GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN / GERMANY

International Max Planck Research School

Molecular Biology

MSc/PhD Program

YEARBOOK 2018 / 2019

Yearbook 2018/2019

MSc/PhD Molecular Biology Program

at the University of Göttingen

International Max Planck Research School

Index

Letter from the President

Success for a comprehensive research university such as our Georg-August University of Göttingen is rooted in excellent science and its integration into an optimal learning environment to educate competent and critical young academics. I am very glad that our university in cooperation with the local Max-Planck Institutes and the German Primate Center has been able to establish conditions, which make top interdisciplinary science possible in an international setting enabling us all to feel the Göttingen Spirit.

The two international MSc/PhD programs in Molecular Biology and Neurosciences truly have contributed to our continued strive for excellence in science-oriented training both by integrating faculty members from university and non-university institutes across institutional borders and by providing comprehensive services especially for international students on the Göttingen Campus. Based on the proven concepts and the experience of these programs the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences (GGNB) was established, which is continuously supported by the federal Excellence Initiative since 2007.

The Molecular Biology and Neuroscience programs remain unique within the GGNB in offering integrated MSc/PhD curricula with a fast track option which allow excellent BSc graduates to directly enter the PhD phase after successfully absolving the initial 1st year training phase. For more than 15 years these international programs have been particularly successful in attracting high numbers of worldwide applicants of good academic quality providing the basis for the selection of the very best candidates. New ideas introduced by these programs have meanwhile been adopted by the Georg-August University School of Science (GAUSS) and other graduate schools for the benefit of the entire University.

While maintaining their successful structure the content and focus of the training curriculum of the programs has continuously been adapted to the changing research topics. Consequently, new faculty members are integrated to reflect novel developments in research. They will further ensure optimal individual supervision and up-to-date research-oriented training. Beyond academia both programs keep close contact with the relevant industries to enhance the opportunities of the graduates for a successful professional career in the private sector.

I would very much like to thank all colleagues and institutions for their committed support of these international programs and, last but not least, the German Academic Exchange Service (DAAD), the Lower Saxony Ministry of Science and Culture, and the various generous donors. The Georg-August University of Göttingen will continue to support these programs to promote international exchange at all levels and for further interaction with our partners worldwide.

Prof. Dr. Ulrike Beisiegel

(President of the Georg-August University of Göttingen)

Letter from the Max Planck Society

The mission of the Max Planck Society is to conduct basic research in science and humanities at the highest level. More than 80 Max Planck Institutes are located on scientific campuses across Germany, most of them close to universities.

Scientific ties between Max Planck Institutes and universities are traditionally strong. In 1998, during the 50th year celebration of the Max Planck Society in Göttingen, the Max Planck Society, together with the Hochschulrektorenkonferenz, launched the International Max Planck Research Schools as a new joint program to further intensify cooperation.

The goals of the International Max Planck Research Schools are

- to attract excellent students from all around the world to intensive Ph.D. training programs in Germany, preparing them for careers in science,
- to integrate Max Planck scientists in top-level scientific training of junior scientists,
- to intensify the ties to the universities owing to the participation of internationally renowned Max Planck scientists in joint teaching activities, and
- to strengthen international relationships by providing individual support to each student and by exposing foreign students to German culture and the German language.

By now, 67 International Max Planck Research Schools have been established involving 73 Max Planck Institutes, 36 German universities and 26 universities abroad. About 3,200 PhD students from 123 countries are presently enrolled.

Since their foundation in the year 2000, the Göttingen International Max Planck Research Schools in Molecular Biology and Neuroscience have met with extraordinary success. Every year, the programs receive hundreds of applications, with the quality of the students consistently being very high. Most students graduated so far have moved on to postdoctoral positions, many at prestigious international institutions. In the past years, the Göttingen Schools received unanimous acclaim during external evaluations and won national awards. For instance they are the only Life Science Programs within Germany that were selected for the “Top Ten International Master’s Degree Courses 2006”. The Schools have also re-shaped the local scientific community, strengthening the ties between the participating institutions, and initiated new scientific collaborations that augment the international reputation of Göttingen as a center of scientific excellence. Furthermore, the Schools served as role models and founding members of the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences, thus being instrumental for the continued support by the German Excellence Initiative provided to the university. We hope that in the years to come the students of the International Max Planck Research Schools will be successful in their professional careers. We also hope that they will remember their training period in Göttingen as an exciting and stimulating phase in their lives.

Martin Stratmann
President
Max Planck Society

Marina Rodnina
Dean of the IMPRS
Molecular Biology

Overview

This yearbook is intended to provide information on the international MSc/PhD Molecular Biology Program in Göttingen, Germany, which was established in the year 2000 as a joint venture of the University of Göttingen and its non-university partners. It is also supported by the Max Planck Society as an International Max Planck Research School (IMPRS). In addition to general information on the program, the yearbook introduces the MSc students of the 2018/19 class, the faculty members, the program committee and the coordination team.

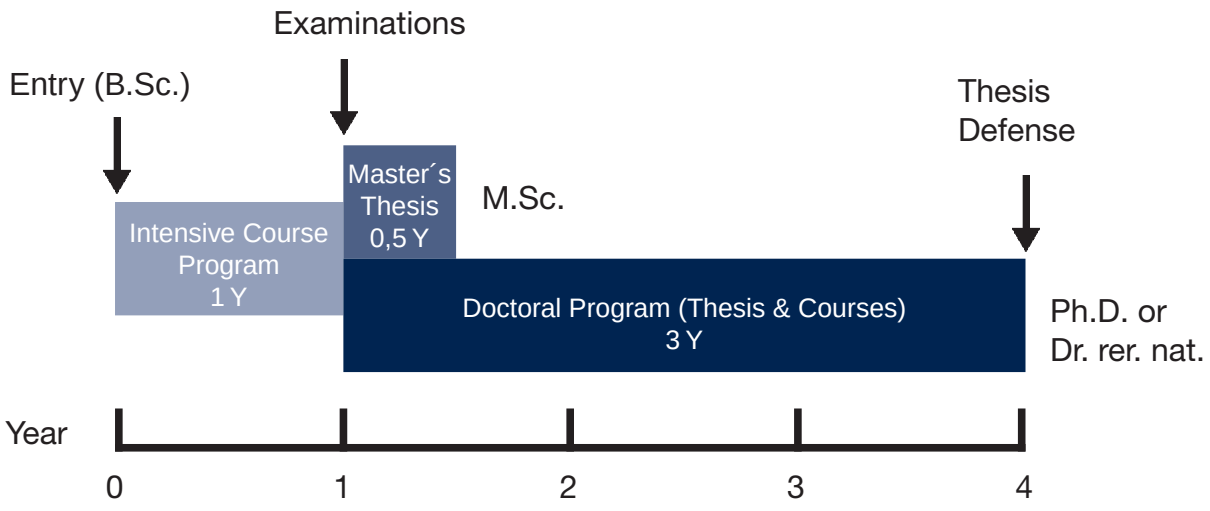
The program belongs to the Göttingen Graduate Center for Neurosciences, Biophysics, and Molecular Biosciences (GGNB), which is funded by the Excellence Initiative of the German Federal and State Governments. It is offered by the Göttingen Center for Molecular Biosciences (GZMB), the Max Planck Institute for Biophysical Chemistry, the Max Planck Institute for Experimental Medicine, and the Leibniz Institute of Primate Research (German Primate Center). Further to their active participation in the Molecular Biology Program and the research activities of the GZMB, the above-mentioned partners closely cooperate in several research alliances, collaborative research centers, and interdisciplinary doctoral programs.

The intensive, research-oriented curriculum of the International MSc/PhD Molecular Biology Program qualifies students for professional work in the fields of molecular and cellular biosciences. The program is open to students from Germany and from abroad, who hold a Bachelor‘s degree (or equivalent) in the biosciences, chemistry, medicine, or related fields. Scholarships are available. All courses are held in English. The academic year starts in October and is preceded by a three-week orientation program. Applications may be submitted until January 15 of the year of enrollment. To ensure a high standard of individual training, the number of participants is limited to 20 students per year.

All students initially participate in one year of intensive course work. This first segment of the program comprises lectures, tutorials, seminars, methods courses, training in professional skills, and individually supervised research projects (laboratory rotations). The traditional German structure of academic semesters is not followed. The condensed schedule allows students to accumulate 90 credits (ECTS) within one year, which would normally require three semesters.

Subsequently, two separate segments are offered:

- **PhD Program:** Good to excellent results after the first year qualify for direct admission to a three-year doctoral project in one of the participating research groups. The Master's thesis requirement is waived in this case. After successful defense of a doctoral thesis, the degree Doctor of Philosophy (Ph.D.) or the equivalent title *Doctor rerum naturalium* (Dr. rer. nat.) is conferred.
- **MSc Program:** Alternatively, students may conclude the program with a Master's thesis, based on six months of experimental scientific research. The degree Master of Science (MSc) is awarded upon successful completion of the Master's thesis.



Intensive Course Program (First Year)

Throughout the first year, current topics in molecular biology are covered by

- lectures
- tutorials
- methods courses
- laboratory rotations
- seminars

Lectures and Tutorials

A comprehensive lecture series is offered in a sequence of 6-12 week units. The following topics are taught at an advanced level throughout the first year (36 weeks, 4 hours per week):

Module M.MolBio.11: DNA and Gene Expression

- architecture of the cell
- DNA and chromatin structure, epigenetics
- DNA replication and repair
- genomics
- transcription, RNA splicing, RNA quality control
- RNA-based regulation of prokaryotes and eukaryotes
- translation, protein structures and folding, posttranslational modification

Module M.MolBio.12: Metabolic and Genetic Networks

- enzyme mechanisms and regulation
- basic metabolism, metabolic networks
- biological membranes
- photosynthesis
- signal transduction
- molecular evolution, microbiomes

Module M.MolBio.13: Cell Biology / Immunology / Neuroscience / Developmental Biology

- biosynthesis of organelles, nucleocytoplasmic transport
- protein sorting and processing, membrane traffic
- ubiquitin, autophagocytosis
- cytoskeleton, cell adhesion
- immunology, infectious diseases, principles of pathogenicity
- cell cycle, meiosis, apoptosis, cancer
- neurons, synapses, synaptic transmission
- glial cells and brain vasculature
- nervous systems, sensory systems
- developmental biology

Module M.MolBio.14: Model Systems / Biotechnology

- stem cells
- fungi, *Arabidopsis*, *Drosophila*
- *C. elegans*, *Xenopus*, zebrafish, mouse
- non-human primate models, use in primate research
- biotechnology (bacteria, fungi, plants, insects)

Each lecture is accompanied by a tutorial session, where students meet with a tutorial in small groups. Tutorials involve exercises, review of lecture material, and a discussion of related topics.

Methods Courses

During the first two months of the Molecular Biology Program, students participate in a series of methods courses to introduce them to principles and practical aspects of basic scientific techniques and the handling of model organisms. During the first two weeks, two 4-day projects with proteins and nucleic acids introduce various basic and advanced techniques. Weeks 3 and 4 provide an overview over various aspects of bioinformatics. Weeks 5 to 7 comprise six 2-day experiments on a variety of different methods indicated below. In addition, students are offered a choice of two (out of four) 5-day special courses with an integrated concept of lectures and hands-on experiments as indicated below. Prior to the course program, students get introduced to programming in R and basis statistics.

Introductory 4-day methods courses (week 1-2)

- proteins
- DNA

Bioinformatics courses (week 3-4)

- next generation sequencing, NGS analysis with R
- protein bioinformatics
- comparative sequence analysis, phylogeny
- gene ontologies & biological networks
- advanced biological networks

Introductory 2-day methods courses (week 5-7)

- analysis or protein-protein and nucleic acid-protein interaction
- RNA analysis
- light microscopy
- analysis of cellular compartments
- cell culture
- expression analysis

Special 5-day methods courses (week 7-8)

- X-ray crystallography
- (3-D-cryo) electron microscopy
- NMR spectroscopy
- mass spectrometry / proteomics

Professional Skills in Science

Additional training is offered in four separate units to prepare the students for professional scientific communication and good scientific practice:

- scientific writing and graphics
- oral presentation of scientific results
- laboratory safety
- good scientific practice
- experimental animal handling

Laboratory Rotations

Starting in January, every student conducts three independent research projects (laboratory rotations) in the participating departments. Each project is individually supervised. It involves seven weeks of experimental work, followed by one week for data analysis and presentation. For each project, a report must be completed in the format of a scientific publication. The laboratory rotations cover three different research areas and methods.

Seminars

Seminars start in March. The class meets weekly for two hours to discuss student presentations. The presentations are research reports based on work from the laboratory rotations.

Examinations

After the first year of intensive training, all students take one written and two oral Master's examinations. The Master's examinations explore the students' theoretical background in topics covered by lectures and tutorials. Each oral examination investigates the qualification in selected topics of the molecular life sciences.

PhD Program

Students who have passed the Master's examinations with good or excellent results qualify for direct admission to a three-year doctoral project in one of the participating research groups without being required to complete a Master's thesis first.

The PhD program emphasizes independent research by the students in the group of a faculty member. The PhD students select three independent faculty members as their thesis advisory committee who closely monitor progress and advise the students in their research project. Laboratory work is accompanied by seminars and lecture series, a wide variety of advanced methods courses, training in scientific writing and oral presentation skills, courses in intercultural communication, career planing, time and project management, bioethics and research ethics, elective courses, and participation in international conferences or workshops. Regular industry excursions are offered to biotechnologyical or pharmaceutical companies, including visits of the R&D facilities and discussions of career options with representatives of the HR departments.

Doctoral students of the program organize the international PhD student symposium "Horizons in Molecular Biology" every year with great success, attracting outstanding speakers and up to 300 participants from all over the world. The meeting was designed by the students to promote scientific exchange between young researchers from different disciplines. Since 2007, a "Career Fair for Scientists" precedes the annual Horizons meetings. The career fair offers a unique and exciting program of career presentations, CV-Check, workshops and interviews and is also organized by the Molecular Biology students. Both events include an increasing number of alumni, sharing their experience.

At the end of the PhD training program, a doctoral thesis is submitted either in the traditional format, or as a collection of scientific publications in internationally recognized journals along with a general introduction and a discussion of the results. The degree of a "Ph.D." or, alternatively, "Dr. rer. nat." is awarded after the successful defense of the doctoral thesis.

Master's Program

After the first year of intensive training, students may conclude the Master's part of the program with a six-month thesis project, leading to a Master of Science degree. The thesis project involves experimental work under the supervision of faculty member of the Molecular Biology Program. Students also have the opportunity to conduct their Master's thesis project at a research institution abroad.

Orientation, Language Courses, Social Activities

A two-week orientation prior to the course program provides assistance and advice for managing day-to-day life in Germany, including arrangements for bank account, health insurance, residence permit, housing, and enrolment. Students have the opportunity to meet faculty members and visit laboratories of the participating institutions. In addition, the orientation program informs students about computing and library facilities, the city and university of Göttingen, sports facilities, and cultural events.

The orientation program also includes several course units to refresh basic knowledge in chemistry and physics and introduces the students to programming in R and basic statistics.

An intensive basic language course in German is offered in cooperation with *Lektorat Deutsch als Fremdsprache* to facilitate the first weeks in Göttingen. Additional language courses and social activities accompany the program.

Application, Selection, and Admission 2018

Applicants must hold a Bachelor's degree or equivalent in biology, biochemistry, chemistry, medicine, or related fields. Applicants who are not native speakers of English should demonstrate adequate competence of the English language by acceptable results in an internationally recognized test.

In the year 2018, the Molecular Biology Program received 814 applications from 74 countries.

Continent	Applications	Admissions
Europe (total)	**128**	**14**
Germany	24	5
other West Europe	19	0
East Europe	85	9
America (total)	**46**	**1**
North America	22	1
Central/South America	24	0
Africa (total)	**214**	**0**
North Africa	69	0
Central/South Africa	145	0
Asia (total)	**426**	**7**
Near East	61	0
Central Asia/ Far East	365	7

Students 2018 / 2019

Name		Home Country
Arjun	Bhatta	Nepal
Margarita	Chudenkova	Russian Federation
Vladyslav	Dembrovskyi	Ukraine
Iga	Grządzielewska	Poland
Aybeg	Günenç	Turkey
Kai-Lin	Hong	Taiwan
Rohan	Kapoor	India
Selay	Kaya	Turkey
Nicole	Kleiber	Brazil / Germany
Barbora	Knotkova	Czech Republic
Hong-Yu	Lee	Taiwan
Florian	Mayr	Germany
Mehar	Monga	India
Vella	Nikolova	Bulgaria
Alexander	Rotsch	Germany
Jennifer	Struck	Germany
Siqi	Sun	China, P.R.
Yuliia	Tereshchenko	Ukraine
Carlos	Vanegas Torres	Mexico
Marcel	Werner	Germany
Yajie	Zhu	China, P.R.
Evi	Zhuleku	Albania

Arjun Bhatta

Nepal

Arjun Bhatta

EDUCATION

College / University

Sharda University

Highest Degree

Bachelor of Technology

Major Subjects

Biotechnology

Lab Experience

Routine microbiological techniques; DNA, RNA and plasmid isolation; PCR, RT-PCR, gradient PCR and RAPD; gene cloning and expression; affinity and ion-exchange chromatography; EMSA; kinetic and end-point enzyme assays.

Projects / Research

06/2017 – 04/2018: “Recombinant production, purification and characterization of rstA, an *A. baumannii* two-component response regulator”; UG Thesis Project under supervision of Dr. Amit K. Singh, Sharda University.

12/2017 – 02/2018: “Molecular docking and dynamic simulation to identify ligands potentially binding to regulatory domain of *A. baumannii* two-component response regulator, rstA.”

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2015 – 2018: Sharda University School of Engineering and Technology Dean’s List.

2014 – 2015: Sharda University Merit-based Entrance Scholarship.

Margarita Chudenkova

Russian Federation

Margarita Chudenkova

EDUCATION

College / University

Lomonosov Moscow State University

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology

Lab Experience

Mitochondria and ribosome isolation, Bradford assay, 1D/2D Blue Native PAGE, SDS-PAGE, in-gel (Coomassie, Ponceau, silver, activity) staining, Western Blot, sucrose density gradient centrifugation and fractionation, PCR, bacterial transformation and cell culture, DNA isolation and purification, affinity chromatography.

Projects / Research

9/2017 – 6/2018: “Changes in mitochondrial respiratory chain supercomplexes in human tumor tissues”, Lomonosov Moscow State University, Laboratory specializing in mitochondrial research.

5/2017 – 7/2017: “The role of AIM23 protein in ribosome splitting in yeast mitochondria”, Lomonosov Moscow State University, Laboratory specializing in mitochondrial research.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

Ukraine

Vladyslav Dembrovskyi

EDUCATION

College / University

Taras Shevchenko National University of Kyiv, Ukraine

Highest Degree

Bachelor of Science

Major Subjects

Biology, Molecular Biology

Lab Experience

Wet lab: SDS-PAGE, Western blot, ELISA, transformation and cloning.

Dry lab: Bash, Python, R + associated libraries and packages (biopython, ggplot2, FastX); programs Trimmomatic, FastQC, MegaBLAST, Centrifuge.

Projects / Research

03/2018 – 05/2018: “Interaction of species in hypersaline environments assessed by whole genome metagenomics”, CRG, Barcelona, Spain.

02/2017 – 07/2017: “Time series bioinformatical analysis of children’s microbiota suffering from an acute infectious diarrhea”, I2SysBio, Valencia, Spain.

01/2016 – 01/2017: “Interactions between human recombinant ITSN2 and clathrin heavy chain in receptor-mediated endocytosis”, IMBG, Kiev, Ukraine.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2014 – 2018: Ukrainian State Scholarship for excellent studying achievements.

2017: Scholarship for Summer School in Bioinformatics “#NGSchool2017”.

2017: ERASMUS exchange semester at the University of Valencia, Spain.

Poland

Iga Grządzielewska

EDUCATION

College / University

Poznan University of Medical Sciences

Highest Degree

Bachelor of Science

Major Subjects

Medical Biotechnology

Lab Experience

PCR, RT-qPCR, HRM, RFLP, molecular cloning, Western blot, flow cytometry, immunoassays, plant tissue culture, mammalian cell culture, enzyme assays, spectroscopic analysis, chromatographic techniques, extraction methods, chromosome staining techniques, fluorescence microscopy.

Projects / Research

01/2018 – 06/2018: “Personalization of melanoma therapeutic vaccination”, supervisor: Dr. Patrycja Czerwińska, Poznan University of Medical Sciences.

2017 – 2018: “Functional analysis of TRIM28 domain mutants in melanoma cell line model”, supervisor: Dr. Patrycja Czerwińska, Poznan University of Medical Sciences.

10/2017 – 06/2018: “The role of long non-coding RNA (lncRNAs) in the regulation of gene expression”, Bachelor’s thesis, supervisor: Prof. Dr. Paweł Jagodziński, Poznan University of Medical Sciences.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2016 – 2018: President’s of Poznan University of Medical Sciences scholarship for outstanding academic performance.

Aybeg Günenç

Turkey

Aybeg Günenç

EDUCATION

College / University

Boğaziçi University

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Genetics

Lab Experience

PCR, qRT-PCR, bacterial culture, molecular cloning, protein purification, CRISPR-Cas9 system, eukaryotic cell culture, transfection, Lentiviral transduction, light and fluorescence microscopy, enzyme-protein assays, live infection assay, electrophoresis (SDS-PAGE and agarose), ELISA, Western blotting, IF-staining, laser-scanning confocal microscopy, *D. melanogaster* maintenance.

Projects / Research

10/2015 – 02/2017: Intern at Plant Research Group, Department of Molecular Biology and Genetics, Boğaziçi University.

06 – 08/2017: "Expression, Purification and Characterization of De Novo Mouse Gene Proteins in *Escherichia coli*", EBB-Evolutionary Bioinformatics Group, Institute of Evolution and Biodiversity, WWU Münster.

09/2017 – 05/2018: "Generation of NLRP7-knockdown THP-1 Cell Line by CRISPR-Cas9", Apoptosis and Cancer Immunology Laboratory, Department of Molecular Biology and Genetics, Boğaziçi University.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

03 – 08/2017: ERASMUS+ Grant for Exchange Semester in WWU Münster.

Kai-Lin Hong

Taiwan

Kai-Lin Hong

EDUCATION

College / University

National Taiwan University

Highest Degree

Master of Science

Major Subjects

Biochemical Science and Technology

Lab Experience

Cell culture, CRISPR/Cas9, bacteria and yeast culture, protein expression and purification, fermentation, molecular cloning, protein analysis.

Projects / Research

2017 – 2018: "Engineering Bacteria as a Smart Drug Delivery Vehicle".

2015 – 2017: "Effects of the Three Tryptophan Residues on the Functions of an Immunomodulatory Protein from *Ganoderma microsporum*, GMI".

2014 – 2015: "Mapping RNA exit channel on transcribing RNA polymerase I by chemical probe, FeBABE".

2013 – 2014: "Sensitive Detection of Aflatoxin B1 by Oligo-nucleotides Conformational Change with Formation of a DNA-adduct".

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2015: Research Achievement Award of NTUBST.

2014 – 2015: College Student Research Fellowship, National Science Council.

2013: Travel grant from College of Life Science, National Taiwan University.

Rohan Kapoor

India

Rohan Kapoor

EDUCATION

College / University

Sri Venkateswara College, University of Delhi

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry, Cell Biology, Molecular Biology, Genetics, Endocrinology, Physiology, Membrane Biology, Immunology

Lab Experience

Spectrophotometry, enzyme assays, protein purification techniques, chromatography, microscopy, cell viability assays and clinical biochemistry; gel electrophoresis, basic RDT techniques; immunological techniques; genetic studies using *Drosophila*; basic bioinformatics.

Projects / Research

2016 – 2018: DBT-STAR Innovation Project “Network Analysis in Systems Biology of Neurological Disorders”, Sri Venkateswara College, DU.

2015: DU Innovation Project “Science in Music”, Sri Venkateswara College, DU.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2017 – 2018: Third prize for presentation on the topic “Bioluminescence, Fireflies and the Next Generation Bio-Lights”, Mindspar, University of Delhi.

Selay Kaya

Turkey

Selay Kaya

EDUCATION

College / University

Middle East Technical University

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Genetics

Lab Experience

SDS-PAGE, agarose gel electrophoresis, qPCR, Western blotting, cDNA synthesis, His/SUMO-tag protein purification, gel filtration and affinity chromatograpy, bacterial/yeast culture, bacterial transformation, gene knockout in yeast, assays for quantitative protein concentration.

Projects / Research

2/2018 – 6/2018 “Identification of transcription factors that interact with Arid4b protein in embryonic stem cells”, Nihal Terzi Çizmecioğlu, Department of Molecular Biology and Genetics, METU

6/2017 – 9-2017 “Protein Homeostasis and Stress Response in Model Organism *Bacillus subtilis*”, Group of K. Turgay, Institut für Mikrobiologie, Leibniz Universität Hannover

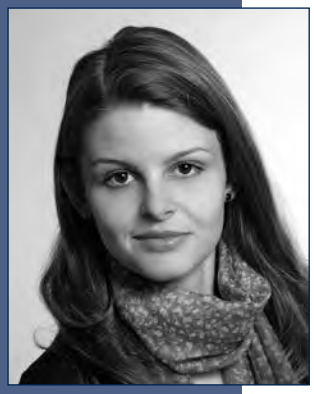
Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2017: Erasmus+ Traineeship Grant.

2013 – 2018: Higher Education Scholarship by The Republic of Turkey General Directorate of Higher Education Credit and Hostels Institution.

Nicole Kleiber



Germany

Nicole Kleiber

EDUCATION

College / University

University of São Paulo (02/2013 – 12/2017)

Ludwig Maximilian University of Munich (10/2015 – 09/2016)

Highest Degree

Bachelor of Science

Major Subjects

Molecular and Cell Biology, Microbiology, Immunology

Lab Experience

Cloning with plasmid vectors, reporter gene assays, transfection assays, ELISA, Western blot, PCR, Sanger sequencing, DNA/RNA extraction, production of RNA *in vitro*, flow cytometry, handling of laboratory animals, fluorescence microscopy.

Projects / Research

03/2017 – 12/2017: "Establishment of RNA vaccine delivery techniques using RNA replicons stabilized by cationic liposomes *in vitro* and *in vivo*", Institute of Biomedical Sciences, University of São Paulo, São Paulo, Brazil.

08/2014 – 06/2015: "The production of monoclonal chimeric antibodies capable of targeting E protein from dengue virus type 2 to the population DEC205 of Dendritic Cells",Institute of Biomedical Sciences, University of São Paulo, São Paulo, Brazil.

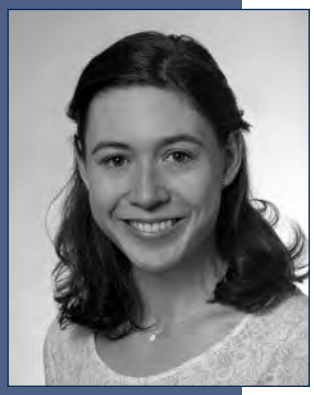
Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2017: São Paulo Research Foundation (FAPESP) fellowship.

2015 – 2016: Brazil's "Science without Borders" scholarship program, funding agency: CAPES.

