (Lipidomics), the Zentrum für Molekulare Biologie Heidelberg, ZMBH (Proteomics), and at the Centre for Organismal Studies Heidelberg, COS (Metabolomics). In addition, expression profiling and genomics has become one of the major methods to tackle scientific questions on a global molecular scale and include both quantitative and qualitative approaches. With the help of Next Generation Sequencing and Nano Stringing, researchers can now profile gene expression on a global scale or subset of selected genes in two Core Facilities, the Deep Sequencing Core Facility and the nCounter Core Facility, to eventually achieve a mechanistic understanding of disease, to identify novel candidate genes for diagnosis, or get insights into novel genomes and transcriptomes and their regulation.



PROTEOMICS

The Core Facilities for Mass Spectrometry and Proteomics was founded in 2000. Their mission is to provide state-of-the-art high-performance mass spectrometry services to researchers on the Campus. These services include not only all aspects of protein characterization, plus qualitative and quantitative proteomics, but also workshops and trainings in the newest methods in this field of research.



The analysis of protein contents, as well as their temporal, qualitative and quantitative changes during development, the reaction to environmental impacts or in pathophysiology can only be explored with the help of established procedures. Therefore the Core facility for Mass Spectrometry and Proteomics has set up targeted proteomics strategies of high accuracy and sensitivity, such as multiple reaction monitoring (MRM), to enable the quantitative analysis of known protein networks. For the analysis of protein mechanics, protein-protein interaction interfaces and ligand-induced allosteric conformational changes, the conformation of proteins can be analyzed using amide hydrogen exchange (HDX) mass spectrometry. In addition, the facility offers protein identification from 1D and 2D-gels, the quantification of proteins based on label-free approaches and isotope labeling techniques, the detection and localization of posttranslational modifications, and the deciphering of the interactome of target proteins.

METABOLOMICS

The Metabolomics Core Technology Platform was initiated in 2013 as part of the Institutional Strategy of Heidelberg University within the Excellence Initiative. The facility is located at the Centre for Organismal Studies Heidelberg (COS) and is a member of the HMLS Core Facility program. All researchers from Heidelberg University, the Heidelberg and Mannheim University Hospital, DKFZ, MPIImF and EMBL are welcome to use the metabolite analysis services offered by MCTP.

Within the last five years, the MCTP has established a highly diversified portfolio of analytical methods and processed samples for over 80 research groups. The primary aims of the MCTP are to offer reliable metabolite fingerprinting by LC-MS, GC-MS and Ion Chromatography as well as high throughput analyses of customer-defined metabolites in various biological sample matrices. Up to now, MCTP has conducted more than 30,000 metabolite analyses for research groups at the University of Heidelberg including BioQuant, DKFZ and the Faculties of Medicine and Biosciences, clearly demonstrating a growing demand for metabolomics in modern research projects.

In 2016, in a joint effort of several major stakeholders of Heidelberg life sciences campus the MCTP was able to acquire a Vion Ion mobility separation QToF mass spectrometer. This new instrument will allow a significant improvement of MCTP's technical portfolio and the implementation of advanced metabolomic techniques required for a number of state-of-the-art analyses, including improved untargeted metabolomics and fluxomics.

Requests for project discussions and analytical services can be placed via the HMLS Research Core Facilities' Management System (<https://hmls.corefacilities.org>). This enables easy communication, transparent status tracking for users, secure data exchange and streamlined project management for core personnel.

LIPIDOMICS

The Lipidomics platform at the Biochemistry Center of Heidelberg University is a research and development unit, which studies the function of lipids in diverse biological systems in collaboration with national and international research partners with the help of mass spectrometry. The research group around Prof. Dr. Britta Brügger, whose work initiated the development of this still young research area, is working on decoding the complex lipid network from a single cell to the systemic interaction/orchestration in various organisms, and for this purpose uses state-of-the-art equipment. The diversity of samples tested requires different ways of analysis over and over again, be it offering the latest methods or the use of new reference substances. "Gaining insights into various research areas, from cancer biology to bionic research, is what makes this work so exciting to me," explains Prof. Brügger. "In addition, the broad spectrum of samples constantly confronts us with new challenges. Therefore, a lavage, a liquid which is obtained from bronchial lavage, cannot be processed the same way for mass spectrometric measurements as a suspension of highly infectious viral particles or a biopsy of a tumor," she adds.