Barbora Knotková



Czech Republic

Barbora Knotková

EDUCATION

College / University

The University of Manchester, UK (2014 –2018)

Highest Degree

Master of Science

Major Subjects

Biochemistry

Lab Experience

Yeast culture, molecular cloning, protein purification, fluorescent microscopy, ImageJ analysis.

Projects / Research

09/2017 – 06/2018: "Investigation of translation factories associated with aromatic amino acid metabolism", Master project under the supervision of Prof. Mark Ashe, The University of Manchester, UK.

06/2017 – 09/2017: Study of interactions between cargo receptors and their cargo at the ER-Golgi interface, Summer project under the supervision of Dr. Liz Miller, MRC Laboratory of Molecular Biology, UK.

07/2016 – 09/2016: GFP-tagging of a bacterial metal ion channel and purification of coronaviral proteins for antigen use, Summer project under the supervision of Prof. Ian Jones, University of Reading, UK.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

06/2017 – 09/2017: LMB research summer studentship.

Hong-Yu Lee

Taiwan

Hong-Yu Lee

EDUCATION

College / University

National Taiwan University

Highest Degree

Bachelor of Science

Major Subjects

Life Science

Lab Experience

Basic biochemical and molecular biology techniques such as DNA/RNA extraction, PCR, transformation, restriction analysis, SDS-PAGE, Western blotting, immunohistochemistry, ELISA.

Projects / Research

07/2017 – 08/2017: “The role of pknB/stp in *Staphylococcus aureus* persistence”, Division of infectious diseases and hospital epidemiology, University Hospital Zurich, University of Zurich, Switzerland.

07/2016 – 08/2016: “Anti-PEG bispecific antibody engineering for nanomedicine in cancer treatment”, Institute of Biomedical Sciences, Academia Sinica, Taiwan.

02/2015 – 06/2017: “The role of secreted frizzled-related protein during regeneration in *Aeolosoma viride*”, Department of Life Science, National Taiwan University, Taiwan.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2018: Dean’s Award, College of Life Science, National Taiwan University.

2017: Abroad Education Scholarship, College of Life Science, National Taiwan University.

Florian Mayr

Germany

Florian Mayr

EDUCATION

College / University

University of Applied Sciences Biberach

Highest Degree

Bachelor of Science

Major Subjects

Cell Biology, Molecular Biology, Microbiology

Lab Experience

General molecular biology techniques such as SDS-PAGE, Western blot, PCR / RT-PCR, cloning, transformation, ELISA. Cultivation of mammalian cell lines (up to 2 L bioreactors), cell viability assays, protein purification using chromatography (SEC, HIC, IEX, AC), RNAi, HPLC, confocal microscopy, high content imaging, Luciferase-reporter assays, flow cytometry.

Projects / Research

03/2017–11/2017: “Exploration of a possible TP53 dependent regulation of *NUDT22* upon cellular stress”, P. Herr, T. Helleday, Division of Translational Medicine and Chemical Biology, Department Medicinal Biochemistry & Biophysics, Karolinska Institutet, Stockholm.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2017: Erasmus+ Stipend.

Mehar Monga

India

Mehar Monga

EDUCATION

College / University

Sri Venkateswara College, University of Delhi

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry, Genetics, Cell Biology, Molecular Biology, Immunology, Endocrinology, Metabolism

Lab Experience

Spectroscopy, protein purification and assay, gel electrophoresis, chromatography, hematology, DNA, RNA and plasmid isolation, PCR, transformation of *E. coli* culture, double immuno diffusion, ELISA, Western blot, *Drosophila* maintenance and cross setting and basic bioinformatics.

Projects / Research

2016–2018: DBT-CIC Star Innovation project: "Network analysis in Systems Biology of Neurological Disorders".

2013: "Inspire Internship Program", Department of Science and Technology, University of Delhi.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2016 – 2018: Stipend for Star Innovation Project by the Cluster Innovation Centre.

2015 – 2018: Kishore Vaigyanik Protsahan Yojna (KVPY) fellowship by the Department of Science and Technology.

Vella Nikolova

Bulgaria

Vella Nikolova

EDUCATION

College / University

Sofia University St. Kliment Ohridski, Sofia, Bulgaria

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology

Lab Experience

Various techniques in biochemistry and molecular biology; different *Arabidopsis* techniques (seed sterilization, growing, analysis of salt stress response, histochemical GUS staining); DNA Gyrase supercoiling and cleavage assays; microbiological techniques; cloning techniques; protein purification.

Projects / Research

10/2015 – 07/2018: "Aberrant DNA methylation patterns affect salinity stress responses of *Arabidopsis thaliana*", Institute of Plant Physiology and Genetics, Bulgarian Academy of Sciences.

10/2016 – 04/2018: Department of Biochemistry, Faculty of Biology, Sofia University.

07/2017 – 08/2017: "The role of Exonuclease VII from *E. coli* in processing DNA Gyrase-DNA complexes", John Innes Centre, Norwich, UK.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

05/2018: Student of the year 2017/2018 award: 3rd place in catego000ry Natural Sciences and Biotechnology.

03/2015 – 07/2018: Stipends for excellent grades at Sofia University.

07/2017 – 08/2017: Grant from Lister Institute of Preventive Medicine.

Alexander Rotsch

Germany

Alexander Rotsch

EDUCATION

College / University

Georg-August-University Göttingen

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry

Lab Experience

DNA and RNA isolation, acrylamide and agarose gel electrophoresis, Western blotting, PCR, Gibson assembly, insect cell culture, protein expression and purification, light and fluorescence microscopy, GC-MS, *in vitro* pollen tube growth, TLC, steady-state kinetics, fluorescence spectroscopy.

Projects / Research

2017 – 2018: "Effect of fusion tags on the ATP sensor ATeam", Bachelor's thesis at the Max-Planck-Institute for Biophysical Chemistry, Göttingen.

2015 – 2017: "Pollen tube metabolism" and "Changes in specialized metabolism due to different red/blue light ratios in *A. thaliana*", internship at the Albrecht-von-Haller-Institute for Plant Sciences, Göttingen.

2015: "Evolution of Brains of marsupials", internship at the University of Queensland.

2014: "Function of lipid droplets in pollen tube development" internship at the Albrecht-von-Haller-Institute for Plant Sciences, Göttingen.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2015 – 2019: German Academic Scholarship Foundation.

Jennifer Struck

Germany

Jennifer Struck

EDUCATION

College / University

Georg-August-University of Göttingen

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry

Lab Experience

PCR, restriction digest, ligation, agarose gel electrophoresis, transformation/cloning, protein purification, SDS-PAGE, CD spectroscopy, liposome reconstitution, DLS, stopped-flow spectroscopy, ITC.

Projects / Research

11/2017 – 02/2018: "Characterization of the Ca^{2+} dependent binding mechanism of Synaptotagmin 1 to membranes", Prof. Dr. Reinhard Jahn, Department of Neurobiology, Max Planck Institute for Biophysical Chemistry, Göttingen.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

12/2016 – 05/2017: Scholarship for the European Community Mobility Program "Experts Sustain" as part of "Erasmus Mundus", Maldives National University.

China, P.R.

Siqi Sun

EDUCATION

College / University

Shandong University, China

Uppsala University, Sweden

Highest Degree

Bachelor of Science

Major Subjects

Biology

Lab Experience

PCR, RNA extraction, Western blot, SDS-PAGE, protein purification (Ni-NTA and anion-exchange chromatography, gel filtration), protein crystallization, enzyme assays, protein structure prediction, Multisite Gateway cloning, and other basic biochemical and microbial techniques.

Projects / Research

03/2018 – 06/2018: "Structure and catalytic activities of 4 glycoside hydrolases in *Gardnerella vaginalis*". Bachelor's thesis, Shandong University, China.

03/2017 – 06/2017: "Comparison of miR165/166's role in primary and lateral root development". Bachelor's thesis, Uppsala University, Sweden.

09/2015 – 06/2016: "Preliminary analysis of extracellular enzymes and anti-fungi activity of 65 mycobiont strains from Arctic and Yunnan Province of China", Internship, Shandong University, China.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2016: International Exchange Scholarship, Shandong University.

2015: Second-class Scholarship (Top 10%), Shandong University.

Ukraine

Yuliia Tereshchenko

EDUCATION

College / University

Taras Shevchenko National University of Kyiv

Highest Degree

Bachelor of Science

Major Subjects

Biology, Chemistry

Lab Experience

I have been working for two years at the Department of Cell Signaling, Institute of Molecular biology and Genetics, NAS, Ukraine.

Projects / Research

Analysis of S6K1 phosphorylation in 2D and 3D cell culture of MCF-7 cell lines.

Generation of MCF-7 cell lines with downregulated expression of different S6K1 isoforms.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

Internal scholarship at Taras Shevchenko National University of Kyiv.

Carlos Vanegas Torres

Mexico

Carlos Vanegas Torres

EDUCATION

College / University

School of Chemistry, National Autonomous University of Mexico (2012 – 2018)

University of California, Santa Cruz (2016)

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry and Microbiology

Lab Experience

Ample experience working with prokaryotic and eukaryotic cells as well as with viral strains. Well-versed in basic molecular biology techniques such as DNA, RNA and protein extraction, quantification (UV-Vis spectrophotometry, band densitometry), separation (acrylamide and agarose gel electrophoresis) and identification (Western blotting, PCR/RT-qPCR). Experience with immunostaining methods, ELISA, optical/fluorescence microscopy, yeast transfection and mutant screening.

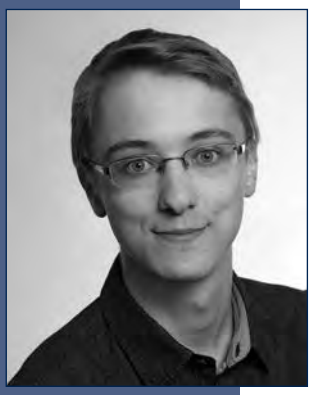
Projects / Research

02/2017 – 06/2018: "Evaluation of the Influenzavirus A(H1N1)- induced expression of adhesion molecules in A549 cells and its effect on the adherence of *Aspergillus fumigatus conidia*", Department of Virology and Mycology, National Institute for Respiratory Diseases.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

Marcel Werner



Germany

Marcel Werner

EDUCATION

College / University

Georg-August-Universität Göttingen

Highest Degree

Bachelor of Science

Major Subjects

Molecular Medicine

Lab Experience

Molecular biology techniques such as PCR/qRT-PCR, Western Blot, FACS, various CRISPR/Cas9 techniques and molecular cloning. Cell culture methods including mammalian cell culture, transfection, chemotherapy treatments and functional assays. Staining techniques (HE, IHC, IF), RNAseq data analysis.

Projects / Research

05/2018 – 08/2018: "Investigating the role of ROBO3 and GDF15 in cell plasticity and therapy resistance of triple-negative mammary carcinoma", F. Wegwitz, Department of Tumor Epigenetics, GZMB, Göttingen.

08/2017 – 10/2017: "Enhancing MYC and EZH2 expression via dCas9 based epigenetic modifications", F. Wegwitz, Department of Tumor Epigenetics, GZMB, Göttingen.

02/2017 – 03/2017: "A characterization of YKT6 under starvation conditions", J. Gross, Department of Developmental Biochemistry, Department of Hematology and Medical Oncology, UMG.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

Yajie Zhu

China, P.R.

Yajie Zhu

EDUCATION

College / University

Tongji University

Highest Degree

Bachelor of Science

Major Subjects

Biotechnology

Lab Experience

Drosophila genetics, *Drosophila* dissection, immunostaining, microscopy.

Projects / Research

2015 – 2017: “Caspase Signaling Promotes Sensory Organ Precursor Cell Fate Determination through Wnt Signaling in *Drosophila*”, Bachelor thesis.

2016 – 2017: “Cka Modulates JNK-Mediated Cell Death in *Drosophila*”.

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

2018 Shanghai Outstanding Graduate.

2017 – 2018: First Class Scholarship of Tongji University.

2014 – 2015: National Encouragement Scholarship by Ministry of Education of China.

2015 – 2016: National Scholarship by Ministry of Education of China.

2014 – 2015, 2015–2016 and 2016–2017: Annual Outstanding Student of Tongji University.

Evi Zhuleku

Albania

Evi Zhuleku

EDUCATION

College / University

Jacobs University

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry and Cell Biology

Lab Experience

Mammalian cell culture and transfection, PCR, site directed mutagenesis, protein purification and expression, Southern blot, SDS-PAGE, Western blot, indirect immunofluorescence, tissue and cell staining, conventional and confocal fluorescence microscopy, fluorescence spectroscopy, differential scanning fluorimetry, size exclusion chromatography, flow cytometry, antibody purification.

Projects / Research

01/2018 – 08/2018: “A Model for the Investigation of Cross-Presentation in Human Embryonic Kidney Cells”, Prof. Dr. Sebastian Springer, Jacobs University

09/2017 – 12/2017: “*In Vitro* Refolding of Murine MHC Class I Molecules with the Use of Dipeptides”, Prof. Dr. Sebastian Springer, Jacobs University

06/2017 – 09/2017: “Characterization of Ribosomal Quality Control in Human Cells”, Prof. Dr. Ulrich Hartl, Max-Planck Institute of Biochemistry

Scholarships / Awards

2018 – 2019: Stipend by the International Max Planck Research School.

06/2017–09/2017: Amgen Scholarship, Ludwig-Maximilians-Universität München.

09/2015 – 06/2018: Merit Scholarship upon admission to Jacobs University.

Faculty

Name		Group / Institution	
Mathias	Bähr	Neurology	U Göttingen
Holger	Bastians	Cellular Oncology	U Göttingen
Rüdiger	Behr	Degenerative Diseases	DPZ
Tim	Beißbarth	Statistical Bioinformatics	U Göttingen
Markus	Bohnsack	Molecular Biology	U Göttingen
Gerhard H.	Braus	Molecular Microbiology and Genetics	U Göttingen
Bertram	Brenig	Molecular Biology of Livestock	U Göttingen
Nils	Brose	Molecular Neurobiology	MPI em
Fabian	Commichau	General Microbiology	U Göttingen
Patrick	Cramer	Molecular Biology	MPI bpc
Rolf	Daniel	Genomic and Applied Microbiology	U Göttingen
Matthias	Dobbelstein	Molecular Oncology	U Göttingen
Roland	Dosch	Molecular Control of Zebrafish Oogenesis	U Göttingen
Jörg	Enderlein	Biophysics	U Göttingen
Alex	Faesen	Biochemistry of Signal Dynamics	MPI bpc
Ivo	Feußner	Plant Biochemistry	U Göttingen
Ralf	Ficner	Molecular Structural Biology	U Göttingen
André	Fischer	Psychiatry and Psychotherapy	U Göttingen
Christiane	Gatz	Plant Molecular Biology and Physiology	U Göttingen
Dirk	Görlich	Cellular Logistics	MPI bpc
Christian	Griesinger	NMR-based Structural Biology	MPI bpc
Uwe	Groß	Medical Microbiology	U Göttingen
Jörg	Großhans	Developmental Biochemistry	U Göttingen
Helmut	Grubmüller	Theoretical and Computational Biophysics	MPI bpc
Ufuk	Günesdogan	Developmental Biology	U Göttingen
Heidi	Hahn	Human Genetics	U Göttingen
Kai	Heimel	Microbial Cell Biology	U Göttingen
Stefan	Hell	NanoBiophotonics	MPI bpc
Claudia	Höbartner	Nucleic Acid Chemistry	U Göttingen
Reinhard	Jahn	Neurobiology	MPI bpc
Andreas	Janshoff	Biophysical Chemistry	U Göttingen

U Göttingen = Georg August University, MPI bpc = Max Planck Institute for Biophysical Chemistry, MPI em = Max Planck Institute for Experimental Medicine, DPZ = German Primate Center

Name		Group / Institution	
Stefan	Jakobs	Mitochondrial Structure and Dynamics	MPI bpc
Steven	Johnsen	Translational Cancer Research	U Göttingen
Dieter	Klopfenstein	Biophysics	U Göttingen
Wilfried	Kramer	Molecular Genetics	U Göttingen
Heike	Krebber	Molecular Genetics	U Göttingen
Volker	Lipka	Plant Cell Biology	U Göttingen
Reinhard	Lührmann	Cellular Biochemistry	MPI bpc
Burkhard	Morgenstern	Bioinformatics	U Göttingen
Tobias	Moser	Auditory Neuroscience	U Göttingen
Klaus-Armin	Nave	Neurogenetics	MPI em
Argyris	Papantonis	Translational Epigenetics	U Göttingen
Vladimir	Pena	X-Ray Crystallography	MPI bpc
Stefanie	Pöggeler	Genetics of Eukaryotic Organisms	U Göttingen
Stefan	Pöhlmann	Infection Biology	DPZ
Peter	Rehling	Biochemistry	U Göttingen
Silvio	Rizzoli	Neuro- and Sensory Physiology	U Göttingen
Marina	Rodnina	Physical Biochemistry	MPI bpc
Melina	Schuh	Meiosis	MPI bpc
Blanche	Schwappach	Molecular Biology	U Göttingen
Halyna	Shcherbata	Gene Expression and Signaling	MPI bpc
Johannes	Söding	Computational Biology	MPI bpc
Holger	Stark	Structural Dynamics	MPI bpc
Alexander	Stein	Membrane Protein Biochemistry	MPI bpc
Claudia	Steinem	Biomolecular Chemistry	U Göttingen
Jörg	Stülke	General Microbiology	U Göttingen
Michael	Thumm	Molecular Cell Biology	U Göttingen
Kai	Tittmann	Molecular Enzymology	U Göttingen
Henning	Urlaub	Bioanalytical Mass Spectrometry	MPI bpc
Lutz	Walter	Primate Genetics	DPZ
Jürgen	Wienands	Cellular and Molecular Immunology	U Göttingen
Ernst	Wimmer	Developmental Biology	U Göttingen

U Göttingen = Georg August University, MPI bpc = Max Planck Institute for Biophysical Chemistry, MPI em = Max Planck Institute for Experimental Medicine, DPZ = German Primate Center

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Mathias Bähr

Professor of Neurology

- 1985 MD, University of Tübingen Medical School, Training in Neurology at University Hospitals in Tübingen and Düsseldorf
- DFG and Max Planck Fellow at the Max Planck Institute for Developmental Biology Tübingen and at the Department of Anatomy and Cell Biology, Washington University St.Louis
- Schilling-Foundation Professor for Clinical and Experimental Neurology, University of Tübingen
- Director at the Department of Neurology, University of Göttingen since 2001

Major Research Interests

Neuronal cell loss is not only a major feature of human neurodegenerative diseases like Parkinson's disease (PD), Alzheimer's disease (AD) or stroke, but can also be observed in neuroinflammatory conditions like Multiple Sclerosis (MS) or after traumatic lesions, e.g. of the optic nerve. We examine the cellular and molecular mechanisms of neuronal dysfunction and neuronal cell death in animal models of the respective disorders with the ultimate goal to detect new targets for a therapeutic neuroprotective intervention.
We have used for many years the retino-tectal system in rodents as our standard model to study de-and regeneration *in vitro* and *in vivo*. Our group has in detail analysed the cellular and molecular cascades that follow lesions of the optic nerve and ultimately lead to cell death of the retinal ganglion cells. To monitor the changes that occur directly after lesions we succeeded in implementing *in vivo* life-imaging of the rat and mouse optic nerve, which offers us a unique opportunity to study the complex processes that follow traumatic or inflammatory lesions of CNS fibre tracts.
In classical neurodegeneration research we have choosen PD as our topic. In this field, a multidisciplinary research team with our participation in the area C2 of the excellence cluster CNMPB examines the role of a-synuclein aggregation for dopaminergic dysfunction and cell death and characterizes other disease related proteins in order to develop new neuroprotective strategies.
In all our model systems we use AAV-mediated viral gene transfer to express different disease-or de-/regeneration associated genes as research tools and also as potential therapeutic factors to manipulate the respective molecular events *in vitro* and *in vivo*. To that end, we have e.g. developed regulatory elements that allow a controlled gene expression in complex *in vivo* models.
The final aim of our research approaches is to describe in detail the molecular pathophysiology that leads to axonal and neuronal loss and to develop new therapeutic strategies, some of which have already been translated into proof of concept studies in human patients.

Selected Recent Publications

Tatenhorst L, Eckermann K, Dambeck V, Fonseca-Ornelas L, Walle H, Lopes da Fonseca T, Koch JC, Becker S, Tönges L, Bähr M, Outeiro TF, Zweckstetter M, Lingor P (2016) Fasudil attenuates aggregation of α-synuclein in models of Parkinson's disease. Acta Neuropathol Commun 4: 39

Doeppner TR, Pehlke JR, Kaltwasser B, Schlechter J, Kilic E, Bähr M, Hermann DM (2015) The indirect NMDAR antagonist acamprosate induces postischemic neurologic recovery associated with sustained neuroprotection and neuroregeneration. J Cereb Blood Flow Metab 35(12): 2089-97

Eckermann K, Kügler S, Bähr M (2015) Dimerization propensities of Synucleins are not predictive for Synuclein aggregation. Biochim Biophys Acta 1852(8): 1658-64

Doeppner TR, Kaltwasser B, Fengyan J, Hermann DM, Bähr M (2013) TAT-Hsp70 induces neuroprotection against stroke via anti-inflammatory actions providing appropriate cellular microenvironment for transplantation of neural precursor cells. J Cereb Blood Flow Metab 33(11): 1778-88

Taschenberger G, Toloe J, Tereshchenko J, Akerboom J, Wales P, Benz R, Becker S, Outeiro TF, Looger LL, Bähr M, Zweckstetter M, Kügler S (2013) β-synuclein aggregates and induces neurodegeneration in dopaminergic neurons. Ann Neurol. 74(1): 109-18

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Further Information

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Holger Bastians

Professor of Cellular Oncology

- Professor of Cellular Oncology, University Medical Center, Göttingen (UMG), since 2013
- Heisenberg-Professor of Cellular Oncology, University Medical Center Göttingen (UMG), 2011 – 2013
- Heisenberg fellow, Philipps-University Marburg, 2008 – 2011
- Group leader, Institute for Molecular Biology and Tumor Research (IMT), Philipps-University Marburg, 2000 – 2010
- Postdoctoral fellow with Prof. Joan Ruderman, Harvard Medical School, Boston, USA, 1996 – 1999
- Dr. rer. nat., German Cancer Research Center (DKFZ), Heidelberg, 1996

Major Research Interests

Mitosis represents the key event during the eukaryotic cell cycle during which the DNA is equally distributed onto the two daughter cells. Defects in mitotic signaling pathways are often detected in human cancer and are directly associated with the missegregation of sister chromatids resulting in chromosomal instability (CIN) and aneuploidy. In fact, this is directly linked to tumorigenesis and represents a major characteristic of human cancer. However, the molecular mechanisms underlying CIN and the genetic lesions causing aneuploidy in human cancer are largely unknown.
In addition to its fundamental role for the maintenance of chromosomal stability, mitosis represents an important target for anti-cancer therapy and many anti-mitotic drugs including taxanes and Vinca alkaloids are frequently used in the clinic to treat various malignancies. However, it is still unclear how the interference with the mitotic progression is linked to tumor cell death, the desired outcome of therapy. A knowledge of this cross-talk is required for the development of future therapy concepts.
Based on these key points of cancer research our lab is focusing on the following main questions:
1. What are the molecular mechanisms of chromosome segregation during mitosis and what are genetic lesions in human cancer responsible for chromosomal instability?
2. What are the molecular mechanisms of mitosis associated cell death after chemotherapeutic treatment and waht are the routes of chemotherapy resistance in human cancer?
3. Based on our investigations of mitotic signaling pathways we are aiming to identify novel mitotic drug targets in order to improve current therapies and to develop novel therapeutic concepts.

Selected Recent Publications

Ertych N, Stolz A, Valerius O, Braus GH, Bastians H (2016) The CHK2-BRCA1 tumor suppressor axis restrains oncogenic AURORA-A to ensure proper mitotic microtubule assembly. Proc Nat Acad Sci USA 113: 1817-1822

Lüddecke S, Ertych N, Stenzinger A, Weichert W, Beissbarth T, Dyczkowski J, Gaedcke J, Valerius O, Braus GH, Kschischo M, Bastians H (2016) The putative oncogene CEP72 inhibits the mitotic function of BRCA1 and induces chromosomal instability. Oncogene 35: 2398-2406

Stolz A, Neufeld K, Ertych N Bastians H (2015). Wnt mediated protein stabilization ensures proper mitotic microtubule assembly and chromosomal stability. EMBO Reports 16: 490-499

Ertych N, Stolz A, Stenzinger A, Weichert W, Kaulfuß S, Burfeind P, Aigner A, Wordeman L, Bastians H (2014) Increased microtubule assembly rates influence chromosomal instability in colorectal cancer cells. Nature Cell Biology 16: 779-791

Stolz A, Ertych N, Kienitz A, Vogel C, Schneider V, Fritz B, Jacob R, Dittmar G, Weichert W, Petersen I Bastians H (2010) The CHK2-BRCA1 tumor suppressor pathway ensures chromosomal stability in human somatic cells. Nature Cell Biology 12: 492-499

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Further Information

http://www.dpz.eu/en/platforms/degenerative-diseases/about-us.html

Rüdiger Behr

Head of Platform Degenerative Diseases, German Primate Center

- 1995 Diploma in Biology, Westfälische Wilhelms-Universität (WWU) Münster, Germany
- 1998 PhD in Biology, Institute of Reproductive Medicine, WWU Münster, Germany
- 1999 – 2005 Post Docs at the Institute of Reproductive Medicine of the WWU Münster; the University of Pennsylvania Medical School, Department of Genetics, Philadelphia, PA, USA; and the Institute of Anatomy, Developmental Biology, University of Essen, Germany
- 2005 – 2008 Head of the Stem Cell Biology Junior Research Group, German Primate Center, Göttingen, Germany
- 2008 – 2015 Head of Stem Cell Biology Unit, German Primate Center, Göttingen, Germany
- Since 2016 Head of Platform Degenerative Diseases, German Primate Center, Göttingen, Germany

Major Research Interests

We are interested in the generation, characterization and genetic modification of primate pluripotent stem cells. We generated embryonic stem cells and induced pluripotent stem cells from the common marmoset monkey and compare these pluripotent stem cell types with natural monkey preimplantation embryos and pre-meiotic germ cells. In addition to this developmental aspect we use pluripotent stem cells in combination with gene editing technology to establish genetic disease models and to test, in collaboration with our partners, cell replacement therapies in pre-clinically relevant settings. Here we currently focus as a member of the Deutsches Zentrum für Herzkreislaufforschung (DZHK) on cardiovascular aspects.