Here, a precise coordination between the collaboration partners is required. Many of the probes submitted help to broaden the range of measurable and analyzable Lipids. Every newly identified lipid molecule provides another piece in the jigsaw puzzle, i.e. the total picture of the complex mixture of naturally occurring lipids, whose exact number is not known so far. The complex interaction of lipids playing a role in changes related to disease can first be explained when

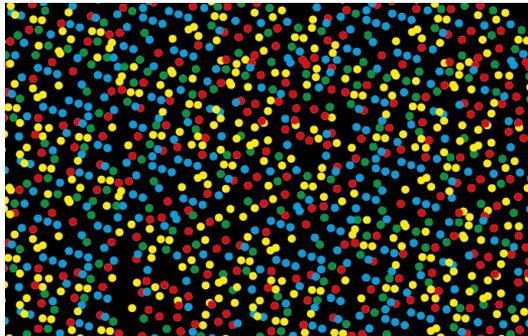
every single one of these components is determined. Examples include diseases from obesity to diabetes, as well as cancer and neurological disorders such as Alzheimer's. This task will stay with the lipidologists for many years to come and will be supported by the development of highly innovative new instruments.

GENOMICS AND TRANSCRIPTOMICS

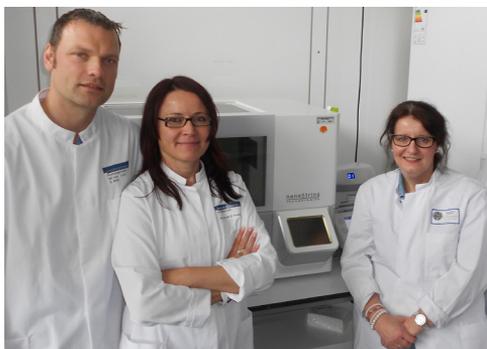
The CellNetworks Deep Sequencing Core Facility was established in 2010 to provide access to Next Generation Sequencing technology and expertise to users on the campus and for the Heidelberg University research community.

The Deep Sequencing Facility provides in-depth support for the project design, consultation on the sequencing mode, long-term expertise in library preparation offering customized protocols and spanning a large range of taxa. Every project is individually discussed, planned and executed, instead of performing standardized high-throughput workflows. On the basis of the focus on the individual project, the scientists benefit most and can obtain the best possible results in the context of their sequencing project, which would not be possible without the intense service provided by the facility. The analyses include a single- or a pair-end sequencing mode, and can be applied to different methods such as RNA-Seq, ChIP-Seq, Methyl/BS-Seq, de novo sequencing and re-sequencing of genomic DNA. More recently single-cell genomic applications have been established.

It is a major drive of the Deep Sequencing Core Facility to act as a methods and technology platform and to continually establish new protocols enabling the processing of challenging samples such as low input or metagenomics samples. For advice on bioinformatics, suitable software solutions and data analysis pipelines, customers can find support in the CellNetworks Math-Clinic Core Facility for Bioinformatics and Image Analysis, which works closely with the Deep Sequencing facility.



NANOSTRING



The CellNetworks nCounter Core Facility was established in 2011 to provide access to one of the current state-of-the-art expression profiling technologies for the Heidelberg University research community. Compared to Real Time PCR (RT PCR) the nCounter technology requires only minute amounts of total RNA (25-50 ng), raw cell lysate, or of genomic DNA (150 ng) and still allows direct counting of individual mRNA/microRNA as well as DNA molecules to study the expression profile or copy number of up to

800 genes from one individual sample. A unique coding technology using fluorescently labeled reporter probes, called 'codeSets', make the system very resistant to lower RNA quality and makes it suitable especially for critical samples, including e.g. formalin-fixed samples. Customized codeSets are designed by nanoString bioinformaticians but the facility also offers the use of commercially available pathway/disease specific codeSets. The nCounter Core Facility also provides help to the customers regarding experimental design. nanoString offers the nSolver software for data analysis free of charge for the customers. The software allows background correction, normalization and fold-change calculations, as well as various data visualization options.