Selected Recent Publications

Wahab F, Drummer C, Schlatt S, Behr R (2016) Dynamic Regulation of Hypothalamic DMXL2, KISS1, and RFRP Expression During Postnatal Development in Non-Human Primates. Mol Neurobiol 2017 Dec; 54(10): 8447-8457

Debowski K, Drummer C, Lentes J, Cors M, Dressel R, Lingner T, Salinas-Riester G, Fuchs S, Sasaki E, Behr R (2016) The transcriptomes of novel marmoset monkey embryonic stem cell lines reflect distinct genomic features. Sci Rep 6: 29122

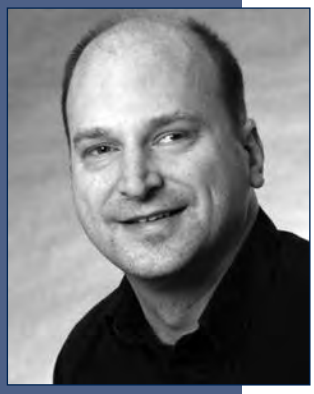
Boroviak T, Loos R, Lombard P, Okahara J, Behr R, Sasaki E, Nichols J, Smith A, Bertone P (2015) Lineage-Specific Profiling Delineates the Emergence and Progression of Naive Pluripotency in Mammalian Embryogenesis. Dev Cell 35: 366-82

Wahab F, Drummer C, Behr R (2015) Marmosets. Curr Biol. 25: R780-2

Debowski K, Warthemann R, Lentes J, Salinas-Riester G, Dressel R, Langenstroth D, Gromoll J, Sasaki E, Behr R (2015) Non-viral generation of marmoset monkey iPS cells by a six-factor-in-one-vector approach. PLoS One 10(3): e0118424

Vogt EJ, Meglicki M, Hartung KI, Borsuk E, Behr R (2012) Importance of the pluripotency factor Lin28 in the mammalian nucleolus during early embryonic development. Development 139: 4514-4523

Müller T, Fleischmann G, Eildermann K, Mätz-Rensing K, Horn P, Sasaki E, Behr R (2009) A novel embryonic stem cell line derived from the common marmoset monkey (Callithrix jacchus) exhibiting germ cell-like characteristics. Hum Reprod 24 (6): 1359-1372



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Tim Beißbarth

Head of Department Medical Bioinformatics

- 2001 Dr. rer. nat, University Heidelberg
- 2001 – 2002 Postdoctoral fellow, Department Computational Molecular Biology, Max-Planck-Institute for molecular Genetics, Berlin
- 2002 – 2005 Postdoctoral fellow, Department Bioinformatics, WEHI, Melbourne, Australia
- 2005 – 2008 Group Leader, Bioinformatics & Modeling, Department Molecular Genome Analysis, DKFZ, Heidelberg
- 2008 – 2018 Professor, Statistical Bioinformatics, Department Medical Statistics, University Medical Center, Göttingen
- Since 2018 Professor, Head of Department Medical Bioinformatics, University Medical Center, Göttingen

Major Research Interests

The Department of Medical Bioinformatics is developing methods in Statistical Bioinformatics as well as Systems Medicine for biomedical research. We are collaborating in biomedical research projects and working in interdisciplinary consortia on the analysis of large heterogeneous high-throughput data-sets. There we apply mainly machine learning approaches as well as analysis and reconstruction methods for biological networks. The focus of the department is the development of methods and tools for the integrative analysis of large biomedical data-sets. These methods are implemented mostly in the statistical computing environment of R.

Selected Recent Publications

Perera-Bel J, Hutter B, Heining C, Bleckmann A, Fröhlich M, Fröhling S, Glimm H, Brors B, Beißbarth T (2018) From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. Genome Med 10(1): 18

Wolff A, Perera-Bel J, Schildhaus HU, Homayounfar K, Schatlo B, Bleckmann A, Beißbarth T (2018) Using RNA-Seq Data for the Detection of a Panel of Clinically Relevant Mutations. Stud Health Technol Inform 253: 217-221

Wolff A, Bayerlová M, Gaedcke J, Kube D, Beißbarth T (2018) A comparative study of RNA-Seq and microarray data analysis on the two examples of rectal-cancer patients and Burkitt Lymphoma cells. PLoS One 13(5): e0197162

Kramer F, Beißbarth T (2017) Working with Ontologies. Methods Mol Biol 1525: 123-135

Wachter A, Beißbarth T (2016) Decoding Cellular Dynamics in Epidermal Growth Factor Signaling Using a New Pathway-Based Integration Approach for Proteomics and Transcriptomics Data. Front Genet 6: 351

von der Heyde S, Sonntag J, Kramer F, Bender C, Korf U, Beißbarth T (2016) Reconstruction of Protein Networks Using Reverse-Phase Protein Array Data. Methods Mol Biol 1362: 227-46

Bayerlová M, Jung K, Kramer F, Klemm +F, Bleckmann A, Beißbarth T (2015) Comparative study on gene set and pathway topology-based enrichment methods. BCM Bioinformatics 16: 334

Becker K, Stauber M, Schwarz F, Beißbarth T (2015) Automated 3D-2D registration of X-ray microcomputed tomography with histological sections for dental implants in bone using chamfer matching and simulated annealing. Comput Med Imaging Graph 44: 62-8

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Markus Bohnsack

Professor of Molecular Biology

- 2005 Dr. rer. nat. (PhD) at the Center for Molecular Biology Heidelberg (ZMBH), University of Heidelberg
- 2006 – 2008 Postdoctoral fellow at the University of Edinburgh, UK
- 2008 – 2012 Group leader at the Goethe University, Frankfurt
- 2009 – 2012 Adjunct Investigator at the Cluster of Excellence Frankfurt
- since 2012 Professor of Molecular Biology, University Medical Centre (UMG), Göttingen

Major Research Interests

RNAs and ribonucleoprotein complexes (RNPs) are involved in many key cellular processes, including translation and at various levels in the regulation of gene expression. Our group is interested in studying the biogenesis, dynamics, nuclear export and functions of several different classes of RNPs in both yeast and mammalian cells. We employ genome-wide techniques such as UV crosslinking and analysis of cDNA (CRAC) as well as proteomics to discover new protein-protein and protein-RNA interactions *in vivo*. Functional analysis is then performed using methods from cell and molecular biology as well as biochemistry, allowing us to gain insights into the many roles of RNP complexes. Several projects aim to understand the biogenesis of ribosomes, a highly energy consuming process that is regulated by proto-oncogenes and tumour suppressors. In particular, we focus on elucidating the roles of key enzymatic factors such as RNA helicases and exo- and endonucleases that catalyse irreversible maturation steps and thereby drive the directionality of the pathway. Determination of the functions of such enzymes also provides the basis for understanding how this process is modulated in response to environmental and developmental cues. Furthermore, multiple genetic diseases, termed ribosomopathies, are caused by mutations in ribosome biogenesis cofactors or ribosomal proteins and the detailed characterisation of these factors enables us to reveal the molecular basis of such disorders. Interestingly, we have recently found that several RNA helicases involved in ribosome biogenesis also function in different cellular processes, indicating that they may play important roles in the cross-regulation of these pathways in RNA metabolism. Another major aspect of our work is the identification of the substrates of RNA methyltransferases. This allows us to determine the roles of the modifications they introduce in regulating the biogenesis and functions of RNAs and RNPs *in vivo*.

Selected Recent Publications

Sloan KE, Bohnsack MT (2018) Unravelling the mechanisms of RNA helicase regulation. Trends Biochem Sci 43: 237-250

Memet I, Doebele C, Sloan KE#, Bohnsack MT# (2017) The G-patch protein NF-KB-repressing factor mediates the recruitment of the exonuclease XRN2 and activation of the RNA helicase DHX15 in human ribosome biogenesis. Nucleic Acids Res 45: 5359-5374

Haag S, Sloan KE, Ranjan N, Warda AS, Kretschmer J, Blessing C, Hübner B, Seikowski J, Dennerlein S, Rehling P, Rodnina MV, Höbartner C, Bohnsack MT (2016) NSUN3 and ABH1 modify the wobble position of mt-tRNAMet to expand codon recognition in mitochondrial translation. EMBO J 35: 2104-2119

Warda AS, Freytag B, Haag S, Sloan KE, Görlich D, Bohnsack MT (2016) Effects of the Bowen-Conradi syndrome mutation in EMG1 on its nuclear import, stability and nucleolar recruitment. Hum Mol Genet 25: 5353-5364

Sloan KE, Bohnsack MT, Watkins NJ (2013) The 5S RNP couples p53 homeostasis to ribosome biogenesis and nucleolar stress. Cell Reports 5: 237-247

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Professor of Microbiology and Genetics

- 1983 Diploma (Biology), Albert-Ludwig University, Freiburg i. Br.
- 1987 Dr.sc.nat., Swiss Federal Institute of Technology (ETH), Zürich (Switzerland)
- 1991 Habilitation (Microbiology), Swiss Federal Institute of Technology (ETH), Zürich (Switzerland)
- 1993 – 1996 Associate Professor of Biochemistry, Friedrich Alexander University, Erlangen
- Since 1996 Professor of Microbiology (since 2001 Professor of Microbiology and Genetics) in Göttingen

Major Research Interests

The major focus of the laboratory is on the control of developmental programs, protein turnover, pathogenicity and the interplay between development and primary and secondary metabolism. Our models are eukaryotic microorganisms (yeasts and filamentous fungi):
(i) We are interested how light coordinates fungal development with fungal secondary metabolism and toxin production.
(ii) Nedd8 is a ubiquitin-like protein which is involved in the control of protein turnover. We study the Nedd8-system including the COP9 signalosome using fungi as model systems.
(iii) We are interested in the molecular control (protein turnover and translation) of adhesion as initial step in infection and biofilm formation.
(iv) We study fungi as models for Parkinson (yeast), fungi as pathogens of immunocompromised patients (*A. fumigatus*) and as plant pathogens (*V. longisporum*).

Selected Recent Publications

Thieme KG, Gerke J, Sasse C, Valerius O, Thieme S, Karimi R, Heinrich AK, Finkgernagel F, Smith K, Bode HB, Freitag M, Ram AFJ, Braus GH (2018) Velvet domain protein VosA represses the zinc cluster transcription factor SclB regulatory network for *Aspergillus nidulans* asexual development, oxidative stress response and secondary metabolism. PLoS Genet 14: e1007511

Kolog Gulko M, Heinrich G, Gross C, Popova B, Valerius O, Neumann P, Ficner R, Braus GH (2018) Sem1 links proteasome stablitiy and specificity to multicellular development. PLoS Genet. 42: e1007141

Shlezinger N, Irmer I, Dhingra S, Beattie SR, Cramer RA, Braus GH, Sharon A, Hohl TM (2017) Sterilizing immunity in the lung relies on targetting fungal apoptosis-like programmed cell death. Science 357: 1037-1041

Opitz N, Schmitt K, Hofer-Pretz V, Neumann B, Krebber H, Braus GH, Valerius O (2017) Capturing the Asc1p/RACK1 microenvironment at the head region of the 40S ribosome with quantitative BioID. Mol Cell Proteomics 16: 2199-2218

Jöhnk B, Bayram Ö, Abelmann A, Heinekamp T, Mattern D, Brakhage AA, Jacobsen ID, Valerius O, Braus GH (2016) SCF ubiquitin ligase F-bxo protein Fbx15 controls nuclear co-repressor localization, stress response and virulence of the human pathogen *Aspergillus fumigatus*. PLoS Pathogens 12(9), e1005899

Kleinknecht A, Popova B, Lázaro DF, Pinho R, Valerius O, Outeiro TF, Braus GH (2016) C-terminal tyrosine residue modifications modulate the protective phosphorylation of serine-129 of α-synuclein in a yeast model of Parkinson´s disease. PLoS Genetics 12, e1006098

Schinke J, Kolog Gulko M, Christmann M, Valerius O, Stumpf SK, Stirz M, Braus GH (2016) The DenA/DEN1 interacting phosphatase DipA controls septa positioning and phosphorylation-dependent stability of cytoplasmatic DenA/DEN1 during fungal development. PLoS Genetics 12, e1005949

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Bertram Brenig

Professor of Molecular Biology of Livestock , Director of the Institute of Veterinary Medicine

- 1979 – 1984 Studies of Veterinary Medicine at the Ludwig-Maximilians-University (Munich) and University of Veterinary Medicine (Vienna)
- 1987 Dr. med. vet. Ludwig-Maximilians-University Munich
- 1987 Postdoctoral researcher at the Institute of Animal Physiology and Genetics Research (Edinburgh, Scotland)
- 1988 Postdoctoral researcher at the Institute of Immunology (LMU, Munich)
- 1988 – 1993 Research assistant and group leader at the Institute of Animal Breeding and Genetics (LMU, Munich) and Max-Planck-Institute for Biochemistry (Martinsried)
- Since 1993 Full professor (C4) and director of the Institute of Veterinary Medicine (University of Göttingen)
- 2016 Prof. h. c. of the Jiangxi Agricultural University (PR China)
- 2018 Prof. h. c. of the Russian State Academy for Biotechnology and Veterinary Medicine Moscow (Russia)

Major Research Interests

We are interested in the structural and functional analysis of mammalian genes and genomes and are investigating the cause of different important genetic traits and defects in domestic animals.
Currently we are working on the following projects:

- Leg and feet disease (digital dermatitis, interdigital hyperplasia) (cattle)
- Early embryonal death (lethal haplotypes) (cattle)
- Male infertility (cattle)
- Developmental skeletal defects (Osteogenesis imperfecta, osteodystrophy) (cattle)
- Hemophilia A and B (dog)

We are using genome wide association studies (high-throughput screening and genotyping, GWAS) and next generation sequencing (NGS) techniques for the identification of chromosomal regions that are linked to the traits or disorders. Fine mapping, positional cloning and candidate gene analysis are used for further elucidation.

Selected Recent Publications

Taher L, Beck J, Liu W, Roolf C, Soller JT, Rutgen BC, Hammer SE, Chodisetti M, Sender S, Sterenczak KA, Fuellen G, Junghanss C, Brenig B, Nolte I, Schutz E, Murua Escobar H (2018) Comparative high-resolution transcriptome sequencing of lymphoma cell lines and *de novo* lymphomas reveals cell-line-specific pathway dysregulation. Sci Rep 8: 6279

Granados-Soler JL, Junginger J, Hewicker-Trautwein M, Bornemann-Kolatzki K, Beck J, Brenig B, Betz D, Schille JT, Murua Escobar H, Nolte I (2018) TiHo-0906: a new feline mammary cancer cell line with molecular, morphological, and immunocytological characteristics of epithelial to mesenchymal transition. Sci Rep 8: 13231

Ferreira DSS, Kato RB, Miranda FM, da Costa Pinheiro K, Fonseca PLC, Tome LMR, Vaz ABM, Badotti F, Ramos RTJ, Brenig B, Azevedo VAC, Benevides RG, Goes-Neto A (2018) Draft genome sequence of Trametes villosa (Sw.) Kreisel CCMB561, a tropical white-rot Basidiomycota from the semiarid region of Brazil. Data Brief 18: 1581-1587

Hollmann AK, Bleyer M, Tipold A, Nessler JN, Wemheuer WE, Schutz E, Brenig B (2017) A genome-wide association study reveals a locus for bilateral iridal hypopigmentation in Holstein Friesian cattle. BMC Genet 18: 30

Hollmann AK, Dammann I, Wemheuer WM, Wemheuer WE, Chilla A, Tipold A, Schulz-Schaeffer WJ, Beck J, Schutz E, Brenig B (2017) Morgagnian cataract resulting from a naturally occurring nonsense mutation elucidates a role of CPAMD8 in mammalian lens development. PLoS One 12: e0180665

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Nils Brose

Professor, Director at the Max Planck Institute for Experimental Medicine

- Undergraduate studies in Biochemistry, Eberhard Karls University, Tübingen, Germany (1981 – 1985)
- MSc in Physiology with Marianne Fillenz, University of Oxford, Oxford, UK (1987)
- PhD in Biology with Reinhard Jahn, Ludwig Maximilians University, Munich, Germany (1990)
- Postdoctoral training with Stephen F. Heinemann (Salk Institute, La Jolla, CA, USA) and Thomas C. Südhof (University of Texas Southwestern Medical Center, Dallas, TX, USA) (1991 – 1995)
- Research Group Leader, Max Planck Institute of Experimental Medicine, Göttingen, Germany (1995 – 2001)
- Director, Department of Molecular Neurobiology, Max Planck Institute of Experimental Medicine, Göttingen, Germany (since 2001)

Major Research Interests

Our research focuses on the molecular mechanisms of nerve cell development and synapse formation and function in the vertebrate central nervous system. To this end, we combine biochemical, morphological, mouse genetic, physiological, and behavioral methods to elucidate the molecular basis of nerve cell differentiation, synapse formation, transmitter release, and postsynaptic transmitter sensing. In selected cases, we explore the dysfunction of corresponding biological processes in neuropsychiatric diseases. Our work in the field of nerve cell development focuses on the role of SUMOylation in cell polarity formation, cell migration, and neuritogenesis, our synaptogenesis research concentrates on synaptic cell adhesion proteins and their role in synapse formation and function, and our studies on the molecular mechanisms of neurotransmitter release focus on components of the presynaptic active zone and their regulatory function in synaptic vesicle fusion.

Selected Recent Publications

Sigler A, Oh WC, Imig C, Altas B, Kawabe H, Cooper BH, Kwon H-B, Rhee J-S*, Brose N* (2017) Formation and maintenance of functional spines in the absence of presynaptic glutamate release. Neuron 94: 304-311 (*joint corresponding authors)

Kawabe H, Mitkovski M, Kaeser PS, Hirrlinger J, Opazo F, Nestvogel D, Kalla S, Fejtova A, Verrier SE, Bungers SR, Cooper BH, Varoqueaux F, Wang Y, Nehring RB, Gundelfinger ED, Rosenmund C, Rizzoli SO, Südhof TC, Rhee J-S, Brose, N (2017) ELKS1 localizes the synaptic vesicle priming protein bMunc13-2 to a specific subset of active zones. J Cell Biol 216: 1143-1161

Lipstein N, Verhoeven-Duif NM, Michelassi FE, Calloway N, van Hasselt PM, Pienkowska K, van Haaften G, van Haelst MM, van Empelen R, Cuppen I, van Teeseling HC, Evelein AMV, Vorstman JA, Thoms S, Jahn O, Duran KJ, Monroe GR, Ryan TA, Taschenberger H, Dittman JS, Rhee J-S, Visser G, Jans JJ*, Brose N* (2017) Synaptic UNC13A protein variant causes increased synaptic transmission and dyskinetic movement disorder. J Clin Invest 127: 1005-1018 (*joint corresponding authors)

Hammer M, Krueger-Burg D, Tuffy LP, Cooper BH, Taschenberger H, Goswami SP, Ehrenreich H, Jonas P, Varoqueaux F, Rhee J-S, Brose N (2015) Perturbed hippocampal synaptic inhibition and gamma-oscillations in a Neuroligin-4 knock-out mouse model of autism. Cell Rep 13: 516-523

Soykan T, Schneeberger D, Tria G, Buechner C, Bader N, Svergun D, Tessmer I, Poulopoulos A, Papadopoulos T, Varoqueaux F, Schindelin H*, Brose N* (2014). A conformational switch in Collybistin determines the differentiation of inhibitory postsynapses. EMBO J 18: 2113-2133 (*joint corresponding authors)

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Fabian Commichau

Group leader: Institute of Microbiology and Genetics, Department of General Microbiology

- 2003 Diploma in Biology, Institute for Biology IV (Microbiology), Rheinisch-Westfälische Technische Hochschule Aachen
- 2006 PhD in Microbiology (Dr. rer. nat.), Department of General Microbiology, University of Göttingen
- 2006 – 2008 Postdoctoral Fellow at the Department of General Microbiology, University of Göttingen
- 2008 – 2009 Postdoctoral Fellow at the Focal Area Infection Biology, Biozentrum, University of Basel, Switzerland
- 2009 – 2011 Scientist, DSM Nutritional Products Ltd, Grenzach-Wyhlen & Kaiseraugst, Germany & Switzerland
- Since 2011 Group leader at the Department of General Microbiology, University of Göttingen
- 2015 Habilitation (Microbiology), University of Göttingen

Major Research Interests

We are interested in the control of glutamate metabolism in the Gram-positive model organism *Bacillus subtilis*. Glutamate is the major amino group donor in every living cell. Therefore, glutamate biosynthesis and degradation have to be tightly regulated. *B. subtilis* possesses two glutamate dehydrogenases that are active in catabolism and in controlling *de novo* synthesis of glutamate by forming a complex with a transcription factor. Currently, we study the molecular details of the regulatory protein complex. We are also interested in genomic adaptation of *B. subtilis* to perturbation of glutamate homeostasis. In this project, we aim at elucidating the underlying molecular mechanisms that are crucial for genome maintenance and adaptability. In collaboration with Prof. Dr. Jörg Stülke, we are working on the construction of Minibacillus, a minimal organism based on *B. subtilis* (www.minibacillus.org). The final goal is to obtain a minimal organism that is equipped with a core genome in which the function of each gene is known. Cyclic di-AMP (c-di-AMP) is a signalling nucleotide that is essential for many bacteria including the human pathogen Listeria monocytogenes. c-di-AMP seems to be the major osmoregulator in many bacteria. By applying genetic as well as biochemical approaches we want to identify the environmental signals that control c-di-AMP synthesis and degradation. Finally, we are working on novel routes for production of the commercially valuable substance vitamin B6 by *B. subtilis*.

Selected Recent Publications

Dormeyer M, Lentes S, Ballin P, Wilkens M, Klumpp S, Kohlheyer D, Stannek L, Grünberger A, Commichau FM (2018) Visualization of tandem repeat mutagenesis in *Bacillus subtilis*. DNA Repair (Amst) 63C: 10-15

Rosenberg J, Yeak KC, Commichau, FM (2018) A two-step evolutionary process establishes a non-native vitamin B6 pathway in *Bacillus subtilis*. Environ Microbiol 20: 156-168

Commichau FM, Gibhardt J, Halbedel S, Gundlach J, Stülke J (2018) A delicate connection: c-di-AMP affects cell integrity by controlling osmolyte transport. Trends in Microbiol 26: 175-185

Dormeyer M, Lübke AL, Müller P, Lentes S, Reuß DR, Thürmer A, Stülke J, Daniel R, Brantl S, Commichau FM (2017) Hierarchical mutational events compensate for glutamate auxotrophy of a *Bacillus subtilis* gltC mutant. Environ Microbiol Rep 9: 279-289

Reuß DR, Altenbuchner J, Mäder U, Rath H, Ischebeck T, Sappa PK, Thürmer A, Guerin C, Nicolas P, Steil L, Zhu B, Feussner I, Klumpp S, Daniel R, Commichau FM, Völker U, Stülke J (2017) Large-scale reduction of the *Bacillus subtilis* genome: Consequences for the transcriptional network, resource allocation, and metabolism. Genome Res 27: 289-299

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Patrick Cramer

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- Study of chemistry at the Universities of Stuttgart and Heidelberg, Research student at the University of Bristol (UK) and Cambridge (UK)
- 1995 Diploma in chemistry at the University of Heidelberg
- 1998 Doctorate at the University of Heidelberg/EMBL Grenoble (France)
- 1995 –1998 Predoctoral fellow in Grenoble (France)
- 1999 – 2000 postdoctoral fellow at Stanford University (USA)
- 2001 – 2003 Tenure-track professor of biochemistry at the University of Munich
- 2004 – 2014 Professor of biochemistry at the University of Munich
- 2004 – 2013 Director at the Gene Center of the University of Munich (LMU)
- Since 2014 Director of the Department for Molecular Biology at the Max Planck Institute of Biophysical Chemistry

Major Research Interests

Molecular Biology: from molecular movies to regulatory systems

Gene transcription is the first step in the expression of the genetic information and a focal point for cellular regulation. Our goal is to understand the molecular mechanisms of gene transcription and the principles of genomic regulation in eukaryotic cells. We use integrated structural biology and complementary functional studies to unravel the three-dimensional and functional architecture of large macromolecular complexes involved in transcription. We also develop functional genomics methods and computational approaches to unravel the cellular mechanisms of genomic regulation. These efforts led to a first molecular movie of transcription and provided insights into gene-regulatory cellular networks. Together, these efforts shape the emerging fields of genome biology and molecular systems biology. Our aim is to understand the functional genome as a regulatory network based on the underlying structural and molecular mechanisms.

Selected Recent Publications

Vos SM, Farnung L, Urlaub H, Cramer P (2018) Structure of paused transcription complex Pol II-DSIF-NELF. Nature 560: 601-606

Vos SM et al, Cramer P (2018) Structure of activated transcription complex Pol II-DSIF-PAF-SPT6. Nature 560: 607-612

Schilbach S et al., Cramer P (2017) Structures of transcription pre-initiation complex with TFIIH and Mediator. Nature 551: 204-209

Nozawa K, Schneider TR, Cramer P (2017) Core Mediator structure at 3.4 Å extends model of transcription initiation complex. Nature 656 (7653): 248-251

Kohler R, Mooney RA, Mills DJ, Landick R, Cramer P (2017) Architecture of a transcribing-translating expressome. Science 356(6334): 194-197

Schwalb B, Michel M, Zacher B, Frühauf K, Demel C, Tresch A, Gagneur J, Cramer P (2016) TT-seq maps the human transient genome. Science 352(6290): 1225-8

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Rolf Daniel

Professor of Genomic and Applied Microbiology

- 2013 – present: Speaker “North German Center of Microbial Genomics” (Norddeutsches Zentrum für Mikrobielle Genomforschung, NZMG)
- 04/2012 – 03/2016: Managing Director of the Institute of Microbiology and Genetics, Georg August University Göttingen
- 02/2012 – present: Full Professor (W3) Genomic and Applied Microbiology, Head of the Dept. of Genomic and Applied Microbiology & Göttingen Genomics Laboratory, Georg August University Göttingen
- 2013: Norddeutscher Wissenschaftspreis (Northern German Science Award)
- 05/2008 – 01/2012: Acting Director of the Department of Genomic and Applied Microbiology and Head of the “Göttingen Genomics Laboratory”, Georg August University Göttingen
- 06/1996 – 04/2008: Group Leader, Department of Genomic and Applied Microbiology, Georg August University Göttingen
- 06/1995 – 05/1996: Research Fellow, University of California (Berkeley, USA), Institute of Molecular and Cell Biology, Head: Prof. Dr. Randy Schekman
- 05/1994 – 05/1995: Research Fellow, Georg August University Göttingen, Department of General Microbiology

Major Research Interests

Research foci are cultivation-independent nucleic acids-based metagenomics and metatranscriptomics of complex microbial assemblages and recovery of novel genes and gene products from environmental samples such as soil, sediments, ice, and biofilms. The metagenomic screenings comprised function-based as well as sequence-based approaches. This work has led, e.g., to the successful identification and characterization proteases, cellulases, oxidoreductases, dehydratases, lipases, and DNA polymerases from metagenomes. To gain insights into the genomes of the uncultivated microorganisms and to determine metabolic potential and key functions of microbial communities in the studied environments direct sequencing and annotation of metagenomic DNA and cDNA (mRNA), and comparative genomics are carried out. Other lines of research include whole-genome sequencing, transcriptomics and functional genomics of archaea, bacteria, and microbial communities. The majority of the analyzed organisms is of industrial importance or pathogenic. The group also develops novel bioinformatic tools for data analysis and visualization.