To date, the Core Facility has carried out 81 projects for customers. The projects include RNA, miRNA and miRGE (that is parallel detection of mRNA and miRNA within one sample) from plasma, serum, total RNA and crude cell lysates, DNA fusion gene and copy number variation detection, on the one hand, and Chip-string detection on DNA level of freshly frozen tissue and pre-fixed material, which in the case of single cells is pre-amplified, on the other. Profiling was performed for more than 3300 samples including drosophila fly, xenopus frog, zebrafish, mouse and human origin. Together with the Math-Clinic, the nCounter Core Facility can be regarded as a showcase example for how Core Facilities can enrich each other by providing expertise and collaboration in the frame work of scientific projects. Expertise can be raised to a higher power and, in addition, the customer greatly benefits from this.

<https://www.klinikum.uni-heidelberg.de/nCounter-Core-Facility.120308.0.htm>

COURSES & WORKSHOPS

22 February 2018	Introduction to bioimage analysis
9 March 2018	Math-Clinic and Nikon joint workshop: Bioimage analysis using NIS Elements 5.0
14 May 2018	Introduction to Programming for Biologists
11 June 2018	Elektronenmikroskopie für Anfänger
1 January 2017	Advanced topics in bioimage analysis
6 February 2017	Next Generation Sequencing: Enrichment Based Targeted Resequencing
13 February 2017	Next Generation Sequencing: Amplicon Based Targeted Resequencing
12 March 2017	Analysis and Integration of Transcriptome and Proteome Data
27 March 2017	RNA Sequencing Library Preparation - How low can you go?
3 April 2017	Advanced R Programming
24 April 2017	Protein Bioinformatics BSc Course
24 April 2017	Practical Course: Single Cell Omics
2 May 2017	Next Generation Sequencing: RNA Sequencing Library Preparation
7 May 2017	Microbial Metagenomics: A 360° Approach
12 May 2017	Introduction to bioimage analysis using Fiji
15 May 2017	Next Generation Sequencing: Enrichment Based Targeted Resequencing
22 May 2017	Next Generation Sequencing: Whole Genome Sequencing Library Preparation
29 May 2017	Next Generation Sequencing: Amplicon Based Targeted Resequencing
6 June 2017	Whole Transcriptome Data Analysis
11 June 2017	CSAMA 2017 – Statistical Data Analysis for Genome Scale Biology
11 June 2017	Statistical Data Analysis for Genome Scale Biology
19 June 2017	BioImage Analysis using ImageJ/Fiji, ilastik and KNIME
19 June 2017	Quantitative Proteomics: Strategies and Tools to Probe Biology

19 June 2017	Software Carpentry Course
25 June 2017	Advanced Fluorescence Imaging Techniques
5 September 2017	Digital PCR
9 September 2017	Analysis of Non-Coding RNAs: quærere et invenietis
21 September 2017	Basic Statistics for Biologists or how to choose the appropriate statistical test
25 September 2017	Introduction to R programming (every semester)
3 October 2017	Whole Transcriptome Data Analysis
4 October 2017	Basic Statistics for Biologists or how to choose the appropriate statistical test
5 October 2017	Basic Statistics for Biologists or how to choose the appropriate statistical test
9 October 2017	Basic StatisticsF for Biologists or how to choose the appropriate statistical test
17 October 2017	Advanced Electron Microscopy
18 October 2017	Software Carpentry
18 October 2017	Introduction to long and short RNA-seq analysis
3 November 2017	Introduction to command line (for Linux and MacOS) and programming
7 November 2017	Galaxy introduction and RNA-seq Analysis
16 November 2017	Galaxy introduction and ChIP-seq Analysis
29 November 2017	Next Generation Sequencing: Whole Genome Sequencing Library Preparation
4 December 2017	PTMs of Proteins by Mass Spectrometry
4 December 2017	Protein Identification by Mass Spectrometry
5 December 2017	Proteomics: Quantification of Proteins in Complex Mixtures
6 December 2017	Targeted Proteomics for Sensitive and Robust Quantification
7 December 2017	Protein crystallization & introduction to protein crystallography
every semester	Electron Microscopy (HBIGS)



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LEAVE YOUR NOTES