Selected Recent Publications

Lüneberg K, Schneider D, Siebe C, Daniel R (2018) Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. Sci Rep 8:1413

Poehlein A, Montoya Solano JD, Flitsch SK, Krabben P, Winzer K, Reid SJ, Jones DT, Green E, Minton NP, Daniel R, Dürre P (2017) Microbial solvent formation revisited by comparative genome analysis. Biotechnol Biofuels 10: 58

Kaiser K, Wemheuer B, Korolkow V , Wemheuer F, Nacke H, Schöning I, Schrumpf M, Daniel R (2016) Driving forces of soil bacterial community structure, diversity, and function in temperate grasslands and forests. Sci Rep 6: 33696

Billerbeck S, Wemheuer B, Voget S, Poehlein A, Giebel H-A, Brinkhoff T, Gram L, Jeffrey WH, Daniel R, Simon M (2016) Biogeography and environmental genomics of the *Roseobacter*-affiliated pelagic CHAB-I-5 lineage. Nature Microbiol 1: 16063

Wemheuer B, Wemheuer F, Hollensteiner J, Meyer F-D, Voget S, Daniel R (2015) The green impact: bacterioplankton response towards a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. Front Microbiol 6: 805

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Matthias Dobbelstein

Professor of Molecular Oncology

- 1993 Dr. med., University of Munich
- 1993 – 1996 Postdoctoral fellow, Princeton University, USA
- 1997 – 2004 Group leader, University of Marburg
- 2004 – 2005 Professor of Molecular Oncology, University of Southern Denmark, Odense
- Since 2005 Head of the Department of Molecular Oncology, Georg-August-Universität Göttingen

Major Research Interests

We are trying to understand the response of cancer cells to chemotherapy. In particular, we are analyzing the impaired replication of DNA and the damage response that results from injury to DNA. Our focus is on the signaling cascades driven by DNA damage, and on the activation of the tumor suppressor p53. Technologies include the use of large scale siRNA transfection, followed by automated fluorescence microscopy, and the analysis of DNA replication by incorporation of artificial nucleosides. As a disease model, we are investigating the response of colorectal cancer to therapy. On top of classical, DNA damaging chemotherapeutics, we are evaluating other broadly acting, yet non-genotoxic drug candidates, e. g. inhibitors of histone deacetylases and heat shock proteins. On long term, we are aiming at improving the response of tumor cells to chemotherapy by combining traditional and targeted therapeutic approaches.

Selected Recent Publications

Klusmann I, Rodewald S, Muller L, Friedrich M, Wienken M, Li Y, Schulz-Heddergott R, Dobbelstein M (2016) p53 Activity Results in DNA Replication Fork Processivity. Cell Rep 17: 1845-1857

Wienken M, Dickmanns A, Nemajerova A, Kramer D, Najafova Z, Weiss M, Karpiuk O, Kassem M, Zhang Y, Lozano G, Johnsen SA, Moll UM, Zhang X, Dobbelstein M (2016) MDM2 Associates with Polycomb Repressor Complex 2 and Enhances Stemness-Promoting Chromatin Modifications Independent of p53. Mol Cell 61(1): 68-83

Zhang X, Schulz R, Edmunds S, Krüger E, Markert E, Gaedcke J, Cormet-Boyaka E, Ghadimi M, Beissbarth T, Levine AJ, Moll UM, Dobbelstein M (2015) MicroRNA-101 Suppresses Tumor Cell Proliferation by Acting as an Endogenous Proteasome Inhibitor via Targeting the Proteasome Assembly Factor POMP. Mol Cell 59(2): 243-57

Alexandrova EM, Yallowitz AR, Li D, Xu S, Schulz R, Proia DA, Lozano G, Dobbelstein M, Moll UM (2015) Improving survival by exploiting tumour dependence on stabilized mutant p53 for treatment. Nature 523(7560): 352-6

Dobbelstein M, Sørensen CS (2015) Exploiting replicative stress to treat cancer. Nat Rev Drug Discov 14(6): 405-23

Dobbelstein M, Moll U (2014) Targeting tumour-supportive cellular machineries in anticancer drug development. Nat Rev Drug Discov 13(3): 179-96

Köpper F, Bierwirth C, Schön M, Kunze M, Elvers I, Kranz D, Saini P, Menon M, Walter D, Sørensen CS, Gaestel M, Helleday T, Schön M P, Dobbelstein M (2013) Damage-induced DNA replication stalling relies on MAPK-activated protein kinase 2 activity. Proc Natl Acad Sci USA 110: 16856-16861

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Roland Dosch

Group Leader at the Dept. of Developmental Biochemistry

- 1994 – 1999 PhD, Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany
- 1999 – 2003 Postdoc University of Pennsylvania, Philadelphia, USA
- 2004 – 2010 Junior group leader, University of Geneva, Switzerland
- 2010 – 2018 Group leader at the Inst. of Developmental Biochemistry, Georg August University, Göttingen
- Since 2018 Group leader at the Inst. of Human Genetics, University Medical Center, Göttingen

Major Research Interests

A fundamental principle of biological systems is their capacity to reproduce, which is not found in other domains of science such as chemistry or physics. In multicellular organisms like humans, this unique activity is achieved by gametes, egg and sperm. To prepare for the development of a novel organism after fertilization, the oocyte shows a fascinating organization into various compartments. The aim of our research is to understand the molecular mechanisms, which control the cellular organization of the oocyte. For our experiments, we take advantage of the zebrafish, which in recent years emerged as an outstanding vertebrate model to investigate molecular processes *in vivo*. We previously isolated a collection of mutations in key regulators, which show defects in the organization of the oocyte. We apply a combination of molecular genetics and cutting edge genomics such as next-generation-sequencing to identify the affected genes in these mutants. In the most interesting mutants, we started to characterize the molecular function of these essential genes. For this purpose, we incorporate biochemical methods with cell biological approaches e.g. imaging to explore the dynamics of protein localization *in vivo*. With these techniques, we discovered proteins controlling the assembly of RNA-granules as an example for a membrane-free compartment. Recently, we also analyzed membrane bound compartments and identified an important regulator of secretion. Our long-term goal is to understand the intricate molecular organization of the oocyte, which prepares it for fertilization and subsequent embryogenesis.

Selected Recent Publications

Krishnakumar P, Riemer S, Perera R, Lingner T, Goloborodko A, Khalifa H, Bontems F, Kaufholz F, El-Brolosy MA, Dosch R (2018) Functional equivalence of germ plasm organizers. PLoS Genet in press

Roovers EF, Kaaij LJT, Redl S, Bronkhorst AW, Wiebrands K, de Jesus Domingues AM, Huang HY, Han CT, Riemer S, Dosch R, Salvenmoser W, Grun D, Butter F, van Oudenaarden A, Ketting RF (2018) Tdrd6a regulates the aggregation of buc into functional subcellular compartments that drive germ cell specification. Dev Cell 46(3): 285-301 e289. doi:10.1016/j.devcel.2018.07.009

Dosch R (2015) Next generation mothers: Maternal control of germline development in zebrafish. Crit Rev Biochem Mol Biol 50: 54-68

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Bontems F, Baerlocher L, Mehenni S, Bahechar I, Farinelli L, Dosch R (2011) Efficient mutation identification in zebrafish by microarray capturing and next generation sequencing. BBRC 405(3): 373-376

Bontems F, Stein A, Marlow F, Lyautey J, Mullins MC, Dosch R (2009) Bucky ball organizes germ plasm assembly in zebrafish. Curr Biol 19 (5): 414-22

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Jörg Enderlein

Professor of Physics

- 1981 – 86 Study of Physics at Ilya-Mechnikov-University Odessa
- 1991 PhD in Physical Chemistry (Humboldt-University Berlin)
- 2000 Habilitation in Physical Chemistry (University of Regensburg)
- 1996 – 97 PostDoc at Los Alamos National Laboratory (USA)
- 1997 – 2000 Assistent Professor (C1) at University of Regensburg
- 2001 – 2006 Heisenberg Fellow of the DFG at Forschungszentrum Jülich
- 2007 – 2008 Professor for Biophysical Chemistry at Eberhard-Karls-University Tübingen
- Since 2008 Professor for Biophysics at Georg-August-University Göttingen

Major Research Interests

Single molecule fluorescence spectroscopy and imaging, protein conformational dynamics and folding

Selected Recent Publications

Gregor I, Spiecker M, Petrovsky R, Großhans J, Ros R, Enderlein J (2017) Rapid nonlinear image scanning microscopy. Nature Methods 14, 2017: 1087-1089

Niehörster T, Löschberger A, Gregor I, Krämer B, Rahn H, Patting M, Koberling F, Enderlein J, Sauer M (2016) Multi-target spectrally resolved fluorescence lifetime imaging microscopy. Nature Methods13: 257-262

Karedla N, Chizhik AI, Gregor I, Enderlein J (2014) Single-Molecule Metal Induced Energy Transfer (smMIET): Resolving nanometer distances at single molecule level. ChemPhysChem, 15,4: 705-11

Chizhik AI, Rother J, Gregor I, Janshoff A, Enderlein J (2014) Metal-induced energy transfer for live cell nanoscopy. Nature Photonics 8: 124-127

Schulz O, Pieper C, Clever M, Pfaff J, Ruhlandt A, Kehlenbach RH, Wouters FS, Großhans J, Bunt G, Enderlein J (2013) Resolution doubling in fluorescence microscopy with Confocal Spinning-Disk Image Scanning Microscopy. PNAS 110: 21000–21005

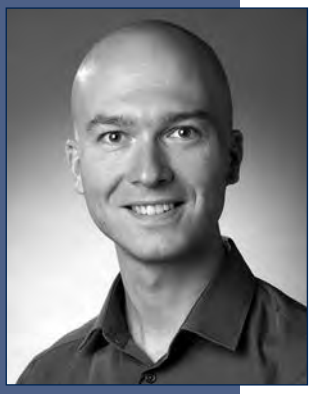
Chizhik AI, Gregor I, Schleifenbaum F, Müller CB, Röling C, Meixner AJ, Enderlein J (2012) Electrodynamic Coupling of Electric Dipole Emitters to a Fluctuating Mode Density within a Nanocavity. Phys Rev Lett 108: 163002

Müller CB, Enderlein J (2010) Image scanning microscopy. Phys Rev Lett 104: 198101

Dertinger T, Colyer R, Iyer G, Weiss S, Enderlein J (2009) Fast, background-free, 3D superresolution optical fluctuation imaging (SOFI). PNAS 106: 22287-22292

Dertinger T, Pacheco C, von der Hocht I, Hartmann R, Gregor I, Enderlein J (2007) Two-Focus fluorescence correlation spectroscopy: a new tool for accurate and absolute diffusion measurements. ChemPhysChem 8: 433-443

Toprak E, Enderlein J, Syed S, McKinney SA, Petschek RG, Ha T, Goldman YE, and Selvin PR (2006) Defocused orientation and position imaging (DOPI) of myosin V. Proc. Natl. Acad. Sci. USA 103: 6495-6499



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- 2003 – 2004 Degree in Technical Management, Eindhoven University of Technology
- 2004 Research trainee, School of Life Sciences, University of Dundee, Advisor: Prof. Dr. D. M. F. van Aalten
- 2000 – 2005 Masters and Bachelor Studies (cum laude (top 5%)), Eindhoven University of Technology, Faculty of BioMedical Engineering, Advisor Master studies: Dr. Maarten Merkx
- 2005 – 2011 Graduate Student, Netherlands Cancer Institute, Amsterdam, Advisor: Prof. Dr. Titia Sixma
- 2012 – 2017 Post-doctoral fellow, Max-Planck Institute of Molecular Physiology, Dortmund, Advisor: Prof. Dr. Andrea Musacchio
- Since 2017 Max-Planck Research Group Leader, Max-Planck Institute of Biophysical Chemistry, Göttingen

Major Research Interests

Spatiotemporal control of protein interactions in signaling pathways is vital in biology. The reversible activation of signaling proteins or complexes through post-translational modifications (PTMs) plays a central role in the regulation of biochemical switches in signal-transducing systems. The primary interest of our research group is in a less studied alternative process in cellular signaling, which is operational in cell division, DNA damage signaling, and autophagy. The signal transduction mechanism relies on the reversible change of a protein's three-dimensional structure to regulate its protein-protein interaction potential. The crucial paradigm emerging from our previous studies in cell division is that structural conversion of HORMA domains is catalyzed, both at the assembly and the disassembly level, by specialized protein machinery, allowing dynamic control of signaling. We are interested in the molecular mechanisms that regulate the topological changes in these signaling protein complexes, which are essential in the initiation of signaling.
Instead of studying these processes in their complex cellular environment, we aim to biochemically reconstitute these dynamic reactions from purified components in vitro. This allows us to study and manipulate all biochemical activities in great detail, identify the minimal set of components, and ultimately reveal the underlying fundamental principles. Typically, our projects use a bottom-up approach, where we build macromolecular machines from scratch to understand them in details using a combination of biochemical reconstitution, structural biology, and biophysical investigations

Selected Recent Publications

Faesen AC, Thanasoula M, Maffini S, Breit C, Müller F, van Gerwen S, Bange T, Musacchio A (2017) Basis of catalytic assembly of the mitotic checkpoint complex Nature Feb 23;542(7642): 498-502

Weir JR, Faesen AC, Klare K, Basilico F, Fischböck, Pentakota S, Keller J, Petrovic A, Pesenti M, Vogt D, Wohlgemuth S, Herzog F, Musacchio A (2016) Insights from biochemical reconstitution into the architecture of human kinetochores Nature Aug 31;537(7619): 249-253

Faesen AC, Luna-Vargas MPA, Sixma TK (2012) The role of UBL domains in Ubiquitin-Specific Proteases. Biochemical Society Transactions June 1; 40(3): 539-545

Faesen AC, Luna-Vargas MPA, Geurink PP, El Oualid F, Clerici M, Ovaa H, Sixma TK (2011) The differential modulation of USP activity by internal regulatory domains, interactors and seven Ub-chain types. Chem. Biol Dec 23; 18(12): 1550-61

Faesen AC, Dirac MG, Shanmugham A, Ovaa H, Perrakis A, Sixma TK (2011) The auto-activation mechanism of USP7/HAUSP by its ubiquitin-like (HUBL) domain is allosterically promoted by GMPS. Mol Cell. Oct 7; 44(1): 147-59

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- 1990 Diploma (Chemistry), Philipps-University, Marburg
- 1993 Dr. rer. nat., Philipps-University, Marburg
- 1997 – 1999 Leader of an independent research group at the Institute for Plant Biochemistry (IPB), Halle/Saale
- 2000 Habilitation (Biochemistry), Martin-Luther-University, Halle/Saale
- 2000 – 2002 Leader of an independent research group at Institute for Plant Genetics and Crop Plant Research (IPK), Gatersleben
- Since 2002 Professor of Biochemistry, Georg-August-University, Göttingen
- 2001 Habilitation-Prize of the Ernst Schering Research Foundation
- 2009 Fellow of the Saxonian Academy of Sciences, Leipzig
- 2012 Terry-Galliard Medal
- 2013 Fellow of the Academy of Sciences, Göttingen

Major Research Interests

The group is currently studying different aspects of the lipid metabolism of plants, algae, mosses and fungi. In this context we are primarily interested in the metabolism of structural lipids and lipid-derived signal transduction processes. For this purpose, we make use of both classical techniques as analytical chemistry and biochemistry as well as of modern approaches in the area of molecular genetics, including the generation of transgenic organisms („gain-of-function“) or mutants („loss-of-function“).
Biochemistry and function of oxylipin metabolism:
We are interested in physiological functions of lipid peroxidation processes. Thus we analyze the function of specific lipoxygenases, i.e. the role of their products, so-called oxylipins (oxygenated fatty acid derivatives), as signals or defence substances during biotic and abiotic stress. Lipid peroxidation reactions are analysed in general by metabolomic approaches. Other studies deal with the role of oxylipins in mosses and algae. In addition the catalytic mechanism of lipoxygenases and related dioxygenases is analysed.
Biochemistry of the biosynthesis of structural lipids:
We study the biochemical pathways or networks that led to an increase in the seed oil content of oilseed crop plants and oleogenous algae. Two other projects deal with the biochemistry and function of sphingolipids in plants with wax ester forming enzymes. In addition we aim to identify chemical signals by metabolomics approaches that are exchanged during the interaction between insects and *Arabidopsis thaliana*.

Selected Recent Publications

Lenarčič T, Albert I, Böhm H, Hodnik V, Pirc K, Zavec AB, Podobnik M, Pahovnik D, Žagar E, Pruitt R, Greimel P, Yamaji-Hasegawa A, Kobayashi T, Zienkiewicz A, Gömann J, Mortimer JC, Fang L, Mamode-Cassim A, Deleu M, Lins L, Oecking C, Feussner I, Mongrand S, Anderluh G, Nürnberger T (2017) Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. Science 358: 1431-1434

Marmon SK, Sturtevant D, Herrfurth C, Chapman KD, Stymne S, Feussner I (2017) Two acyltransferases contribute differently to linolenic acid levels in seed oil. Plant Physiol 173: 2081-2095

Newie J, Neumann P, Werner M, Mata RA, Ficner R, Feussner I (2017) Lipoxygenase 2 from Cyanothece sp. controls dioxygen insertion by steric shielding and substrate fixation. Sci Rep 7: 2069

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Ralf Ficner

Professor of Structural Biology

- Dr. rer. nat. (1992) and Postdoc (1993), Max Planck Institute for Biochemistry, Martinsried
- Postdoctoral fellow, EMBL Heidelberg, 1994 – 1996
- Junior Group Leader, University of Marburg, 1997 – 2000
- Appointed 2001 as Head of the Department of Molecular Structural Biology at the University of Göttingen

Major Research Interests

In order to understand the relationship between the three-dimensional structure and the cellular function of biological macromolecules we determine the structures of proteins and protein-RNA complexes by means of X-ray crystallography. Our current projects concern proteins involved in the splicing and modification of RNA and, as well, proteins required for the nucleocytoplasmic transport.

Selected Recent Publications

Tauchert MJ, Fourmann JB, Lührmann R, Ficner R (2017). Structural insights into the mechanism of the DEAH-box RNA helicase Prp43. eLife 6, e21510

Fischer N, Neumann P, Konevega AL, Bock LV, Ficner R, Rodnina MV, Stark H (2015) Structure of the *E. coli* ribosome-EF-Tu complex at <3 Å resolution by Cs-corrected cryo-EM. Nature 520: 567-570

Kuhle B, Ficner R (2014) A monovalent cation acts as structural and catalytic cofactor in translational GTPases. EMBO J 33: 2547-2563

Neumann P, Lakomek K, Naumann P-T, Erwin W, Lauhon C, Ficner R (2014) Crystal structure of a 4-thiouridine synthetase - RNA complex reveals specificity of tRNA U8 modification. Nucleic Acids Res 42: 6673-6685

Kuhle B, Ficner R (2014) eIF5B employs a novel domain release mechanism to catalyze ribosomal subunit joining. EMBO J 33: 1177-1191

Ahmed YL, Gerke J, Park HS, Bayram O, Neumann P, Ni M, Dickmanns A, Kim SC, Yu JH, Braus GH, Ficner R (2013) The velvet family of fungal regulators contains a DNA-binding domain structurally similar to NF-kappaB. PLoS Biol 11: e1001750

Monecke T, Haselbach D, Voss B, Russek A, Neumann P, Thomson E, Hurt E, Zachariae U, Stark H, Grubmüller H, Dickmanns A, Ficner R (2013) Structural basis for cooperativity of CRM1 export complex formation. Proc Natl Acad Sci USA 110: 960-965

Khoshnevis S, Hauer F, Milon P, Stark H, Ficner R (2012) Novel insights into the architecture and protein interaction network of yeast eIF3. RNA 18: 2306-2319

Lehwess-Litzmann A, Neumann P, Parthier C, Lüdtke S, Golbik R, Ficner R, Tittmann K (2011) Twisted Schiff base intermediates and substrate locale revise transaldolase mechanism. Nat Chem Biol 7(10): 678-684

Güttler T, Madl T, Neumann P, Deichsel D, Corsini L, Monecke T, Ficner R, Sattler M, Görlich D (2010) NES consensus redefined by structures of PKI-type and Rev-type nuclear export signals bound to CRM1. Nature Struct Mol Biol 17: 1367-1376

Schulz E-C, Dickmanns A, Urlaub H, Schmitt A, Mühlenhoff M, Stummeyer K, Schwarzer D, Gerardy-Schahn R, Ficner R (2010) Crystal structure of a novel intramolecular chaperone mediating triple ß-helix folding. Nature Struct Mol Biol 17: 210-215

Monecke T, Güttler T, Neumann P, Dickmanns A, Görlich D, Ficner R (2009) Crystal structure of the nuclear export receptor CRM1 in complex with Snurportin1 and RanGTP. Science 324(5930): 1087-91

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André Fischer

Professor for Psychiatry and Psychotherapy

- 2003 – 2006: Postdoctoral Associate in the lab of Li-Huei Tsai; Harvard Medical School, Department of Pathology, Boston, USA; Picower Center for Learning and Memory, M.I.T, Cambridge, USA
- 2007 – 2011: Independent Group Leader at ENI
- since 2011: W3 Professor at the Department for Psychiatry and Psychotherapy, University Medical Center Göttingen
- since 2011: Speaker of the German Center for Neurodegenerative Diseases (DZNE) site Göttingen

Major Research Interests

The long-term goal of our research is to understand the cellular and molecular mechanisms underlying brain diseases and to develop neuroprotective and neurodegenerative therapeutic approaches. There is now accumulating evidence that on an individual level health or disease critically depends on the interaction between genes and environment. Epigenetic mechanisms such as histone-modification, DNA-methylation and non-coding RNA-mediated processes are key-regulators of gene-environment interactions. Importantly, such epigenetic mechanisms have recently been implicated with the pathogenesis of neurodegenerative and psychiatric diseases. Thus our current hypothesis is that deregualtion of genome-environment interactions, especially via epigenetic gene-expression, is a key feature of neurodegenerative diseases such as Alzheimer's disease. We combine studies in patient material, mouse and cellular models, behavioral, molecular, genetic, and bioinformatic techniques to address these questions.

Selected Recent Publications

Bahari-Javan S, Varbanov H, Halder R, Benito E, Kaurani L, Burkhardt S, Anderson-Schmidt H, Anghelescu I, Budde M, Stilling RM, Costa J, Dietrich D, Figge C, Folkerts H, Gade K, Heilbronner U, Koller M, Konrad C, Nussbeck SY, Scherk H, Spitze C, Stierl S, Stöckel J, Thiel J, Hagen M, Zimmermann J, Zitzelsberger A, Schulz A, Schmitt A, Delalls I, Falkai P, Schulze TG, Dityatev A, Sananbenesi F, Fischer A (2017) HDAC1 links early life stress to schizophrenia-like phenotypes. Proc Natl Acad Sci USA 114(23): E4686–E4694

Benito E, Urbanke U, Ramachandran B, Barth J, Halder R, Awasthi A, Jain G, Capece V, Burkhardt S, Navarro-Sala M, Nagarajan N, Schütz AL, Johnsen SA, Bonn SA, Lührmann R, Dean C, Fischer A (2015) Reinstating transcriptome plasticity and memory function in models for cognitive decline. Journal of Clinical Investigation 125(9): 3572-84

Stilling R, et al. Fischer A (2014) K-Lysine acetlytransferase 2A regulates a hippocampal gene-expression network linked to memory formation. EMBO J 33(17): 1912-1927

Kerimoglu C, et al. Fischer A (2013) Histone-methyltransferase MLL2 (kmt2b) is required for memory formation in mice. J Neurosci 8: 3452-3464

Zovoilis A, Agbemenyah HY, Agis-Balboa RC, Stilling RM, Edbauer D, Rao P, Farinelli L, Delalle I, Schmitt A, Falkai P, Bahari-Javan S, Burkhardt S, Sananbenesi F, Fischer A (2011) microRNA-34c is a novel target to treat dementias. EMBO J 30(20): 4299-308

Peleg S, Sananbenesi F, Zovoilis A, Burkhardt S, Bahari-Javan S, Agis-Balboa RC, Cota P, Wittnam JL, Gogol-Doering A, Opitz L, Salinas-Riester G, Dettenhoffer M, Farinelli L, Chen W, Fischer A (2010) Altered histone H4 lysine 12 acetylation is associated with age-dependent memory impairment in mice. Science 328: 753

Fischer A*, Sananbenesi F, Wang X, Dobbin M, Tsai LH (2007) Recovery of learning and memory is associated with chromatin remodeling. Nature 447: 178-82 (* Corresponding author)

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Christiane Gatz

Professor of Plant Molecular Biology

- Dr. rer. nat. (1985) at the Institute for Biochemistry, Technical University Darmstadt
- Postdoctoral fellow at the University of Wisconsin, Madison, USA (1985 – 1987)
- Habilitation in Molecular Genetics at the Freie Universität Berlin in 1992
- Professor at the University of Bielefeld (1993 – 1995)
- Alfried Krupp von Bohlen und Halbach-Award for young university professors (1994)
- Professor at the University of Göttingen since 1996

Major Research Interests

Our laboratory is interested in the molecular mechanisms establishing plant innate immunity. We focus on the elucidation of signal transduction mechanisms that lead to transcriptional reprogramming in the course of plant defense responses against bacteria and fungi. Plants have developed multiple layers of defense responses against pathogens. In general, infection of the model plant *Arabidopsis thaliana* with biotrophic pathogens (pathogens that exploit resources of living cells) leads to the activation of salicylic acid (SA)-mediated defense responses, whereas infection with necrotrophic pathogens (pathogens that kill cells to obtain access to nutrients) elicits jasmonic acid/ethylene (JA/ET)-dependent responses. If plants are infected by both types of pathogens, the SA pathway represses the JA/ET pathway (cross-talk). Members of the TGA family of transcription factors have been identified as essential regulators of both responses. While the SA-mediated mechanisms that activate TGA factors have been elucidated in considerable detail it has remained unknown how these factors mediate the negative effect of SA on the JA/ET response (Zander et al., 2010; Zander et al., 2014). In this context, we have identified the family of plant-specific ROXY-type glutaredoxins, which interact with TGA factors to influence defense responses (Ndamukong at al., 2007; Zander et al., 2012). A central question in our lab is as to how ROXYs regulate the activity of TGA factors. We combine genetic (e.g. analysis of mutants and double mutants, generation of mutants using the CRISPR/Cas genome editing system), molecular (e.g. gene expression analysis by real-time RT PCR), cell biological (subcellular localization and protein-protein-interaction studies in living cells) and biochemical (e.g. chromatin immunoprecipitation, biotin switch assays to study the *in vivo* redox state of proteins) approaches to gain novel insights into these complex mechanisms.
A further project analyzes the function of the JA receptor COI1 in the defense against the vascular pathogen *Verticillium longisporum*. Whereas COI1 usually promotes defense responses against necrotrophic fungi when activated by JA, it promotes susceptibility independently from JA in response to infection with *V. longisporum* (Ralhan et al., 2012). Our aim is to understand the activation and the downstream effects of this novel COI1 function. Moreover, we aim to elucidate the evolution of JA synthesis and COI1-dependent JA signaling in non-seed plants.

Selected Recent Publications

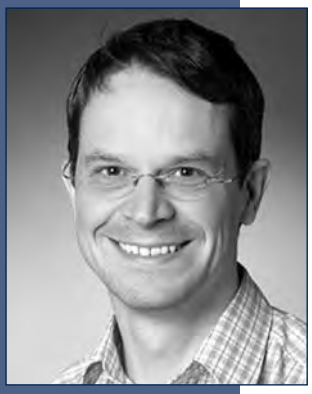
Uhrig JF, Huang LJ, Barghahn S, Willmer M, Thurow C, Gatz, C (2016) CC-type glutaredoxins recruit the transcriptional co-repressor TOPLESS to TGA-dependent target promoters in *Arabidopsis thaliana*. Biochim Biophy Acta 1860: 218-226

Zander M, Thurow C, Gatz C (2014) TGA transcription factors activate the salicylic acid-suppressible branch of the ethylene-induced defense program by regulating ORA59 expression. Plant Physiol 65: 1671-1683

Ralhan A, Schottle S, Thurow C, Iven T, Feussner I, Polle A, Gatz C (2012) The vascular pathogen *Verticillium longisporum* requires a jasmonic acid-independent COI1 function in roots to elicit disease symptoms in *Arabidopsis* shoots. Plant Physiol 159: 1192-1203

Zander M, Chen S, Imkampe J, Thurow C, Gatz C (2011) Repression of the *Arabidopsis thaliana* jasmonic acid/ethylene-induced defense pathway by TGA-interacting glutaredoxins depends on their C-Terminal ALWL motif. Mol Plant 5: 831-40

Zander M, La Camera S, Lamotte O, Metraux JP, Gatz C (2010) *Arabidopsis thaliana* class-II TGA transcription factors are essential activators of jasmonic acid/ethylene-induced defense responses. Plant J 61: 200-210



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Dirk Görlich

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- 1989 Diploma (Biochemistry), Martin-Luther-Universität in Halle
- 1990 – 1993 Graduate studies (Laboratory of T.A. Rapoport, Berlin)
- 1993 Dr. rer. nat. (Biochemistry) Humboldt-Universität Berlin
- 1993 – 1995 Postdoc (Laboratory of R.A. Laskey, Cambridge, England)
- 1996 – 2007 Research group leader at the ZMBH Heidelberg
- 2001 – 2007 Professor for Molecular Biology (Universität Heidelberg)
- 2007 – Director, Dept. Cellular Logistics, MPI for Biophysical Chemistry, Göttingen
- 2018 – 2019 Managing Director of the Institute

Major Research Interests

- Nuclear pore complexes, their function and assembly
- Hydrogels, “smart” materials, phase separations
- Structural biology
- Importins and Exportins, cargo recognition
- Recombinant antibodies, protein engineering

Selected Recent Publications

Frey S, Rees R, Schünemann J, Ng SC, Fünfgeld K, Huyton T, Görlich D (2018) Surface properties determining passage rates of proteins through nuclear pores. Cell 174: 202-217.e9

Aksu M, Pleiner T, Karaca S, Kappert C, Dehne HJ, Seibel K, Urlaub H, Bohnsack MT, Görlich D (2018) Xpo7 is a broad-spectrum exportin and a nuclear import receptor. J Cell Biol 217: 2329-2340

Pleiner T, Bates M, Görlich D (2018) A toolbox of anti-mouse and anti-rabbit IgG secondary nanobodies. J Cell Biol 217: 1143-1154

Aksu M, Trakhanov S, Görlich D (2016) Structure of the exportin Xpo4 in complex with RanGTP and the hypusine-containing translation factor eIF5A. Nat Commun 7: 11952

Schmidt HB, Görlich D (2015) Nup98 FG domains from diverse species spontaneously phase-separate into particles with nuclear pore-like permselectivity. eLife 4: e04251

Pleiner T, Bates M, Trakhanov S, Lee CT, Schliep J E, Chug H, Böhning M, Stark H, Urlaub H, Görlich D (2015) Nanobodies: site-specific labeling for super-resolution imaging, rapid epitope-mapping and native protein complex isolation. eLife 4: e11349

Chug H, Trakhanov S, Hülsmann BB, Pleiner T, Görlich D (2015) Crystal structure of the metazoan Nup62•Nup58•Nup54 nucleoporin complex. Science 350: 106-110

Kirli K, Karaca S, Dehne H J, Samwer M, Pan T, Lenz C, Urlaub H, Görlich D (2015) A deep proteomics perspective on CRM1-mediated nuclear export and nucleocytoplasmic partitioning. eLife 4: e11466

Hülsmann BB, Labokha A, Görlich D (2012) The permeability of reconstituted nuclear pores provides direct evidence for the selective phase model. Cell 150: 738-751

Frey S, Görlich D (2007) A saturated FG-repeat hydrogel can reproduce the permeability properties of nuclear pore complexes. Cell 130: 512-523

Frey S, Richter RP, Görlich D (2006) FG-rich repeats of nuclear pore proteins form a three-dimensional meshwork with hydrogel-like properties. Science 314: 815-817

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Christian Griesinger

Professor, Director at the Max Planck Institute for Biophysical Chemistry, Göttingen

- Dr. phil. nat. University of Frankfurt (1986, Prof. Dr. H. Kessler)
- Postdoctoral Fellow at Lab. for Physical Chemistry, ETH Zürich (1986 – 1989, Prof. Dr. R. R. Ernst)
- Full Professor for Organic Chemistry at the University of Frankfurt (1990 – 2000)
- Appointed as Director at the Max Planck Institute for Biophysical Chemistry (1999)

Major Research Interests

In the department, we develop NMR spectroscopic methods and apply them to the investigation of water soluble and membrane proteins, nucleic acids and their complexes as well as drug/target complexes. We are specifically focussing on the dynamics of biomolecules. Structural biology projects are performed in the context of signal transduction, ion channels, cytoskeletal proteins, enzymes and drug/target complexes using NMR as well as X-ray crystallography to characterize structure and dynamics. An applied project is the investigation of proteins involved in neurodegenerative diseases that are studied in the context of the CNMPB and involve NMR and other biophysical methods as well as chemical synthesis. Methods developments are aimed at pushing the limits of sensitivity for NMR spectroscopic detection (e.g. DNP), developing the measurement of structurally and dynamically relevant parameters, establishing methods to describe structural ensembles for folded and intrinsically disordered proteins. For solid state NMR investigations, pulse sequences that allow structure determination of uniformly labelled membrane proteins as well as oligomers and fibrils formed from proteins involved in neurodegenerative diseases have been successfully developed.

Selected Recent Publications

Turriani E, LázaroDF, Ryazanov S,Leonov A, Giese A, Schön M, Schön MP, Griesinger C, Outeiro TF, Arndt-Jovin DJ, Becker D (2017) Treatment with diphenyl-pyrazole compound anle138b/c reveals that a-synuclein protects melanoma cells from autophagic cell death. Proc Natl Acad Sci USA 114(25): E4971-E4977

Salvi M, Schomburg B, Giller K, Graf S, Unden G, Becker S, Lange A, Griesinger C (2017) Sensory domain contraction in histidine kinase CitA triggers transmembrane signaling in the membrane bound sensor. Proc Natl Acad Sci USA 114: 3115-3120

Weisenburger S, Böning D, Schomburg B, Giller K, Becker S, Griesinger C, Sandoghdar V (2017) Crygenic optical localization provides 3D protein structure data with Angstrom resolution. Nat Meth 14: 141-144

Smith CA, Ban D, Pratihar S, Giller K, Paulat M, Becker S, Griesinger C, Lee D, de Groot BL (2016) Allosteric switch regulates protein-protein binding through collective motion. Proc Natl Acad Sci USA 113: 3296-74

Kühn J, Wong LE, Pirkuliyeva S, Schulz K, Schwiegk C, Fünfgeld KG, Keppler S, Batista FD, Urlaub H, Habeck M, Becker S, Griesinger C, Wienands J (2016) The adaptor protein CIN85 assembles intracellular signaling clusters for B cell activation. Sci Signaling 9(434): ra66

Carneiro MG, Reddy JG, Griesinger C, Lee D (2015) Speeding-up exchange-mediated saturation transfer experiments by Fourier transform. J Biomol NMR 63(3): 237-244

Wagner J, Krauss S, Shi S, Ryazanov S, Steffen J, Miklitz C, Leonov A, Kleinknecht A, Göricke B, Weishaupt JH, Weckbecker D, Reiner AM, Zinth W, Levin J, Ehninger D, Remy S, Kretzschmar HA, Griesinger C, Giese A, Fuhrmann M (2015) Reducing tau aggregates with anle138b delays disease progression in a mouse model of tauopathies. Act Neuropath 130: 619-631

Pilger J, Mazur A, Monecke P, Schreuder H, Elshorst B, Bartoschek S, Langer T, Schiffer A, Krimm I, Wegstroth M, Lee D, Hessler G, Wendt KU, Becker S, Griesinger C (2015) A combination of spin diffusion methods for the determination of protein-ligand complex structural ensembles. Angew Chem Int Ed 54: 6511-15

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Uwe Groß

Professor of Medical Microbiology

- Professor of Bacteriology and Head, Institute of Medical Microbiology, University Medical Center Göttingen since 1999 (co-opted Professorship, Faculty of Biology since 2005)
- Professor of Medical Parasitology, University of Würzburg 1998/1999
- Postdoctoral fellow, UC Los Angeles, California, 1987 – 1989
- M.D., University of Hamburg 1987

Major Research Interests

The Institute of Medical Microbiology is trying to understand infectious diseases by linking applied and basic sciences, e.g. aspects of epidemiology and pathogenesis. In regards to bacteriology, we are focusing on the intestinal pathogens *Campylobacter jejuni* and *Clostridium difficile*, where we use molecular approaches to identify and characterize virulence-associated factors, such as those involved in invasion (*Campylobacter*) or in spore regulation (*Clostridium*). In addition, the epidemiology of both pathogens in different regions and environments is under investigation.
Fungal infections caused by *Candida* and *Aspergillus* is a second major research topic. Like in bacterial infections, antimicrobial resistances are an emerging threat in mycology as well. Therefore, we focus on analyzing the epidemiology and the mechanisms of antifungal resistances, but are also investigating fungal factors and mechanisms that are involved in pathogenesis of mycoses.
The protozoan parasite *Toxoplasma gondii* usually causes asymptomatic infections in immunocompetent adults leading to lifelong persistence especially in the brain and in muscle tissue. Infections are especially dangerous during pregnancy and in immuno-compromised individuals (i.e. patients suffering from AIDS). We are interested in the epidemiology of toxoplasmosis as well as in the cross-talk between the parasite and its host cell on a molecular level. Here, we investigate how the parasite (i) modulates the host cell capacity for MHC-restricted antigen presentation and (ii) inhibits apoptosis of the infected cell. Both mechanisms allow intracellular persistence.
Recently, we also started to develop the theme Global Health in regards to infectious diseases and cooperate with scientists from Ghana, Kenya, and Tanzania

Selected Recent Publications

Janssen I, Cooper P, Gunka K, Rupnik M, Wetzel D, Zimmermann O, Groß U (2016) High prevalence of nontoxigenic Clostridium difficile isolated from hospitalized and non-hospitalized individuals in rural Ghana. Int J Med Microbiol 306: 652-656

Mössner R, Diering N, Bader O, Forkel S, Overbeck T, Groß U, Grimbacher B, Schön MP, Buhl T (2016) Ruxolitinib induces interleukin 17 and ameliorates chronic mucocutaneous candidiasis caused by STAT1 gain-of-function mutation. Clin Infect Dis 62: 951-3

Zautner AE, Goldschmidt AM, Thürmer A, Schuldes J, Bader O, Lugert R, Groß U, Stingl K, Salinas G, Lingner T (2015) SMRT sequencing of the *Campylobacter coli* BfR-CA-9557 genome sequence reveals unique methylation motifs. BMC Genomics 16: 1088

Zautner AE, Masanta WO, Weig M, Groß U, Bader O (2015) Mass spectrometry-based phyloproteomics (MSPP): A novel microbial typing method. Sci Rep 5: 13431

Herrmann DC, Maksimov P, Hotop A, Groß U, Däubener W, Liesenfeld O, Pleyer U, Conraths FJ, Schares G (2014) Genotyping of samples from German patients with ocular, cerebral and systemic toxoplasmosis reveals a predominance of *Toxoplasma gondii* type II. Int J Med Microbiol 304: 911-916

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Jörg Großhans

Professor of Developmental Biochemistry

- 1993 Diplom Biochemistry, Tübingen
- 1993 – 1996 Doctoral research with C Nüsslein-Volhard, Max-Planck-Institut für Entwicklungsbiologie, Tübingen
- 1997 – 2001 Post-doc with E Wieschaus, Princeton (USA)
- 2002 – 2008 ZMBH and Emmy-Noether research group, Heidelberg
- since 2009 Professor, Universitätsmedizin Göttingen

Major Research Interests

Biological structure formation and ageing.
Our group is interested in the molecular and cell-biological mechanisms how biological structures are formed. We analyse structure formation in the early *Drosophila* embryo employing genetical, biochemical and embryological experiments as well as live-imaging. Specifically we investigate how nuclear shape is determined and how the farnesylated protein Kugelkern is involved, how the cells are regularly arranged, how apical-basal polarity is established and how the number of synchronous cell divisions is robustly controlled. Based on our studies nuclear shape we have studied the function of the nuclear lamina and lamina proteins, such as lamin and Kugelkern, in ageing and stem cell proliferation and differentiation in the adult fly.

Selected Recent Publications

Winkler F, Kriebel M, Clever M, Gröning S, Großhans J (2017) Essential Function of the Serine Hydroxymethyl Transferase (SHMT) Gene During Rapid Syncytial Cell Cycles in *Drosophila*. G3 7: 2305–2314

Liu B, Großhans J (2017) Link of zygotic genome activation and cell cycle control. Meth Mol Biol 1605: 11-30

Kong D, Wolf F, Großhans J (2017) Forces directing germ-band extension in *Drosophila* embryos. Mech Dev 144: 11-22

Lv Z, Großhans J (2016) A radial actin network in apical constriction. Dev Cell 39: 280-282

Koke C, Kanesaki T, Großhans J, Schwarz US, Dunlop CM (2014) A computational model of nuclear self-organisation in syncytial embryos. J Theor Biol 359: 92-100

Zhang Y, Kong D, Reichl L, Vogt N, Wolf F, Großhans J (2014) The glucosyltransferase Xiantuan of the endoplasmic reticulum specifically affects E-Cadherin expression and is required for gastrulation movements in *Drosophila*. Dev Biol, 390: 208-220

Bogdan S, Schulz J, Großhans J (2013) Formin' cellular structures - physiological roles of Diaphanous (Dia) in actin dynamics. (review). Comm Integ Biol 6: e27634

Yan S, Lv Z, Winterhoff M, Wenzl C, Zobel T, Faix J, Bogdan S, Großhans J (2013) The F-BAR protein Cip4/Toca-1 antagonizes the formin Diaphanous in membrane stabilization and compartmentalization. J Cell Sci 126 1796-1805.

Sung H-W, Spangenberg S, Vogt N, Großhans J (2013) Number of nuclear divisions in the *Drosophila* blastoderm controlled by onset of zygotic transcription. Curr Biol 23: 133-138

Albrecht SC, Barata A, Großhans J, Teleman AA, Dick TP (2011) *In vivo* mapping of hydrogen peroxide and oxidaized glutathione reveals chemical and regional specificity of redox homeostasis. Cell metabolism 14: 819-829

Kanesaki T, Edwards C, Schwarz U, Großhans J (2011) Dynamic ordering of nuclei in syncytial embryos: a quantitative analysis of the role of cytoskeletal networks. Integ Biol 3: 1112-1119

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Helmut Grubmüller

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1994 Dr. rer nat. (Physics), Technical University of Munich
- 1997 EMBO fellow at the Institute for Molecular Biology and Biophysics, Federal Institute of Technology (ETH) Zurich, Switzerland
- 1998 – 2003 Head of the Theoretical Molecular Biophysics Group at the Max Planck Institute for Biophysical Chemistry, Göttingen
- 2003 Associate Professor for Biomolecular Sciences at the École Polytechnique Fédérale de Lausanne (EPFL)
- 2003 - Director at the Max Planck Institute for Biophysical Chemistry, Göttingen, Head of the Theoretical and Computational Biophysics Department
- 2005 - Honorary Professor for Physics at the University of Göttingen

Major Research Interests

The question 'How do proteins work?' is our driving force. We study biomolecular dynamics and function by atomistic molecular dynamics and qm/mm simulations. Emphasis is on protein function, as well as on protein/DNA/RNA interactions.
Available projects address nuclear pore transport, the ribosome, molecular motors such as F-ATPase, protein unfolding as well as the interaction with radiation with a focus at single molecules, typically in close collaboration with experimental groups. The simulation of single molecule AFM experiments by force probe techniques helps us to reveal mechanisms of protein function involving mechanical stress such as the muscular force sensor titin kinase, and so do improved methods to calculate thermodynamic quantities from simulations. We are continuously advancing our simulation techniques and scalability on massively parallel computers. The group of ca. 20 PhD students and postdocs shares a strong background mainly in physics, and scientific computing, but also in chemistry and biology. We enjoy exclusive access to a high-performance linux cluster of ca. 18.000 processor cores and ca. 950 GPUs.

Selected Recent Publications

Bock LV, Blau C, Vaiana AC, Grubmüller H (2015) Dynamic contact network between ribosomal subunits enables rapid large-scale rotation during spontaneous translocation. Nucleic Acids Res 43(14): 6747-60

Risselada HJ, Bubnis G, Grubmüller H (2014) Expansion of the fusion stalk and its implication for biological membrane fusion. Proc Natl Acad Sci USA 111(30): 11043-8

Czub J, Grubmüller H (2014) Rotation triggers nucleotide-independent conformational transition of the empty β subunit of F-ATPase. J Am Chem Soc 136(19): 6960-8

Bock LV, Blau C, Schröder GF, Davydov II, Fischer N, Stark H, Rodnina MV, Vaiana AC, Grubmüller H (2013) Energy barriers and driving forces in tRNA translocation through the ribosome. Nat Struct Mol Biol 20(12): 1390-6

Czub J, Grubmüller H (2011) Torsional elasticity and energetics of F1-ATPase. Proc Natl Acad Sci USA 108(18): 7408-7413

Lange OF, Lakomek NA, Fares C, Schröder GF, Walter KFA, Becker S, Meiler J, Grubmüller H, Griesinger C, de Groot BL (2008) Recognition dynamics up to microseconds revealed from an RDC-derived ubiquitin ensemble in solution. Science 320: 1471-1475

Sieber JJ, Willig KI, Kutzner C, Gerding-Reimers C, Harke B, Donnert G, Rammner B, Eggeling C, Hell SW, Grubmüller H, Lang T (2007) Anatomy and dynamics of a supramolecular membrane protein cluster. Science 317: 1072-1076

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Ufuk Günesdogan

Group Leader, Developmental Biology

- Undergraduate studies in biology at the University of Braunschweig
- 2006 – 2010 Predoctoral fellow at the Max Planck Institute for Biophysical Chemistry, Göttingen
- 2010 – 2015 Postdoctoral Research Associate at the Gurdon Institute, University of Cambridge, UK
- 2015 – 2017 Leverhulme Early Career Fellow at the Gurdon Institute, University of Cambridge, UK
- Since 2017 Group Leader at the University of Göttingen

Major Research Interests

Our research focuses on understanding the development of mammalian primordial germ cells (PGCs), the precursors of sperm or egg. Hence, PGCs represent the only cell type that transmits genetic and epigenetic information to the next generation. In mammals, the developing embryo forms the postimplantation epiblast, the founder cell population of all embryonic cell types. While most of these cells give rise to organs and tissues, a few are set aside to become PGCs. Shortly after, PGCs undergo reprogramming including extensive transcriptional changes accompanied by epigenetic alterations. Our work addresses the fundamental questions: How is the transcriptional programme controlled and what are the functional implications of epigenetic modifications in PGCs? To address these questions, we make use of *in vivo* and *in vitro* model systems of PGC differentiation, genome-wide techniques and the CRIPSR/Cas9 genome editing tool.

Selected Recent Publications

Murakami K, Günesdogan U, Zylicz JJ, Tang WWC, Sengupta R, Kobayashi T, Kim S, Butler R, Dietmann S, Surani MA (2016) NANOG alone induces germ cells in primed epiblast *in vitro* by activation of enhancers. Nature 529: 403–407

Günesdogan U, Surani MA (2016) Developmental Competence for Primordial Germ Cell Fate Curr Top Dev Biol 117: 471–496

Zylicz, JJ, Dietmann S, Günesdogan U, Hackett JA, Cougot D, Lee C, Surani MA (2015) Chromatin dynamics and the role of G9a in gene regulation and enhancer silencing during early mouse development. Elife 4: e09571

Kim S, Günesdogan U, Zylicz JJ, Hackett JA, Cougot D, Bao S, Lee C, Dietmann S, Allen, GE, Sengupta R (2014) PRMT5 Protects Genomic Integrity during Global DNA Demethylation in Primordial Germ Cells and Preimplantation Embryos. Mol. Cell 56: 564–579

Günesdogan U, Magnúsdóttir E, Surani MA (2014) Primordial germ cell specification: a context-dependent cellular differentiation event. Philos Trans R Soc Lond B Biol Sci: 369

Günesdogan U, Jäckle H, Herzig A (2014) Histone supply regulates S phase timing and cell cycle progression. Elife 3: e02443

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Heidi Hahn

Professor of Molecular Developmental Genetics

- Dr. med., University of Würzburg, 1992
- Postdoctoral Fellow, National Institutes of Health, Bethesda, Maryland, USA (1993 – 1998)
- Junior Group Leader (BioFuture), Technical University of Munich (1999 – 2000)
- Professor of Molecular Developmental Genetics, University of Göttingen since 2001

Major Research Interests

Cancer is a disease that results from inappropriate cell division induced by hyperproliferation. In many cases, the development of cancer is associated with genes or signaling pathways important for patterning during embryogenesis.
We investigate the role of the Hedgehog/Patched (Hh/Ptch) signaling cascade in the development of solid tumors. The focus is on rhabdomyosarcoma and basal cell carcinoma. In addition, we are investigating the role of Hh/Ptch signaling in cutaneous squamous cell carcinoma and adenoma of the pituitary gland.
The first aim is the discovery of molecular and cellular events that trigger the initiation of Hh associated tumors. The second aim is to elucidate the function Hh signaling during tumor progression. The third goal is the identification of drugs that target Hh/Ptch-associated solid tumors. To test the anti-tumor activity of the drugs we use tumor-bearing Ptch mutant mice.

Selected Recent Publications

Nitzki F, Cuvelier N, Dräger J, Schneider A, Braun T, Hahn H (2016) Hedgehog/Patched-associated rhabdomyosarcoma formation from Delta1-expressing mesodermal cells. Oncogene 35(22): 2923-31

Uhmann A, Heß I, Frommhold A, König S, Zabel S, Nitzki F, Dittmann K, Lühder F, Christiansen H, Reifenberger J, Schulz-Schaeffer W, Hahn H (2014) DMBA/TPA treatment is necessary for BCC formation from Patched deficient epidermal cells in Ptchflox/floxCD4Cre+/- mice. J Invest Dermatol 134: 2620-2629

Pelczar P, Zibat Z, van Dop WA, Heijmans J, Bleckmann A, Gruber W, Nitzki F, Uhmann A, Guijarro MV, Hernando E, Dittmann K, Wienands J, Dressel R, Wojnowski L, Binder C, Taguchi T, Beissbarth T, Hogendoorn PCW, Antonescu CR, Rubin BP, Schulz-Schaeffer W, Aberger F, van den Brink GR, Hahn H (2013) Inactivation of patched1 in mice leads to development of gastrointestinal stromal-like tumors that express pdgfrα but not kit. Gastroenterology 144(1): 134 -144.e6

Nitzki F, Zibat A, Frommhold A, Schneider A, Schulz-Schaeffer W, Braun T, Hahn H (2011) Uncommitted precursor cells might contribute to increased incidence of embryonal rhabdomyosarcoma in heterozygous Patched1 mutant mice. Oncogene 30: 4428-36

Nitzki F, Zibat A, Konig S, Wijgerde M, Rosenberger A, Brembeck F, Carstens PO, Frommhold A, Uhmann A, Klingler S, Reifenberger J, Pukrop T, Aberger F, Schulz-Schaeffer W, Hahn H (2010) Tumor stroma-derived Wnt5a induces differentiation of basal cell carcinoma of Ptch mutant mice via CaMKII. Cancer Research 70: 2739-48

Uhmann A, Dittmann K, Nitzki F, Dressel R, Koleva M, Frommhold A, Zibat A, Binder C, Adham I, Nitsche M, Heller T, Armstrong V, Schulz-Schaeffer W, Wienands J, Hahn H (2007) The Hedgehog receptor Patched controls lymphoid lineage commitment. Blood 110: 1814-23

Hahn H, Wicking C, Zaphiropoulos P, Gailani M, Shanley S, Chidambaram A, Vorechovsky I, Holmberg E, Unden A, Gillies S, Negus K, Smyth I, Pressman C, Leffell D, Gerrard B, Goldstein A, Wainright B, Toftgard R, Chenevix-Trench G, Dean M, Bale A (1996) Mutations of the human homologue of *Drosophila* patched in the nevoid basal cell carcinoma syndrome. Cell 85: 841-51

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Stefan Hell

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1987 Diploma in Physics, University of Heidelberg
- 1990 Doctorate in Physics, University of Heidelberg (summa cum laude)
- 1991 – 1993 Postdoctoral Researcher, EMBL (European Molecular Biology Laboratory)
- 1993 – 1996 Principal Investigator, Laser Microscopy Group; University of Turku, Finland
- 1996 Habilitation in Physics, University of Heidelberg; Physics teaching since 02/1996
- 1997 – 2002 Head, Max-Planck Junior Group High Resolution Optical Microscopy, at the Max Planck Institute for Biophysical Chemistry Göttingen, Germany
- Since 10/2002 Director at the Max Planck Institute for Biophysical Chemistry, Head of Department of NanoBiophotonics
- Since 12/2003 Apl. Prof., Faculty of Physics, University of Heidelberg
- 2003 – 2017 Head of High Resolution Optical Microscopy Division, DKFZ Heidelberg
- Since 01/2004 Hon. Prof., Faculty of Physics, University of Göttingen
- 2014 Nobel Prize in Chemistry
- 2014 Kavli Prize in Nanoscience
- Since 11/2015 Director at the Max Planck Institute for Medical Research, Head of Department of Optical Nanoscopy

Major Research Interests

Optical microscopy beyond the diffraction barrier with far-field optics. Invention of STED, RESOLFT, GSDIM and 4Pi microscopy and related techniques.

Selected Recent Publications

Eilers Y, Ta H, Gwosch KC, Balzarotti F, Hell SW (2018) MINFLUX monitors rapid molecular jumps with superior spatiotemporal resolution. Proc Natl Aacad Sci USA 115: 6117-6122

Balzarotti F, Eilers Y, Gwosch KC, Gynna AH, Westphal V, Stefani FD, Elf J, Hell SW (2017) Nanometer resolution imaging and tracking of fluorescent molecules with minimal photon fluxes. Science 355: 606-612

Heine J, Reuss M, Harke B, D'Este E, Sahl SJ, Hell SW (2017) Adaptive-illumination STED nanoscopy. Proc Natl Aacad Sci USA 114: 9797-9802

Ta H, Keller J, Haltmeier M, Saka SK, Schmied J, Opazo F, Tinnefeld P, Munk A, Hell SW (2015) Mapping molecules in scanning far-field fluorescence nanoscopy. Nat Commun 6: 7977

Schneider J, Zahn J, Maglione M, Sigrist SJ, Marquard J, Chojnacki J, Kräusslich HG, Sahl SJ, Engelhardt J, Hell SW (2015) Ultrafast, temporally stochastic STED nanoscopy of millisecond dynamics. Nat Methods 12(9): 827-30

Hell SW (215) Nanoscopy with Focused Light (Nobel Lecture). Angew Chem Int Ed Engl 54(28):8054-66

Berning S, Willig KI, Steffens H, Dibaj P, Hell SW (2012) Nanoscopy in a Living Mouse Brain. Science 335: 551

Eggeling C, Ringemann C, Medda R, Schwarzmann G, Sandhoff K, Polyakova S, Belov VN, Hein B, von Middendorff C, Schönle A, Hell SW (2009) Direct observation of the nanoscale dynamics of membrane lipids in a living cell. Nature 457: 1159-1163

Willig KI, Rizzoli SO, Westphal V, Jahn R, Hell SW (2006) STED-microscopy reveals that synaptotagmin remains clustered after synaptic vesicle exocytosis. Nature 440: 935-939

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Kai Heimel

Professor of Microbial Cell Biology

- Since 04/2012: Junior Professor for Microbial Cell Biology, Georg-August-University Göttingen
- 2012: Teaching stand-in for W3 Professorship of Genetics and Cell Biology, Karlsruhe Institute of Technology (KIT)
- 2010 – 2011: Postdoctoral fellow at the Karlsruhe Institute of Technology (KIT)
- 2010: Dr. rer. nat., Philipps-University Marburg
- 2005 – 2010: Doctoral thesis, Max-Planck Institute for Terrestrial Microbiology, Marburg and Karlsruhe Institute of Technology (KIT) (Germany)
- 2000 – 2005: Diploma (Biology), Philipps-University Marburg (Germany)

Major Research Interests

Research in our laboratory is focused on the Unfolded Protein Response (UPR) in development and disease signaling. Cells need to re-adjust and modify their cellular programs in response to a wide range of biotic and abiotic stimuli. The UPR is a highly conserved cellular response to maintain homeostasis of the endoplasmic reticulum (ER). In situations of increased demands for protein production and secretion, potentially harmful un- or mis-folded proteins accumulate in the ER and activate the UPR pathway. Defects in UPR signaling are associated with a wide range of developmental, metabolic and neurodegenerative disorders. Besides the role as a cellular stress response, recent work demonstrated that the UPR pathway is also involved in control of developmental processes. We uncovered that UPR signaling in the phytopathogenic fungus Ustilago maydis is required for disease development and directly coupled to the pathways that control parasitic growth of the fungus. Our future studies will aim to characterize these connections on a molecular level and further explore the role of UPR signaling in controlling cellular behavior and responses to different environments.

Selected Recent Publications

Hampel M, Jakobi M, Schmitz L, Meyer U, Finkernagel F, Doehlemann G, Heimel K (2016) Unfolded Protein Response (UPR) Regulator Cib1 Controls Expression of Genes Encoding Secreted Virulence Factors in *Ustilago maydis*. PLoS One 11: e0153861

Lo Presti L, López Díaz C, Turrà D, Di Pietro A, Hampel M, Heimel K, Kahmann R (2015) A conserved co-chaperone is required for virulence in fungal plant pathogens. New Phytol 209(3): 1135-1148

Heimel K (2015) Unfolded protein response in filamentous fungi - Implications in biotechnology. Appl Mircobiol Biotechnol 99: 121-132

Kellner N, Heimel K, Obhof T, Finkernagel F, Kämper J (2014) The SPF27 homologue Num1 connects splicing and kinesin 1-dependent cytoplasmic trafficking in *Ustilago maydis*. PLoS Genetics 10: e1004046; featured in Faculty of 1000 prime

Heimel K., Freitag J., Hampel M., Ast J, Bölker M., Kämper J (2013) Crosstalk between the Unfolded Protein Response and Pathways That Regulate Pathogenic Development in *Ustilago maydis*. Plant Cell 25: 4262-4277

Heimel K, Scherer M, Schuler D, Kämper J (2010) The *Ustilago maydis* Clp1 Protein Orchestrates Pheromone and b-Dependent Signaling Pathways to Coordinate the Cell Cycle and Pathogenic Development. Plant Cell (8): 2908-22

Heimel K*, Scherer M*, Vranes M, Wahl R, Pothiratana C, Schuler D, Vincon V, Finkernagel F, Flor-Parra I, Kämper J (2010) The transcription factor Rbf1 is the master regulator for bmating type controlled pathogenic development in *Ustilago maydis*. PLoS Pathog 6(8): e1001035 (*equal contribution)

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Claudia Höbartner

Professor, Institute for Organic and Biomolecular Chemistry

- 2004 Dr. rer. nat. (PhD), University of Innsbruck, Austria
- 2005 – 2007 Erwin Schrödinger postdoctoral Fellowship, FWF (Austrian Science Fund), University of Illinois at Urbana-Champaign, USA
- 2007 – 2008 Hertha Firnberg Fellowship, funded by FWF & bmwf (federal ministry of science and research), University of Innsbruck, Austria
- Since 2008 Independent Research Group Leader, Max Planck Institute for Biophysical Chemistry, Göttingen
- 2014 – 2017 Professor at the Institute for Organic and Biomolecular Chemistry, University of Göttingen
- Since 2017 Professor at the Institute of Organic Chemistry, Julius-Maximilians-University Würzburg

Major Research Interests

Our research is focused on the chemistry and biochemistry of natural and artificial nucleic acids.
Functional nucleic acids with new properties can be identified in the laboratory by *in vitro* selection. We use this method to develop catalytic DNA and RNA for labeling and ligation reactions of biomolecules, and we explore functional and structural properties of deoxyribozymes and fluorogenic aptamers. Recently we reported the first crystal structure of a catalytic DNA which allowed mechanistic insights into the regioselectivity of DNA-catalyzed RNA ligation and enabled engineering of DNA enzymes for substrates that could previously not be used in DNA-catalyzed ligations.
In addition, we investigate natural modifications of DNA and RNA and develop labeling methods for their biochemical and spectroscopic detection, with particular emphasis on the emerging field of posttranscriptional RNA modification.

Selected Recent Publications

Ponce-Salvatierra A, Wawrzyniak-Turek K, Steuerwald U, Höbartner* C, Pena* V, (2016) Crystal structure of a DNA catalyst. Nature 529: 231-234 (* corresponding authors)

Samanta B, Seikowski J, Höbartner, C (2016) Fluorogenic labeling of 5-formylpyrimidines in DNA and RNA. Angew Chem Int Ed 55: 1912-1916

Javadi-Zarnaghi F, Höbartner C (2016) Functional hallmarks of a catalytic DNA that makes lariat RNA. Chem Eur J 22: 3720-3728

Halbmair K, Seikowski J, Tkach I, Höbartner* C, Sezer* D, Bennati* M (2016) High-resolution measurement of long-range distances in RNA: pulse EPR spectroscopy with TEMPO-labeled nucleotides. Chem Sci 7: 3172-3180 (*corresponding authors)

Haag S, Sloan KE, Ranjan N, Warda AS, Kretschmer J, Blessing C, Hübner B, Seikowski J, Dennerlein S, Rehling P , Rodnina MV, Höbartner* C, Bohnsack* MT (2016) NSUN3 and ABH1 modify the wobble position of mt-tRNAMet to expand codon recognition in mitochondrial translation. EMBO J 35(19): 2104-2119 (* corresponding authors)

Büttner L, Javadi-Zarnaghi F, Höbartner C (2014) Site-specific labeling of RNA at internal ribose hydroxyl groups: terbium-assisted deoxyribozymes at work. J Am Chem Soc 136: 8131-7

Wawrzyniak-Turek K, Höbartner C (2014) Deoxyribozyme-mediated ligation for incorporating EPR spin labels and reporter groups into RNA. Methods Enzymol 549: 85-104

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Reinhard Jahn

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1981 Dr. rer. nat., University of Göttingen
- 1985 Assistant Professor, The Rockefeller University, New York (USA)
- 1986 Junior Group leader, Max Planck Institute for Psychiatry, Martinsried
- 1991 Associate Professor of Pharmacology and Cell Biology, Yale University, and Investigator, Howard Hughes Medical Institute, New Haven (USA)
- 1995 Professor of Pharmacology and Cell Biology, Yale University, New Haven
- 1997 Director, Max Planck Institute for Biophysical Chemistry, Göttingen
- 1997 – 2001 Adjunct Professor of Pharmacology, Yale University School of Medicine, New Haven, USA
- 2001 Adjunct Professor of Biology, University of Göttingen
- 2019 Emeritus Group Leader, Max Planck Institute for Biophysical Chemistry, Göttingen

Major Research Interests

Our group is interested in the mechanisms of membrane fusion, with the main emphasis on regulated exocytosis in neurons. Intracellular membrane fusion events are mediated by a set of conserved membrane proteins, termed SNAREs. For fusion to occur, complementary sets of SNAREs need to be present on both of the fusing membranes, which then assemble in a zipper-like fashion to initiate membrane merger. The neuronal SNAREs are among the best characterized. They are the targets of the toxins responsible for botulism and tetanus, and they are regulated by several addtional proteins including synaptotagmin, the calcium sensor for neurotransmitter release. To understand how these proteins mediate fusion, we study their properties in vitro with biochemical and biophysical approaches using native and artificial membranes.
In a second set of projects, we are interested in the mechanisms by which synaptic vesicles sequester and store neurotransmitters. Uptake is mediated by specific vesicular neurotransmitter transporters that are energized by an electrochemical proton gradient across the membrane. Presently we aim for a better understanding of the transport mechanisms using a variety of biochemical and biophysical approaches including imaging of single vesicles. Finally, we use quantitative proteomics to better understand how the presynaptic protein network contributes to the regulation of synaptic release, focusing on protein phosphorylation.

Selected Recent Publications

Jakhanwal S, Lee CT, Urlaub H, Jahn R (2017) An activated Q-SNARE/SM protein complex as a possible intermediate in SNARE assembly. EMBO J 36: 1788-1802

Farsi Z, Preobraschenski J, van den Bogaart G, Riedel D, Jahn R*, Woehler A (2016) Single-vesicle imaging reveals different transport mechanisms between glutamatergic and GABAergic vesicles. Science 351: 981-984 *corresponding author

Ryo J-K, Min D, Rah S-H, Kim SJ, Park Y, Kim H, Kim H-M, Jahn R*, Yoon T-Y* (2015) Spring-loaded unraveling of a single SNARE complex by NSF in one round of ATP turnover. Science 347: 1485-1489 *corresponding authors

Binotti B, Pavlos NJ, Riedel D, Wenzel D, Vorbrüggen G, Schalk AM, Kühnel K, Boyken J, Erck C, Martens H, Chua JJE, Jahn R (2015) The GTPase Rab26 links synaptic vesicles to the autophagy pathway. eLife 4: e05597

Par Y, Seo JB, Fraind A, Perez-Lara A, Yavuz H, Han K, Jung SR, Kattan I, Walla PJ, Choi MY, Cafiso DS, Koh D, Jahn R (2015) Synaptotagmin-1 binds to PI(4,5) P2-containing membranes but not to SNAREs in a physiological ionic environment. Nature Struct Mol Biol 10: 815-823

Honigmann A, van den Bogaart G, Iraheta E, Risselada HJ, Milovanovic D, Mueller V, Müllar S, Diederichsen U, Fasshauer D, Grubmüller H, Hell SW, Eggeling C, Kühnel K, Jahn R (2013) Phosphatidylinositol 4,5-bisphosphate clusters act as molecular beacons for vesicle recruitment. Nat Struct Mol Biol 20: 679-686

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Stefan Jakobs

Professor of High Resolution Microscopy in Neurodegenerative Diseases

- 1995 – Diploma, University of Kaiserslautern
- 1995 – 1999 Graduate studies (MPI for Plant Breeding Research, Cologne, Germany and John-Innes-Centre, Norwich, GB)
- 1999 Dr. rer. nat. University of Cologne
- 1999 Postdoc (Laboratory of J. Schell/K. Palme, MPI for Plant Breeding Research, Cologne)
- 1999 – 2005 Postdoc (MPI for Biophysical Chemistry, Laboratory of S.W. Hell)
- 2005 – Research group leader at the MPI for Biophysical Chemistry
- 2007 Habilitation (Botany/Cell Biology) at the Georg-August-University Göttingen
- 2010 – Professor (W2) of High Resolution Microscopy in Neurodegenerative Diseases, University of Göttingen Medical School, Dept. of Neurology

Major Research Interests

Our two major research interests are the investigation of the nanoscale architecture and dynamics of mitochondria and the analysis of reversibly switchable fluorescent proteins (RSFPs) as probes for super-resolution microscopy. Mitochondria are essential organelles in all eukaryotic cells and their dysfunction is involved in many devastating (neurodegenerative) diseases. We want to understand the organization of mitochondria on the nanoscale in healthy and challenged cells and investigate the molecular mechanisms that determine their intricate structure. We utilize a wide array of techniques, including molecular biology, biochemical methods as well as electron and super-resolution microscopy.
RSFPs are fluorescent proteins that may be switched by light between a non-fluorescent and a fluorescent state. Their unique properties open up numerous applications in microscopy and cell biology. We investigate the molecular switching mechanisms and aim to improve the properties of these fascinating proteins as probes for live-cell super-resolution microscopy.

Selected Recent Publications

Sahl SJ, Hell SW, Jakobs S (2017) Fluorescence nanoscopy in cell biology, Nature Rev Mol Cell Biol, doi:10.1038/nrm.2017.71

Große L, Wurm CA, Brüser C, Neumann D, Jans DC, Jakobs S (2016) Bax assembles into large ring-like structures remodeling the mitochondrial outer membrane in apoptosis. EMBO J 35: 402-413

Schnorrenberg S, Grotjohann T, Vorbrüggen G, Herzig A, Hell S, Jakobs S (2016) *In vivo* super-resolution RESOLFT microscopy of *Drosophila melanogaster*. eLife 5: e15567

Jans DC, Wurm CA, Riedel D, Wenzel D, Stagge F, Deckers M, Rehling P, Jakobs S (2013) STED super-resolution microscopy reveals an array of MINOS clusters along human mitochondria. Proc Natl Acad Sci USA 110: 8936-41

Grotjohann T, Testa I, Leutenegger M, Bock H, Urban NT, Lavoie-Cardinal F, Willig KI, Eggeling C, Jakobs S*, Hell SW* (* shared corresponding authors) (2011) Diffraction-unlimited all-optical imaging and writing with a photochromic GFP. Nature 478: 204-208

Brakemann T, Stiel AC, Weber G, Andresen M, Testa I, Grotjohann T, Leutenegger M, Plessmann U, Urlaub H, Eggeling C, Wahl MC, Hell SW, Jakobs S (2011) A reversibly photoswitchable GFP-like protein with fluorescence excitation decoupled from switching. Nature Biotech 29(10): 942-947

Andresen M, Stiel AC, Fölling J, Wenzel D, Schönle A, Egner A, Eggeling C, Hell SW, Jakobs S (2008) Photoswitchable fluorescent proteins enable monochromatic multilabel imaging and dual color fluorescence nanoscopy. Nature Biotech 26: 1035-1040

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Andreas Janshoff

Professor of Biophysical Chemistry

- 1987 – 1989 Studies of Biology at the University of Münster
- 1989 – 1994 Studies of Chemistry at the University of Münster, with honor
- 1994 – 1997 PhD thesis under supervision of Prof. Dr. H.-J. Galla
- 1997 – 1998 Postdoctoral Researcher at the Scripps Research Institute (La Jolla, CA, USA)
- 1999 – 2001 Habilitation in Biochemistry at the University of Münster in the group of Prof. Dr. H.-J. Galla and Prof. Dr. H. Fuchs
- 2001 – 2006 Associate Professor (C3) for Physical Chemistry at the University of Mainz
- 2006 – 2008 Full Professor (W3) for Biophysical Chemistry at the University of Mainz
- since 2008 Full Professor (W3) for Biophysical Chemistry at the University of Göttingen

Major Research Interests

- Membrane Biophysics
- Cell mechanics
- Sensor design
- Single-molecule force spectroscopy

Selected Recent Publications

Block J, Witt H, Candelli A, Danes JC, Peterman EJ, Wuite GJ, Janshoff A, Köster S (2018) Viscoelastic properties of vimentin originate from nonequilibrium conformational changes. Science Advances 4(6): eaat1161

Seiwert D, Witt H, Janshoff A, Paulsen H (2017) The non-bilayer lipid MGDG stabilizes the major light-harvesting complex (LHCII) against unfolding. Scientific Reports 7: 5158

Schütte OM, Mey I, Enderlein J, Savić F, Geil B, Janshoff A, Steinem C (2017) Size and mobility of lipid domains tuned by geometrical constraints. Proceedings of the National Academy of Sciences 114 (30): E6064-E6071

Baronsky T, Ruhlandt D, Brückner BR, Schäfer J, Karedla N, Isbaner S, Hähnel D, Gregor I, Enderlein J, Janshoff A, Chizhik AI (2017) Cell-Substrate Dynamics of the Epithelial-to-Mesenchymal Transition. Nano Letters 17 (5): 3320-3326

Brückner BR, Nöding H, Janshoff A (2017) Viscoelastic Properties of Confluent MDCK II Cells Obtained from Force Cycle Experiments. Biophysical Journal 112 (4): 724-735

Oelkers M, Witt H, Halder P, Jahn R, Janshoff A (2016) SNARE-mediated membrane fusion trajectories derived from force-clamp experiments. Proceedings of the National Academy of Sciences 113 (46): 13051-13056

Brückner BR, Pietuch A, Nehls S, Rother J, Janshoff A (2015) Ezrin is a Major Regulator of Membrane Tension in Epithelial Cells. Scientific Reports 5: 14700

Rother J, Nöding H, Mey I, Janshoff A (2014) AFM-based microrheology reveals significant differences in the viscoelastic response between malign and benign cell lines. Open Biology 4: 140046

Bao C, Pähler G, Geil B, Janshoff A (2013) An Optical Fusion Assay Based on Membrane Coated Spheres in a 2D Assembly. Journal of the American Chemical Society 135 (33): 12176-12179

Krick R, Busse RA, Scacioc A, Stephan M, Janshoff A, Thumm M, Kühnel K (2012) Structural and functional characterization of the two phosphoinositide binding sites of PROPPINs, a beta-propeller protein family. Proceedings of the National Academy of Sciences 109 (30): E2042 -E2049

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Steven Johnsen

Full Professor for Translational Cancer Research

- 1999 – 2002 Ph.D. Mayo Clinic College of Medicine, Rochester, MN, USA
- 2003 – 2006 Doctoral Fellow, Center for Molecular Neurobiology (ZMNH), Hamburg, Germany
- 2006 – 2007 Post-Doctoral Fellow, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
- 2007 – 2012 Assistant Professor in Molecular Oncology, University of Göttingen Medical Faculty, Göttingen, Germany
- 2012 – 2014 Assoc. Professor in Tumor Biology, University Medical Center Hamburg-Eppendorf, Hamburg, Germany
- Since 2014 Professor for Translational Cancer Research, University Medical Center Göttingen, Göttingen, German

Major Research Interests

Cell fate determination during normal physiological processes requires the integration of multiple extrinsic and intrinsic signaling pathways which ultimately converge on the genome to induce stable changes in gene expression. These gene expression changes require an intricate interplay between sequence-specific transcription factors and epigenetic regulatory proteins. Importantly, many major tumor genome sequencing projects have uncovered frequent alterations in epigenetic regulatory proteins, suggesting that genetic changes occurring during tumorigenesis or tumor progression help promote the effects elicited by the activation of oncogenic signaling to reverse cell differentiation programs and lead to pathogenesis. Our group is examining the role of specific epigenetic regulators both in both normal physiological differentiation (e.g., in human osteoblasts) and in cancer (especially colorectal and pancreatic cancer, but also lung, prostate and breast cancer). In order to achieve this we utilize a variety of cell culture and molecular techniques to perform genome- and transcriptome-wide analyses of gene regulatory function and complement these with *in vivo* analysis of conditional gene knockouts and patient samples. Our goal is to gain a thorough understanding of the molecular epigenetic defects in specific subtypes of cancer which will allow us to uncover targeted therapy approaches which can be used in a “precision medicine” approach to treat cancer.

Selected Recent Publications

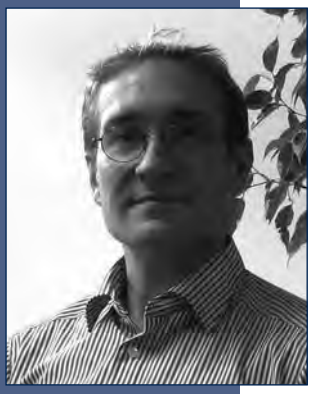
Mishra VK, Wegwitz F, Kosinsky RL, Sen M, Baumgartner R, Wulff T, Siveke JT, Schildhaus HU, Najafova Z, Kari V, Kohlhof H, Hessmann E, Johnsen SA (2017) Histone deacetylase class-I inhibition promotes epithelial gene expression in pancreatic cancer cells in a BRD4- and MYC-dependent manner. Nucleic Acids Res 45(11): 6334-6349

Xie W, Nagarajan S, Baumgart SJ, Kosinsky RL, Najafova Z, Kari V, Hennion M, Indenbirken D, Bonn S, Grundhoff A, Wegwitz F, Mansouri A, Johnsen SA (2017) RNF40 regulates gene expression in an epigenetic context-dependent manner. Genome Biol 18(1): 32

Najafova Z, Tirado-Magallanes R, Subramaniam M, Hossan T, Schmidt G, Nagarajan S, Baumgart SJ, Mishra VK, Bedi U, Hesse E, Knapp S, Hawse JR, Johnsen SA (2017) BRD4 localization to lineage-specific enhancers is associated with a distinct transcription factor repertoire. Nucleic Acids Res 45(1): 127-141

Nagarajan S, Hossan T, Alawi M, Najafova Z, Indenbirken D, Bedi U, Taipaleenmäki H, Ben-Batalla I, Scheller M, Loges S, Knapp S, Hesse E, Chiang CM, Grundhoff A, Johnsen SA (2014) Bromodomain protein BRD4 is required for estrogen receptor-dependent enhancer activation and gene transcription. Cell Rep 8(2): 460-9

Karpiuk O, Najafova Z, Kramer F, Hennion M, Galonska C, König A, Snaidero N, Vogel T, Shchebet A, Begus-Nahrmann Y, Kassem M, Simons M, Shcherbata H, Beissbarth T, Johnsen SA (2012) The histone H2B monoubiquitination regulatory pathway is required for differentiation of multipotent stem cells. Mol Cell 46(5): 705-13



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Dieter Klopfenstein

Junior Group Leader at the Center for Molecular Physiology of the Brain, University of Göttingen

- Dr. phil. nat. (Ph.D.) University of Basel, 1999
- Postdoctoral fellow at the University of California San Francisco, 1999 – 2003
- Since 2003 head of an independent Junior Research Group

Major Research Interests

The long-range transport of membrane organelles in neurons depends primarily upon microtubules and motor proteins that move unidirectionally along these tracks. One type of microtubule-based motor proteins powering membrane transport is the kinesin superfamily. We are interested in how these motors achieve specificity in cargo binding, elicit membrane transport, and the regulation of transport activity. In addition, the fascinating organization of the muscle's sarcomere guides our research in understanding the orchestration of individual constituents in muscle contraction. Using fluorescently tagged motor and vesicle markers we investigate these questions in the nervous system of the nematode *C. elegans* serves us as a model system for microscopic tools (confocal, TIRF, FRET FLIM) and biochemical transport assays *in vitro*.

Selected Recent Publications

Butkevich E, Härtig W, Nikolov M, Erck C, Grosche J, Urlaub H, Schmidt CF, Klopfenstein DR, Chua JJ (2016) Phosphorylation of FEZ1 by Microtubule Affinity Regulating Kinases regulates its function in presynaptic protein trafficking. Sci Rep 6: 26965

Butkevich E, Bodensiek K, Fakhri N, von Roden K, Schaap IA, Majoul I, Schmidt CF, Klopfenstein DR (2015) Drebrin-like protein DBN-1 is a sarcomere component that stabilizes actin filaments during muscle contraction. Nat Commun 6: 7523

Düselder A, Fridman V, Thiede C, Wiesbaum A, Goldstein A, Klopfenstein DR, Zaitseva O, Janson ME, Gheber L, Schmidt CF (2015) Deletion of the Tail Domain of the Kinesin-5 Cin8 Affects Its Directionality. J Biol Chem 290(27): 16841-50

Fakhri N, Wessel AD, Willms C, Pasquali M, Klopfenstein DR, MacKintosh FC, Schmidt CF (2014)High-resolution mapping of intracellular fluctuations using carbon nanotubes. Science 344(6187): 1031-5

Chia PH, Patel MR, Wagner OI, Klopfenstein DR, Shen K (2013)Intramolecular regulation of presynaptic scaffold protein SYD-2/liprin-. Mol Cell Neurosci 56: 76-84

Chua JJ, Butkevich E, Worseck JM, Kittelmann M, Grønborg M, Behrmann E, Stelzl U, Pavlos NJ, Lalowski MM, Eimer S, Wanker EE, Klopfenstein DR, Jahn R (2012)Phosphorylation-regulated axonal dependent transport of syntaxin 1 is mediated by a Kinesin-1 adapter. Proc Natl Acad Sci USA 109(15): 5862-7

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Wilfried Kramer

Privatdozent Molecular Biology and Genetics

- Diploma (Biology), University of Cologne, Germany, 1982
- Dr. rer. nat., University of Cologne, Germany, 1986
- Postdoctoral Fellow, University of California, Berkeley, USA, 1986 – 1989
- Habilitation in Molecular Biology and Genetics, University of Göttingen, Germany, 2000
- At the Dept. of Molecular Genetics since 1989

Major Research Interests

In the Department of Molecular Genetics, headed by Prof. Dr. H. Krebber, I try to identify new factors that might be involved in the export of mRNA from the nucleus in *Saccharomyces cerevisiae*. To this end, ordered mutants arrays are screened for genetic interactions with selected mutants by the so called SGA technique, which makes use of the genetic features offered by budding yeast to rapidly construct double mutants and compare their growth with that of single mutants. Furthermore, we want to extend these studies in different collaborations to microscopic screenings of those mutant arrays for export defects using automated microscopes. In a collaboration with Prof. Dr. S. Emmert from the medical faculty we want to analyse the function of the yeast *MPH1* gene and of its human homologue *FANCM*. The latter is a determining factor of the hereditary disease Fanconi anemia, which is – besides other symptoms - characterised by chromosome instability and increased incidence of cancer. Both are associated to homologous recombination and at least Mph1 is very likely involved in the error-free bypass of lesions, which are caused by DNA damaging agents and are blocking DNA replication, posing a very serious threat to the survival of the cell. Understanding these cellular responses to DNA damage will allow a better insight into central processes involved in the malignant transformation of cells.

Selected Recent Publications

Popova B, Schubert S, Bulla I, Buchwald D, Kramer W (2015) A Robust and Versatile Method of Combinatorial Chemical Synthesis of Gene Libraries via Hierarchical Assembly of Partially Randomized Modules. PLoS One 10(9): e0136778

Ede C, Rudolph CJ, Lehmann S, Schürer KA, Kramer W (2011) Budding yeast Mph1 promotes sister chromatid interactions by a mechanism involving strand invasion. DNA Repair 10: 45-55

Schomacher L, Schürer KA, Ciirdaeva E, McDermott P, Chong J, Kramer W, Fritz HJ (2010) Archaeal DNA uracil repair via direct strand incision: A minimal system reconstituted from purified components. DNA Repair 9: 438-447

Panico ER, Ede C, Schildmann M, Schürer KA, Kramer W (2010) Genetic evidence for a role of *Saccharomyces cerevisiae* Mph1 in recombinational repair under replicative stress. Yeast 27: 11-27

Prakash R, Satory D, Dray E, Papusha A, Scheller J, Kramer W, Krejci L, Klein H, Haber JE, Sung P, Ira G (2009) Yeast Mph1 helicase dissociates Rad51-made D-loops: implications for crossover control in mitotic recombination. Genes Dev 23: 67-79

Schürer KA, Rudolph C, Ulrich HD, Kramer W (2004) Yeast MPH1 gene functions in an error-free DNA damage bypass pathway that requires genes from homologous recombination, but not from postreplication repair. Genetics 166: 1673-1686

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Heike Krebber

Professor of Molecular Genetics

- 1996 Dr. rer. nat., Deutsches Krebsforschungszentrum, DKFZ, Heidelberg (Germany)
- 1996 Visiting Scientist, Weizman Institute of Science, Rehovot (Israel)
- 1996 – 1999 Scientist, Dana-Farber Cancer Institute, Harvard Medical School, Boston (USA)
- 1999 – 2010 Junior group leader, Institute für Molekularbiologie und Tumorforschung, Philipps-Universität Marburg (Germany)
- 2005 Habilitation in Molecular Biology
- 2006 Heisenberg Fellow
- since 2010 Professor for Molecular Genetics, Georg-August Universität Göttingen (Germany)

Major Research Interests

Messenger RNAs are transcribed in the nucleus and translated in the cytoplasm of eukaryotic cells. It has to be assured that intron containing pre messenger RNAs are retained in the nucleus until processing is completed. Only fully processed and spliced mRNAs are transported and translated. The otherwise resulting gene products can be toxic to cells and harmful to organisms. Several examples exist where not fully processed pre-mRNAs reach the cytoplasm, resulting in diseases like cancer or neurodegenerative diseases. Our projects aim to identify and characterize the requirements for mRNA processing, transport and translation. Moreover, we study the principles of mRNA quality control. Interestingly, proteins of the nuclear quality control machinery also bind to noncoding RNAs. Their functions are the focus of a second topic in the lab. *Saccharomyces cerevisiae* has been proven to be a useful model organism for eukaryotic cells and we use a combination of genetics, biochemistry and cell biology to uncover these processes.

Selected Recent Publications

Zander G, Krebber H (2017) Quick or Quality? How mRNAs escapes nuclear quality control during stress. RNA Biology Jul 14:1-7. doi: 10.1080/15476286.2017.1345835

Zander G, Hackmann A, Bender L, Becker D, Lingner T, Salinas G, Krebber H (2016) mRNA quality control is bypassed for an immediate export of stress responsive transcripts. Nature 540: 593-596

Wu H, Becker D, Krebber H (2014) Telomerase RNA TLC1 shuttling to the cytoplasm requires mRNA export factors and is important for telomere maintenance. Cell Rep 8: 1-9

Hackmann A, Wu H, Schneider UM, Meyer K, Jung K, Krebber H (2014) Quality control of spliced mRNAs requires the shuttling SR proteins Gbp2 and Hrb1. Nat Commun 5: 3123

Baierlein C, Hackmann A, Gross T, Henker L, Hinz F, Krebber H (2013) Monosome formation during translation initiation requires the serine/arginine-rich protein Npl3. Mol Cell Biol 33(24): 4811-23

Hackmann A, Gross T, Baierlein C, Krebber H (2011) The mRNA export factor Npl3 mediates the nuclear export of large ribosomal subunits. EMBO-Rep doi: 10.1038/embor.2011.155

Baierlein C, Krebber H (2010) Translation termination: New factors and insights. RNA-Biology 7: issue 5: 548 – 550

Khoshnevis S, Gross T, Rotte C, Baierlein C, Ficner R, Krebber H (2010) The iron-sulfur protein Rli1 functions in translation termination. EMBO-Rep 11: 214 – 219

Gross T, Siepmann A, Sturm D, Windgassen M, Scarelli J, Cole CN, Seedorf M, Krebber H (2007) The DEAD-box RNA-helicase Dbp5 functions in translation termination. Science 315 (5812): 646-649

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Volker Lipka

Professor of Plant Cell Biology

- Dr. rer.nat. at the Department for Plant Molecular Biology, Technical University Aachen, 1999
- Postdoctoral fellow at the SainsburyLaboratory, John Innes Centre, Norwich, UK, 1999 – 2000
- Postdoctoral fellow at the Max-Planck Institute for Plant Breeding Research, Cologne, 2000 – 2004
- Leader of an independent research group at the Department for Plant Biochemistry, Centre for Plant Molecular Biology, University of Tübingen, 2004 – 2007
- Leader of an independent research group at the Sainsbury Laboratory, John Innes Centre, Norwich, UK, 2007 – 2009
- Professor at the University of Göttingen since 2009

Major Research Interests

Our laboratory is interested in the molecular analysis of plant innate immunity. Our research is focused on 1) the molecular dissection of mechanisms that control activation of basal defence in the plant model *Arabidopsis thaliana* 2) the analysis of defence mechanisms that contribute to resistance against fungal pathogens 3) the identification of fungal effector molecules that interfere with the plant defence machinery and allow host plant colonization
In nature, plants are constantly exposed to above- and below-ground attack by a vast array of potential pathogens. However, most plants are immune to the majority of would-be pathogens and susceptible to only a relatively small number of adapted microbes. Using a novel plant-fungus interaction model system we recently identified several molecular components that are required for the activation (Gimenez-Ibanez et al., 2009) and execution of basal plant defence (Collins et al., 2003; Lipka et al., 2005; Stein et al., 2006; Kwon et al., 2008; Lipka et al., 2008). As a consequence, receptor-mediated recognition, pathogen-induced intracellular transport processes, dynamic organelle translocation and cytoskeletal rearrangements represent major research topics in our department. Suppression of these defence mechanisms is a key requirement for adapted pathogens and we recently began studies to identify secreted fungal effector molecules that are likely to be involved. We combine genetic, cell, molecular and biochemical experimental strategies to gain novel insights into these complex mechanisms.

Selected Recent Publications

Fuchs R, Kopischke M, Klapprodt C, Hause G, Meyer AJ, Schwarzländer M, Fricker MD, Lipka V (2016) Immobilized Subpopulations of Leaf Epidermal Mitochondria Mediate PENETRATION2-Dependent Pathogen Entry Control in Arabidopsis. Plant Cell 28: 130-145

Petutschnig EK, Stolze M, Lipka U, Kopischke M, Horlacher J, Valerius O, Rozhon W, Gust AA, Kemmerling B, Poppenberger B, Braus GH, Nürnberger T, Lipka V (2014) A novel *Arabidopsis* CHITIN ELICITOR RECEPTOR KINASE 1 (CERK1) mutant with enhanced pathogen-induced cell death and altered receptor processing. New Phytologist 204(4): 955-67

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Petutschnig EK, Jones AM, Serazetdinova L, Lipka U, Lipka V (2010) The Lysin Motif Receptor-like Kinase (LysM-RLK) CERK1 Is a Major Chitin-binding Protein in *Arabidopsis thaliana* and Subject to Chitin-induced Phosphorylation. Journal of Biological Chemistry 285(37): 28902-28911

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- 1975 Dr. rer. nat (PhD), University of Munster
- 1981 – 1988 Research group leader, Max Planck Institute for Molecular Genetics, Berlin
- 1988 – 1999 Professor of Biochemistry and Molecular Biology at the University of Marburg
- Since 1999 Director, Dept. of Cellular Biochemistry, Max Planck Institute for Biophysical Chemistry, Göttingen
- Honorary Professor at the Georg August University of Göttingen

Major Research Interests

Most metazoan pre-mRNAs contain multiple introns and exons. In order to generate mature mRNA, the introns must be excised from the pre-mRNA, a process termed pre-mRNA splicing. In many cases, alternative splicing generates different mRNAs from a single pre-mRNA by the regulated removal of different sections of the RNA, a process which greatly expands the complexity of the repertoire of proteins that can be expressed from relatively small genomes. Splicing is catalysed by a large macromolecular machine, termed the spliceosome which consists of the small nuclear RNAs (U1, U2, U4, U5 and U6) and more than 150 proteins, 50 of which are associated with the snRNAs to form snRNPs.
In our laboratory, intense efforts are focussed on understanding how the spliceosome recognizes and binds the intron ends and discriminates them from exons. This is an especially confounding problem in metazoans because, in contrast to lower eucaryotes such as yeast, pre-mRNA introns are often extremely long (104-105 nucleotides), while exons are generally small (less than 300 nucleotides). Another major goal of our research is the elucidation of the mechanisms by which the spliceosome assembles into a catalytically active machine and catalyses intron excision. None of the building blocks of the spliceosome contains an active site. Instead, the catalytically active domain must be assembled anew on to each intron, a highly dynamic process which entails dramatic structural rearrangements of the RNP structure of the spliceosome, and which is orchestrated by the successive action of more than 10 enzymes such as RNA helicases and GTPases, as well as by posttranslational phosphorylation of a multitude of spliceosomal proteins. Our studies involve a large number of experimental approaches, including biochemical purification of entire spliceosomes or large protein ensembles, and characterization of their proteins by mass spectrometry; RNA biology methods such as enzymatic engineering of RNA molecules, RNA structure probing and RNA interference methods; production of recombinant proteins and antibodies; procedures for the investigation of protein-protein and protein-RNA interactions *in vitro* and *in vivo*; and biophysical methods such as fluorescence spectroscopy.
Finally, we are investigating the 3D structure of purified spliceosomes or major building blocks thereof using electron microscopic approaches and X ray crystallography. Our studies on the regulatory mechanisms of constitutive and alternative pre-mRNA splicing involve mainly mammalian systems. As the basic mechanisms of splicing catalysis appear to be evolutionarily highly conserved, we are also taking advantage of molecular genetic approaches in baker yeast to elucidate the structure and function of the catalytic core domain of the spliceosome.

Selected Recent Publications

Haselbach D, Komarov I, Agafonov DE, Hartmuth K, Graf B, Dybkov O, Urlaub H, Kastner B, Lührmann R, Stark H (2018) Structure and conformational dynamics of the human spliceosomal bact complex. Cell 172: 454-464

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Bertram K, Agafonov DE, Dybkov O, Haselbach D, Leelaram MN, Will CL, Urlaub H, Kastner B, Lührmann R, Stark H (2017) Cryo-EM structure of a pre-catalytic human spliceosome primed for activation. Cell 170: 701-713

Bertram K, Agafonov DE, Liu WT, Dybkov O, Will CL, Hartmuth K, Urlaub H, Kastner B, Stark H, Lührmann R (2017) Cryo-EM structure of a human spliceosome activated for step 2 of splicing. Nature 542: 318-323

Sidarovich A, Will CL, Anokhina MM, Ceballos J, Sievers S, Agafonov DE, Samatov T, Bao P, Kastner B, Urlaub H, Waldmann H, Lührmann R. (2017) Identification of a small molecule inhibitor that stalls splicing at an early step of spliceosome activation. Elife: pii: e23533. doi: 10.7554/eLife.23533

Rauhut R, Fabrizio P, Dybkov O, Hartmuth K, Pena V, Chari A, Kumar V, Lee CT, Urlaub H, Kastner B, Stark H, Lührmann R (2016) Molecular architecture of the *Saccharomyces cerevisiae* activated spliceosome. Science 353 (6306): 1399-1405

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Professor of Bioinformatics

- 1993 Diploma (Mathematics), LMU München
- 1996 PhD (Dr. Math.), Universität Bielefeld
- 1997 – 1998 Visiting Scientist, North Carolina State University, Raleigh, NC, USA
- 1998 – 2000 RPR/Aventis, Dagenham, Essex, UK
- 2000 – 2001 MIPS, MPI fuer Biochemie, Martinsried and GSF, Neuherberg
- 2001 – 2002 Group leader and faculty member at International Graduate School in Bioinformatics and Genome Research, Universität Bielefeld
- Since 2002 Professor of Bioinformatics, Universität Göttingen

Major Research Interests

The focus of our research work is algorithm and software development for nucleic acid and protein sequence analysis; the multiple-alignment program "DIALIGN" and the gene-finding program "AUGUSTUS" are widely used tools that have been developed in our department. More recently, we started to work on word-matching statistics and on alignment-free approaches to comparative sequence analysis, here we developed the tools "kmacs", "Prot-SpaM" and "Multi-SpaM".
Other areas of research in our department include phylogeny reconstruction, metagenomics, motif discovery and remote homology detection using machine learning methods, genome annotation for prokaryotes, recombinations in viral genomes and HIV classification using coalescent theory.

Selected Recent Publications

Leimeister C-A, Dencker T, Morgenstern B (2018) Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. Bioinformatics, in press, doi:10.1093/bioinformatics/bty592

Leimeister C-A, Schellhorn J, Schöbel S, Gerth M, Bleidorn C, Morgenstern B (2018) Prot-SpaM: Fast alignment-free phylogeny reconstruction based on whole-proteome sequences bioRxiv, https://doi.org/10.1101/306142

Dencker T, Leimeister C-A, Gerth M, Bleidorn C, Snir S, Morgenstern B (2018) Multi-SpaM: a maximum-likelihood approach to phylogeny reconstruction based on multiple spaced-word matches. In: M. Blanchette, A. Ouangraoua (Eds.), Comparative Genomics, LNBI 11183, Springer, Proc. RECOMB-CG 2018 (in press)

Morgenstern B, Schöbel S, Leimeister C-A (2017) Phylogeny reconstruction based on the length distribution of k-mismatch common substrings. Algorithms for Molecular Biology 12: 27

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Hahn L, Leimeister C-A, Ounit R, Lonardi S, Morgenstern B (2016) *rasbhari*: Optimizing spaced seeds for database searching, read mapping and alignment-free sequence comparison. PLOS Computational Biology 12(10): e1005107

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Leimeister C-A, Morgenstern B (2014) kmacs: the k-Mismatch Average Common Substring Approach to alignment-free sequence comparison. Bioinformatics 30: 2000-2008

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Tobias Moser

Professor of Auditory Neuroscience

- 1995 MD University of Jena
- 1994 – 1997 Postdoc with E. Neher at the MPI for Biophysical Chemistry
- 1997 – 2001 Junior Group Leader at the MPI for Biophysical Chemistry, Göttingen
- 1997 – 2002 Residency in Otolaryngology, University Medical Center Göttingen
- Since 2001 Group Leader at the Department of Otolaryngology, University Medical Center Göttingen
- Since 2014 Research Group Leader at MPI for Biophysical Chemistry, MPI of Experimental Medicine and German Primate Center, Göttingen
- 2015 Director, Institute for Auditory Neuroscience, University Medical Center Göttingen

Major Research Interests

Auditory Neuroscience - Synaptic Physiology and Pathophysiology – Audiology and Neuroprosthetics

Our work focuses on the molecular physiology and pathophysiology of sound encoding at the hair cell ribbon synapse and its restoration. We have physiologically and morphologically characterized synapses of wild-type and mutant mice with defects in hair cell synaptic coding from the molecular to the systems level. This way we have contributed to the understanding of structure and function of the hair cell ribbon synapse and co-initiated the concept of auditory synaptopathy. Molecular dissection and detailed physiological characterization of ribbon synapse function employ a spectrum of molecular, biophysical, physiological, psychophysical and clinical approaches. Towards restoration of hearing we pursue the optogenetic stimulation of cochlea and gene replacement therapy.

Selected Recent Publications

Neef J, Ohn TL, Urban NT, Frank T, Jean P, Hell SW, Willig KI, Moser T (2018) Quantitative optical nanophysiology of Ca^{2+}-signaling at inner hair cell active zones. Nat commun, 18;9(1): 290

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Klaus-Armin Nave

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- 1987 PhD, University of California, San Diego
- 1987 – 1991 Postdoc, The Salk Institute, la Jolla, California
- 1991 Junior Group Leader, ZMBH, University of Heidelberg
- 1998 Professor of Molecular Biology (C4), ZMBH, University of Heidelberg

Major Research Interests

We are studying the interactions of neurons and glial cells in the mammalian nervous system with a special interest in the role of oligodendrocytes and Schwann cells, best known as myelin forming cells of the central and peripheral nervous system. These highly specialized glial cells enwrap axons with a multilayered sheath that provides electrical insulation for rapid impulse propagation. However the biology of these axon-glia interactions is complex. Using mouse genetics, originally to study the role of proteins in the myelin architecture and in neurogenetic disorders, we made the unexpected discovery of a novel function of oligodendrocytes, which even precedes myelin in nervous system evolution: the glial metabolic support of axonal conduction, axonal transport and long-term integrity. We determined that oligodendrocytes and Schwann cells take up glucose and deliver lactate, here the product of aerobic glycolysis, to the axonal compartment. This supportive function helps maintaining axon functions especially when ATP demands are increased at higher firing rates, also because access of axons to extracellular metabolites is restricted by myelin itself. Here, the fine architecture of the myelin sheath that we visualize with advanced electron microscopic techniques appears critical. Specialized cytoplasmic connections within the myelin sheath ('myelinic nanochannels') must provide a pathway of continuous communication between oligodendrocytes and the encapsulated axon. In neurological diseases, in which myelin is structurally affected or even destroyed, such as in multiple scleroses, leukodystrophies and various peripheral neuropathies, there is invariably secondary axonal degeneration that we propose is caused by the lack of adequate metabolic support. We are investigating the underlying molecular mechanisms of these diseases in detail, using corresponding animal models that we have generated with a range of genetic techniques. A further goal is to understand the role of myelinating glial cells in higher brain functions and psychiatric diseases, which we approach in close collaboration with the Department of Hannelore Ehrenreich at our institute.

Selected Recent Publications

Saab AS, Tzvetavona ID, Trevisiol A, Baltan S, Dibaj P, Kusch K, Möbius W, Goetze B, Jahn HM, Huang W, Steffens H, Schomburg ED, Pérez-Samartín A, Pérez-Cerdá F, Bakhtiari D, Matute C, Löwel S, Griesinger C, Hirrlinger J, Kirchhoff F, Nave KA (2016) Oligodendroglial NMDA receptors regulate glucose import and axonal energy metabolism. Neuron 91: 119-32

Goebbels S, Wieser GL, Pieper A, Spitzer S, Weege B, Yan K, Edgar JM, Yagensky O, Wichert SP, Agarwal A, Karram K, Renier N, Tessier-Lavigne M, Rossner MJ, Káradóttir RT, Nave KA (2016) A neuronal PI(3,4,5)P3-dependent program of oligodendrocyte precursor recruitment and myelination. Nat Neurosci. 20: 10-15

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Nave K-A (2010) Myelination and support of axonal integrity by glia. Nature 468: 244-252

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Professor, University Medical Center

- 2002–2008 Ph.D., National & Kapodistrian University of Athens, Greece
- 2008–2013 Postdoctoral fellow, Oxford University, United Kingdom
- 2012–2013 Lecturer for Biochemistry, University College Oxford, United Kingdom
- 2009 Grad Junior Group Leader for Systems Biology, University of Cologne
- Since 2018 Professor of Translational Epigenetics, University Medical Center Göttingen

Major Research Interests

We wish to uncover the rules governing gene expression in response to developmental and extra-cellular cues. Genome architecture is thought to be a major determinant in this. What we strive to understand is how chromatin (re)folds to accommodate responses to such cues in 3D nuclear space and dynamically over time. In the end, we anticipate these rules to be general ones, which once deciphered will allow us to predict how a cell might respond upon signalling, in the context of disease, or during cellular ageing.

Selected Recent Publications

Rada-Iglesias A, Grosveld FG, Papantonis A (2018) Forces driving the three-dimensional folding of eukaryotic genomes. Mol Syst Biol 14: e8214

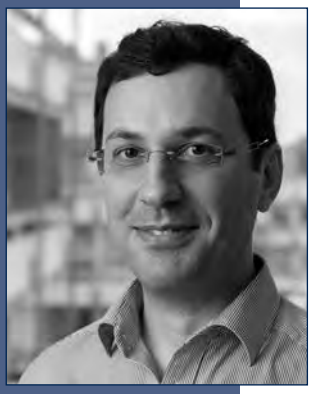
Zirkel A, Nikolic M, Sofiadis K, Mallm JP, Brackley CA, Gothe H, Drechsel O, Becker C, Altmüller J, Josipovic N, Georgomanolis T, Brant L, Franzen J, Koker M, Gusmao EG, Costa IG, Ullrich RT, Wagner W, Roukos V, Nürnberg P, Marenduzzo D, Rippe K, Papantonis A (2018) HMGB2 loss upon senescence entry disrupts genomic organization and induces CTCF clustering across cell types. Mol Cell 70: 730-744

Brant L, Georgomanolis T, Nikolic M, Brackley CA, Kolovos P, van Ijcken W, Grosveld FG, Marenduzzo D, Papantonis A (2016) Exploiting native forces to capture chromosome conformation in mammalian cell nuclei. Mol Syst Biol 12: 891

Kolovos P, Georgomanolis T, Koeferle A, Larkin JD, Brant L, NikolićM, Gusmao EG, Zirkel A, Knoch TA, van Ijcken WF, Cook PR, Costa IG, Grosveld FG, Papantonis A (2016) Binding of nuclear factor ðB to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. Genome Res 26: 1478-1489

Binding of nuclear factor ðB to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. Genome Res. 26:1478-1489., Papantonis A (2016) Isolation of the protein and RNA content of active sites of transcription from mammalian cells. Nat Protoc 11: 553-565

Kelly S, Georgomanolis T, Zirkel A, Diermeier S, O'Reilly D, Murphy S, Längst G, Cook PR, Papantonis A (2015) Splicing of many human genes involves sites embedded within introns. Nucleic Acids Res 43: 4721-4732



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Vladimir Pena

Research Group Leader at the MPI for Biophysical Chemistry

- Study of biochemistry at the University of Bucharest (1995 – 2000)
- Research assistant with Stefan Szedlacsek at the Institute of Biochemistry, Bucharest (1999 – 2001)
- PhD with Klaus Scheffzek at the European Molecular Biology Laboratory (EMBL), Heidelberg (2001 – 2005)
- Postdoctoral fellow with Markus Wahl at the Max Planck Institute (MPI) for Biophysical Chemistry, Göttingen (2006 – 2010)
- Group Leader in the Department of Reinhard Lührmann, MPI Göttingen (2010 – 2013)
- Research Group Leader at the MPI, Göttingen (since 2014)

Major Research Interests

The majority of genes in higher eukaryotes contain protein-coding exons that can be joined in a combinatorial fashion. The process, termed pre mRNA splicing, is an essential step in gene expression, and it expands tremendously the proteome and the complexity of an organism. Our goal is to understand the structural basis of pre-mRNA splicing. Here we place particular emphasis on the spliceosome's regulation, as well as on the misregulation that causes various diseases.
DNA catalysts are an increasingly important topic in the work pursued in our laboratory. The surprisingly complex fold that these molecules adopt raises questions about the structural importance of DNA in the cell, and it enables us to manipulate the molecules' properties for technological applications.
For our investigations we make use of biochemistry, X ray crystallography and – increasingly – electron microscopy.

Selected Recent Publications

Cretu C, Schmitzová J, Ponce-Salvatierra A, Dybkov O, De Laurentiis EI, Sharma K, Will CL, Urlaub H, Lührmann R, Pena V (2016) Molecular architecture of SF3b and structural consequences of its cancer-related mutations. Molecular Cell 64(2): 307-319

Rauhut R, Fabrizio P, Dybkov O, Hartmuth K, Pena V, Chari A, Kumar V, Lee CT, Urlaub H, Kastner B, Stark H, Lührmann R (2016) Molecular architecture of the *Saccharomyces cerevisiae* activated spliceosome. Science 353(6306):1399-1405

Ponce-Salvatierra A, Wawrzyniak-Turek K, Steuerwald U, Höbartner C, Pena V (2016) Crystal structure of a DNA catalyst. Nature 529(7585): 231-4

De I, Schmitzova J, Pena V (2016) The organization and contribution of helicases to RNA splicing. WIREs RNA 7(2): 259-74

De I, Bessonov S, Hofele R, dos Santos K, Will CL, Urlaub H, Lührmann R, Pena V (2015) The RNA helicase Aquarius exhibits structural adaptations mediating its recuitment to spliceosomes. Nature Struct Mol Biol 22(2): 138-44

Schmitzová J, Pena V (2012) Emerging views about the molecular structure of the spliceosomal catalytic centre. RNA Biol 9 (11): 1311-1318

Schmitzová J, Rasche N, Dybkov O, Kramer K, Fabrizio P, Urlaub H, Lührmann R, Pena V (2012) Crystal structure of Cwc2 reveals a novel architecture of a multipartite RNA-binding protein. EMBO J 31: 2222-34

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Stefanie Pöggeler

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- 1993 – 1995 Research associate
- 1995 – 2001 Postdoctoral research fellow and group leader
- 1997 Visiting Scientist, Institut de Génétique et Microbiologie, Laboratory of Dr. D. Zickler, Université Paris-Sud, Orsay, France
- 2000 Habilitation (Botany), Ruhr-Universität Bochum
- 2001 – 2003 Associate Professor of Botany (stand-in), University of Münster
- 2003 – 2006 University lecturer (Hochschuldozentin) and group leader, Ruhr-Universität Bochum
- since 2006 Associate Professor of Genetics of Eukaryotic Microorganisms, Georg-August-Universität Göttingen

Major Research Interests

Fruiting-body development in filamentous ascomycetes
Fruiting-body development in filamentous ascomycetes is a complex cellular differentiation process that requires special environmental conditions and is controlled by many developmentally regulated genes. We are interested in the genes regulating this development process. We use the homothallic (self-fertile) ascomycete *Sordaria macrospora* as a model organism. Numerous mutants which are blocked at various stages of fruiting-body development have been generated and molecular genetic procedures have been applied to isolate genes involved in fruiting-body development. In addition to mutants generated by chemical mutagenesis, several mutants affecting fruiting-body development were produced by knock-out of mating-type genes, pheromone and receptor genes, as well as genes involved in autophagy and bicarbonate metabolism.

Autophagy in filamentous ascomycetes
Autophagy is defined as a tightly controlled non-selective degradation process in which eukaryotic cells digest their own proteins and organelles in response to starvation or stress conditions. In filamentous ascomycetes, autophagy is involved in various developmental processes. However, the exact role of autophagy in multicellular fruiting-body development is largely unknown.
Using a reverse genetics approach, we have recently shown that the autophagy genes *Smatg8* and other conserved genes required for core functions of the selective and non-selective autophagic machinery are essential for fruiting-body development in the filamentous ascomycete *Sordaria macrospora*. Our aim is to understand how selective autophagy contributes to vegetative growth and fruiting-body development in filamentous ascomycetes.

Selected Recent Publications

Peter M, Kohler A, Ohm RA, Kuo A, Krützmann J, Morin E, Arend M, Barry KW, Binder M, Choi C, Clum A, Copeland A, Grisel N, Haridas S, Kipfer T, LaButti K, Lindquist E, Lipzen A, Maire R, Meier B, Mihaltcheva S, Molinier V, Murat C, Pöggeler S, Quandt CA, Sperisen C, AnTritt A, Tisserant E, Crous PW, Henrissat B, Nehls U, Egli S, Spatafora JW14, Grigoriev IV, Martin FM (2016) Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus *Cenococcum geophilum*. Nat Commun 7: 12662

Frey S, Lahmann Y, Hartmann T, Seiler S, Pöggeler S (2015) Deletion of Smgpi1 encoding a GPI-anchored protein suppresses sterility of the STRIPAK mutant ΔSmmob3 in the filamentous ascomycete *Sordaria macrospora*. Mol Microbiol 97: 676-697

Lehneck R, Elleuche S, Pöggeler S (2014) The filamentous ascomycete *Sordaria macrospora* can survive in ambient air without carbonic anhydrases. Mol Microbiol 92: 931-944

Lehneck R, Neumann P, Vullo D, Elleuche S, Supuran CT, Ficner R, Pöggeler S (2014) Crystal structures of two tetrameric β-carbonic anhydrases from the filamentous ascomycete *Sordaria macrospora*. FEBS Journal 281: 1759-1772

Böhm J, Hoff B, O'Gorman CM, Wolfers S, Klix V, Binger D, Zadra I, Kürnsteiner H, Pöggeler S Dyer P, Kück U (2013) Sexual recombination and mating type-mediated strain development in the penicillin producing fungus *Penicillium chrysogenum*. Proc Natl Acad Sci USA 110: 1476-1481

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- 2000: Ph.D., Friedrich-Alexander-University Erlangen-Nürnberg
- 2000 – 2003: Postdoctoral Fellow, University of Pennsylvania
- 2003 – 2007: Head of a SFB Junior Research Group, Institute of Clinical and Molecular Virology, Friedrich-Alexander-University Erlangen-Nürnberg
- 2007 – 2010: Professor for Experimental Virology, Hannover Medical School
- 2010: Professor for Infection Biology at Georg-August-University Göttingen (Brückenprofessur) and Head of the Infection Biology Unit of the German Primate Center

Major Research Interests

The Infection Biology Unit is studying virus-host cell interactions and their contribution to viral spread and pathogenesis in the host. One focus of our work is on activation of viruses by host cell proteases. Our recent studies provided evidence that the cellular protease TMPRSS2 is essential for influenza virus spread in mice and primate respiratory epithelium, indicating that TMPRSS2 is an attractive target for antiviral intervention. Therefore, our future work seeks to define the antiviral activity of TMPRSS2 inhibitors in non-human primates.
The interferon system constitutes the first barrier against virus infection. A second focus of our studies is on the question how antiviral effector proteins of the interferon system inhibit viral spread and how viruses counter their antiviral activity. To answer this question, we employ siRNA and CRISPR/Cas9 approaches, life cell imaging, reporter viruses, genetic analyses and *ex vivo* cultures of primate organs.
Another goal of the Infection Biology Unit is the diagnosis of viral infections of non-human primates. Transmission of herpes B virus from macaques to humans and transmission of herpes B-related viruses between non-human primates can result in fatal disease. Therefore, our work is focused on establishing herpes virus diagnostics.

Selected Recent Publications

Hoffmann M, Crone L, Dietzel E, Paijo J, González-Hernández M, Nehlmeier I, Kalinke U, Becker S, Pöhlmann S (2017) A Polymorphism within the Internal Fusion loop of the Ebola virus glycoprotein modulates host cell entry. J Virol 91(9)

Pöhlmann S, Suntz M, Akimkin V, Bleyer M, Kaul A (2017) Herpes B virus replication and viral lesions in the liver of a cynomolgus macaque which died from severe disease with rapid onset. J Med Primatol, doi: 10.1111/jmp.12269

Zmora P, Molau-Blazejewska P, Bertram S, Walendy-Gnirß K, Nehlmeier I, Hartleib A, Moldenhauer AS, Konzok S, Dehmel S, Sewald K, Brinkmann C, Curths C, Knauf S, Gruber J, Mätz-Rensing K, Dahlmann F, Braun A, Pöhlmann S (2017) Non-human primate orthologues of TMPRSS2 cleave and activate the influenza virus hemagglutinin. PLoS One 12(5)

Gierer S, Müller MA, Heurich A, Ritz D, Springstein BL, Karsten CB, Schendzielorz A, Gnirß K, Drosten C, Pöhlmann S (2014) Inhibition of proprotein convertases abrogates processing of the middle eastern respiratory syndrome coronavirus spike protein in infected cells but does not reduce viral infectivity. J Infect Dis 211(6): 889-97

Hatesuer B, Bertram S, Mehnert N, Bahgat MM, Nelson PS, Pöhlmann S, Schughart K (2013) Tmprss2 is essential for influenza H1N1 virus pathogenesis in mice. PLoS Pathog 9(12): e1003774

Kühl A, Münch J, Sauter D, Bertram S, Glowacka I, Steffen I, Specht A, Hofmann H, Schneider H, Behrens G, Pöhlmann S (2010) Calcium-modulating cyclophilin ligand does not restrict retrovirus release. Nat Med 16: 155-6

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Peter Rehling

Professor, Director of the Dept. of Cellular Biochemistry

- 1996 Dr. rer. nat. (Biology), University of Bochum
- 1996 – 1998 Postdoctoral fellow (Laboratory of W.-H. Kunau, Bochum)
- 1998 – 2000 Postdoctoral fellow (S.D. Emr, HHMI, University of California San Diego, USA)
- 2000 – 2004 Research Group leader at the Institute for Biochemistry and Molecular Biology, Freiburg
- 2003 Habilitation (Biochemistry and Molecular Biology), University of Freiburg
- 2004 – 2007 Assistant Professor Institute for Biochemistry and Molecular Biology, Freiburg
- Since 2007 Professor of Biochemistry and Director of the Dept. of Biochemistry II University of Göttingen
- Since 2010 Group associated with the Max Planck Institute for Biophysical Chemistry

Major Research Interests

We are interested in understanding the molecular mechanisms by which proteins are transported across the mitochondrial membranes and to find out how multi-protein complexes in the inner membrane (TIM complexes; translocation machineries of the inner membrane) mediate this task. In another aspect of our work we address how translation of mitochondrial-encoded proteins on organellar ribosomes is regulated. The analysis of the principles of the biogenesis of mitochondrial proteins and protein complexes is of central importance for our understanding of the molecular basis of human mitochondrial disorders. In this context we analyze the molecular pathology of a number of human disease models utilizing mice models, knock out cell lines, and iPSC-derived cardiomyocytes. Our analyses aim to understand how mitochondrial functions are integrated into the cellular context.

Selected Recent Publications

Schendzielorz AB, Bagosewski P, Naumenko N, Gomkale R, Schulz C, Guiard B, Chacinska A, Rehling P (2018) Motor-recruitment to the TIM23 channel's lateral gate restricts polypeptide release into the mitochondrial inner membrane. Nature comm (In press)

Naumenko N, Morgenstern M, Rucktäschel R, Warscheid B, Rehling P (2017) INA complex liaises the F1Fo-ATP synthase membrane motor modules. Nature comm 8: 1237

Richter-Dennerlein R, Oeljeklaus S, Lorenzi I, Ronsör C, Bareth B, Schendzielorz AB, Wang C, Warscheid B, Rehling P*, Dennerlein S (2016) Mitochondrial protein synthesis adapts to influx of nuclear-encoded protein. Cell 67: 471-483 (*corresponding and lead author)

Dudek J, Cheng I Chowdhury A, Wotnzy K, Balleininger M, Reinhold R, Grunau S, Callegari S, Toischer K, Wanders RJA, Hasenfuß G, Guan K, Brügger B, Guan K, Rehling P (2016) Cardiac-specific Succinate Dehydrogenase Deficiency in Barth Syndrome. EMBO Mol Med 8: 139-154

Mick D.U, Dennerlein S, Wiese H, Reinhold R, Pacheu-Grau D, Lorenzi I, Sasarman F, Weraarpachai W, Shoubridge EA, Warscheid B, Rehling P (2012) MITRAC links mitochondrial protein translocation to respiratory-chain assembly and translational regulation. Cell 151: 1528-1541

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Silvio Rizzoli

Group Leader STED Microscopy of Synaptic Function

- 2000 – 2004 Research assistant with William Betz at the Dep. of Physiology and Biophysics, University of Colorado Health Sciences Center (USA)
- 08/2004 PhD degree (Physiology) awarded by the University of Colorado
- 2004 – 2007 Post doctoral fellow with Reinhard Jahn at the Neurobiology
- Department of the Max Planck Institute for Biophysical Chemistry in Göttingen (Germany)
- since 2007 Group Leader (STED Microscopy) at the European Neuroscience Institute Göttingen (ENI-G)

Major Research Interests

Conventional fluorescence microscopy is limited by the diffraction of light: fluorescent objects that are close together cannot be discerned. Stimulated emission depletion (STED) is a recent advancement in optical physics that breaks the diffraction barrier, allowing microscopes to obtain much clearer images.
The diffraction barrier has been particularly problematic for imaging synaptic vesicles, which are among the smallest known organelles (30-50 nm in diameter). They are located in small areas in the synapses (about 1 micron in diameter). The group takes advantage of the increased imaging resolution provided by STED to investigate synaptic vesicle function, with an emphasis on synaptic vesicle recycling. Since STED microscopy also allows imaging of protein domains, the group aims at studying the patterning of protein domains in the synapse, in order to understand its molecular architecture.

Selected Recent Publications

Vreja IC, Nikić I, Göttfert F, Bates M, Kröhnert K, Outeiro TF, Hell SW, Lemke EA, Rizzoli SO (2015) Super-resolution Microscopy of Clickable Amino Acids Reveals the Effects of Fluorescent Protein Tagging on Protein Assemblies. ACS ACS Nano 9(11): 11034-41

Vreja IC, Kabatas S, Saka SK, Kröhnert K, Höschen C, Opazo F, Diederichsen U, Rizzoli SO (2015) Secondary-ion mass spectrometry of genetically encoded targets. Angew Chem Int Ed Engl 54(19): 5784-8

Saka SK, Honigmann A, Eggeling C, Hell SW, Lang T, Rizzoli SO (2014) Multi-protein assemblies underlie the mesoscale organization of the plasma membrane. Nat Commun 5: 4509

Wilhelm BG, Mandad S, Truckenbrodt S, Kröhnert K, Schäfer C, Rammner B, Koo SJ, Claßen GA, Krauss M, Haucke V, Urlaub H, Rizzoli SO. Composition of isolated synaptic boutons reveals the amounts of vesicle trafficking proteins. Science 344(6187): 1023-8

Saka SK, Vogts A, Kröhnert K, Hillion F, Rizzoli SO, Wessels JT (2014) Correlated optical and isotopic nanoscopy. Nat Commun 5: 3664

Opazo F, Levy M, Byrom M, Schäfer C, Geisler C, Groemer TW, Ellington AD, Rizzoli SO (2012) Aptamers as potential tools for super-resolution microscopy. Nat Methods 9: 938-939

Denker A, Bethani I, Kröhnert K, Körber C, Horstmann H, Wilhelm BG, Barysch SV, Kuner T, Neher E, Rizzoli SO (2011a) A small pool of vesicles maintains synaptic activity *in vivo*. Proc Natl Acad Sci USA 108: 17177-17182

Denker A, Kröhnert K, Bückers J, Neher E, Rizzoli SO (2011b) The reserve pool of synaptic vesicles acts as a buffer for proteins involved in synaptic vesicle recycling. Proc Natl Acad Sci USA 108: 17183-17188

Wilhelm BG, Groemer TW, Rizzoli SO (2010) The same synaptic vesicles drive active and spontaneous release. Nat Neurosci 13: 1454-1456

Hoopmann P, Punge A, Barysch SV, Westphal V, Bückers J, Opazo F, Bethani I, Lauterbach MA, Hell SW, Rizzoli SO (2010) Endosomal sorting of readily releasable synaptic vesicles. Proc Natl Acad Sci USA 107: 19055-19060

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Marina Rodnina

Professor of Biochemistry

- PhD, Institute of Molecular Biology and Genetics, Academy of Science Ukraine, Kiew, Ukraine, 1989
- Research Fellow of the Alexander von Humboldt Foundation, University of Witten, Germany, 1990 – 1992
- Research Fellow at the Institute of Molecular Biology, University of Witten/Herdecke, 1992 – 1998
- Associate Professor for Physical Biochemistry at the Institute of Molecular Biology, University of Witten/Herdecke, 1998 – 2000
- Full Professor, Head of the Institute of Physical Biochemistry, University of Witten/Herdecke, 2000 – 2008
- Director of Department of Physical Biochemistry, Max Planck Institute for Biophysical Chemistry, Göttingen, since 2008

Major Research Interests

1. Ribosome function and dynamics
2. Regulation and fidelity of translation
3. Ribosome-catalyzed reactions

Protein synthesis from amino acids in the cell is performed on ribosomes, large ribonucleoprotein particles that consist of several RNA molecules and over 50 proteins, augmented by auxiliary translation factors. One important unresolved question is the relation between the speed and fidelity of protein synthesis, which are two fundamental parameters that define viability and fitness of cells. While normal decoding is very accurate, is special cases the ribosome can overcome the rules of normal translation to recode parts of the genome in an alternative way. Incorporation of unusual amino acids, such as selenocysteine, requires highly specialized machinery for delivery. Understanding the the movement of tRNAs and mRNA through the ribosome remains a major challenge. Finally, the processivity of the ribosome on the mRNA track, discontinuous translation and vectorial co-translational protein folding are open challenging questions. We investigate translation using a combination of techniques from Biochemistry, Structural Biology and Physical Biochemistry. Development of highly efficient and controlled ribosome translation systems on a highly sophisticated technological level is important for production of proteins with desired properties for purposes of proteomics and high-throughput structural studies emerging in the post-genomic era. The translational apparatus is a major target for antibiotics. Better understanding of the mechanisms of antibiotic action, resistance mechanisms and the interplay between resistance and bacterial fitness will be increasingly important for developing new antimicrobials and combating the major infectious diseases.

Selected Recent Publications

Caliskan N, Wohlgemuth I, Korni, N, Pearson M, Peske F, Rodnina MV (2017) Conditional switch between frameshifting regimes upon translation of dnaX mRNA. Mol Cell 66: 558-567

Belardinelli R, Sharma H, Caliskan N, da Cunha CEL, Peske F, Wintermeyer W, Rodnina MV (2016) Choreography of molecular movements during ribosome progression along mRNA. Nat Struct Molec Biol 23: 342-348

Holtkamp W, Kokic G, Jäger M, Mittelstaet J, Komar AA, Rodnina MV (2015) Co-translational protein folding on the ribosome monitored in real time. Science 350: 1104-1107

Maracci C, Peske F, Dannies E, Pohl C, Rodnina MV (2014) Ribosome-induced tuning of GTP hydrolysis by a translational GTPase. Proc Natl Acad Sci USA 111: 14418-14423

Doerfel LK, Wohlgemuth I, Kothe C, Peske F, Urlaub H, Rodnina MV (2013) EF-P is essential for rapid synthesis of proteins containing consecutive proline residues. Science 339: 85-88

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Melina Schuh

Director at the Max Planck Institute for Biophysical Chemistry

- 2004 Diploma in Biochemistry, University of Bayreuth, Germany
- 2004 – 2008 Ph.D. Student, Laboratory of Jan Ellenberg, EMBL Heidelberg, Germany
- 2008 Dr. rer. nat., University of Heidelberg and EMBL Heidelberg, Germany
- 2009 – 2010 Senior Investigator Scientist, MRC LMB, Cambridge, UK
- 2010 – 2014 Programme Leader Track, MRC LMB, Cambridge, UK
- 2014 – 2015 Programme Leader (Tenured), MRC LMB, Cambridge, UK
- since 2016 Director of the Department of Meiosis, MPI for Biophysical Chemistry, Göttingen, Germany

Major Research Interests

We study meiosis in mammalian oocytes, the progenitor cells of eggs. This topic is of great interest for fundamental research because meiosis is still much more poorly understood than mitosis, especially in mammals. It is also of direct medical relevance because defects in eggs are the leading cause of pregnancy loss and several congenital disorders such as Down's syndrome. Our main aim is to understand how defects at the interface between chromosomes and cytoskeletal structures lead to aneuploid eggs and pregnancy loss in mammals. To this end, we study how the meiotic spindle is organized, how it segregates the chromosomes and how the spindle interacts with actin to drive the meiotic divisions. To have a solid foundation for future research, we are also developing new tools to study meiosis in mammalian oocytes. For instance, we have been able to carry out the first high content screen for meiotic genes in mammals. We also developed Trim Away, a method for rapid degradation of endogenous proteins. We have also been able to establish methods that now allow us for the first time to study the causes of chromosome segregation errors directly in live human oocytes. This has opened an exciting new area of research in my laboratory that we plan to expand significantly in the future.

Selected Recent Publications

Clift D, McEwan W, Labzin LL, Konieczny V, Mogessie M, James LC, Schuh M1 (2017) A method for the acute and rapid degradation of endogenous proteins. Cell doi: 10.1016

Mogessie B, Schuh M (2017) Actin protects mammalian eggs against chromosome segregation errors. Science 357: eaal1647

Webster A, Schuh M (2017) Mechanisms of aneuploidy in mammalian eggs. Review invited by Trends Cell Biol 27: 55-68

Pfender S, Kuznetsov V, Pasternak M, Tischer T, Santhanam B, Schuh M (2015) Live imaging RNAi screen reveals genes essential for meiosis in mammalian oocytes. Nature 524: 239-242

Holubcová Z, Blayney M, Elder K, Schuh M (2015) Error-prone chromosome-mediated spindle assembly favors chromosome segregation defects in human oocytes. Science 348: 1143-1147

Clift, D, Schuh M (2013) Restarting life: fertilization and the transition from meiosis to mitosis. Nat Rev Mol Cell Biol 14: 549-562

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Blanche Schwappach

Professor, Director of Molecular Biology

- 1996 Dr rer nat (Biology), Centre for Molecular Neurobiology (ZMNH), University of Hamburg
- 1997 – 2000 Postdoctoral fellow (Laboratory of Lily Jan, University of California, San Francisco, USA)
- 2000 – 2007 Research group leader at the Centre for Molecular Biology (ZMBH), University of Heidelberg
- 2004 Habilitation (Molecular Biology and Cell Biology) at the ZMBH
- 2007 – 2010 Wellcome Trust Senior Research Fellow, Faculty of Life Sciences, University of Manchester, UK
- since 2010 Professor of Biochemistry and Director of Molecular Biology
- since 2010 the group is associated with the Max Planck Institute for Biophysical Chemistry

Major Research Interests

The group works on different aspects of membrane protein biogenesis and its integration into the physiology of organs such as the brain or the heart. We study the early life of tail-anchored proteins that are post-translationally targeted to the endoplasmic reticulum for membrane integration. Other projects address the role of sorting motifs during the passage of ion channels and neurotransmitter receptors through the secretory pathway. One channel under investigation (the KATP channel) couples cellular metabolism to insulin secretion in pancreatic beta cells. In the brain and the heart KATP channels play less defined roles that we currently address employing biochemical methods. We study biogenesis and trafficking under (patho)physiological conditions in genetically tractable model organisms such as yeast or mouse. Besides membrane protein biochemistry we use GFP-based physiological sensors for small molecules and ions in cellular compartments. This allows us to tackle how ion channels and transporters contribute to different physicochemical milieus inside cells.

Selected Recent Publications

Arakel E, Schwappach B (2018) Formation of COPI-coated vesicles at a glance. J Cell Sci 2018 131: jcs209890

Arakel E, Richter K, Clancy A, Schwappach B (2016) delta-COP contains a helix C-terminal to its longin domain key to COPI dynamics and function. Proc Natl Acad Sci USA 113(25): 6916-21

Kilisch M, Lytovchenko O, Arakel EC, Bertinetti D, Schwappach B (2016) A dual phosphorylation switch controls 14-3-3-dependent cell surface expression of TASK-1. J Cell Sci 129: 831-42

Pfaff J, Rivera Monroy J, Jamieson C, Rajanala K, Vilardi F, Schwappach B, Kehlenbach RH (2016) Emery-Dreifuss muscular dystrophy mutations impair TRC40-mediated targeting of emerin to the inner nuclear membrane. J Cell Sci 129: 502-16

Vilardi F, Stephan M, Clancy A, Janshoff A, Schwappach B (2014) WRB and CAML are necessary and sufficient to mediate tail-anchored protein targeting to the ER membrane. PLoS One 9(1): e85033

Arakel EC, Brandenburg S, Uchida K, Zhang H, Lin YW, Kohl T, Schrul B, Sulkin MS, Efimov IR, Nichols CG, Lehnart SE, Schwappach B (2014) Tuning the electrical properties of the heart by differential trafficking of KATP ion channel complexes. J Cell Sci 127(Pt 9): 2106-19

Voth W, Schick M, Gates S, Li S, Vilardi F, Gostimskaya I, Southworth DR, Schwappach B, Jakob U (2014) The protein targeting factor GET3 functions as an ATP-independent chaperone under oxidative stress conditions. Molecular Cell 56: 116-127

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Halyna Shcherbata

Max Planck Research Group Leader

- 1996 Ph.D., Genetics, Kyiv Institute for Plant Physiology and Genetics, Ukraine
- 1996 – 2003 Scientific Researcher, then Assistant Professor, Lemberg (Lviv) National University, Ukraine
- 2003 – 2008 Postdoc, then Research Professor, Biochemistry Department, Institute for Stem cell and Regenerative Medicine, University of Washington, Seattle, WA, USA
- 2008 – present Max Planck Research Group Leader, MPI for Biophysical Chemistry, Göttingen, Germany
- 2012 Habilitation in Developmental Biology, Georg-August University, Göttingen, Germany

Major Research Interests

My lab is focused on understanding of biological roles of miRNAs in cell differentiation and maintenance under normal, stress, and disease conditions in *Drosophila*. We show that the miRNAs-based regulatory network is accomplished via feedback-feedforward signaling, which allows to reduce transcriptional noise and fine-tune gene expression to regulate the entire gene expression profile. In addition, tissue-specific miRNAs direct differentiation toward corresponding lineages by suppressing alternative cell fates and ensuring the robustness of cell identity. Under stress and in chronic pathological states, miRNA levels are misregulated which disrupts tissue regeneration and homeostasis due to miRNA influence on cell proliferation and differentiation programs. We found that miRNAs act as spatio-temporal cell fate determinants, differentiation guardians and canalization factors, and stress response elements. We use *Drosophila* as a model organism that can serve as a valuable model system for conserved mechanisms underlying human disorders. One of our scientific interests is the analysis of the Dystrophin Glycoprotein Complex (DGC), perturbation in which results in muscular dystrophies and brain abnormalities in humans. We found that stress induces muscle degeneration even in wild type animals and accelerates age-dependent muscular dystrophy. In view of the facts that miRNAs have been implicated in stress response and the DGC has an effect on miRNA expression in vertebrates, we have conducted a miRNA microarray screen in stressed and not stressed wild type and dystrophic animals. The second line of the research that is actively conducted in my lab is focused on studying the role of the microRNA pathway in stem cells, where the *Drosophila* germline and neuronal stem cells are used as model systems. Our findings show that hormonal signaling and miRNAs direct neuronal and germline stem cell differentiation. Not only do steroid hormones control the miRNA expression, miRNAs also act in feedback loops to regulate the strength of the hormonal signaling. This provides the means to fine-tune the signals managing stem cell division, maintenance, and differentiation in response to ever-changing extracellular conditions.

Selected Recent Publications

Çiçek IO, Karaca S, Brankatschk M, Eaton S, Urlaub H Shcherbata HR (2016) The *mir*-310s target Hh signaling to rebalance the metabolic status and sustain healthy homeostasis upon dietary changes. Genetics 202(3): 1167-83

König A, Shcherbata HR (2015) Soma influences GSC progeny differentiation via the cell adhesion-mediated steroid-let-7-Wingless signaling cascade that regulates chromatin dynamics. Biology Open 4(3): 285-300

Yatsenko AS, Shcherbata HR (2014) *Drosophila* miR-9a targets the ECM receptor Dystroglycan to canalize myotendinous junction formation. Developmental Cell 28(3): 335-48

Fagegaltier D, König A, Gordon A, Lai EC, Gingeras TR, Hannon GJ, Shcherbata HR (2014) A Genome-Wide Survey of Sexually Dimorphic Expression of *Drosophila* miRNAs Identifies the Steroid Hormone-Induced miRNA let-7 as a Regulator of Sexual Identity. Genetics 198(2): 647-68

Yatsenko AS, Marrone AK, Shcherbata HR (2014) miRNA-based buffering of the cobblestone-lissencephaly-associated extracellular matrix receptor dystroglycan via its alternative 3'-UTR'. Nature Communications 5: 4906

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Johannes Söding

Research Group Leader at the Max Planck Institute for Biophysical Chemistry

- 1992 Diploma in physics at the University of Heidelberg
- 1996 PhD in physics at the University of Heidelberg
- 1996 – 1998 Post-doc with C. Cohen-Tannoudji and J. Dalibard at the École Normale Supérieure in Paris
- 1999 – 2002 Strategy management consultant for the Boston Consulting Group in Frankfurt
- 2002 – 2007 Staff scientist with Andrei Lupas at the Max-Planck-Institute for Developmental Biology in Tübingen
- 2007 – 2013 Group leader at the Gene Center and Department of Biochemistry, University of Munich (LMU)
- Since 2014 Group Leader of the Computational Biology Group at the Max Planck Institute of Biophysical Chemistry

Major Research Interests

We are interested in two broad areas of research. First, we develop computational methods for predicting the structure, function, and evolution of proteins from sequence. We develop statistical methods that enable us to make use of the vast amount of sequence information that is becoming available at an ever-increasing pace. The goal is to provide life scientists with more and more powerful tools for predicting the functions and structures of proteins in order to guide their experimental work.
Second, we want to understand how transcriptional regulation, which represents the most important level of cellular regulation, is encoded in each gene's regulatory regions. We develop computational methods to analyse regulatory sequences and to detect regulatory motifs. We also want to predict transcription rates, using probabilistic modeling, statistical physics, and machine learning techniques. We collaborate extensively with experimental groups to elucidate the molecular processes regulating transcription initiation, elongation, mRNA processing, and chromatin states.

Selected Recent Publications

Kiesel A, Roth C, Ge W, Wess M, Meier M, Söding J (2018) The BaMM web server for de-novo motif discovery and regulatory sequence analysis. Nucleic Acids Res

Steinegger M, Söding J (2018) Clustering huge protein sequence sets in linear time. Nature Commun

Steinegger M, Söding J (2017) MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. Nature Biotechnol, accepted. bioRxiv

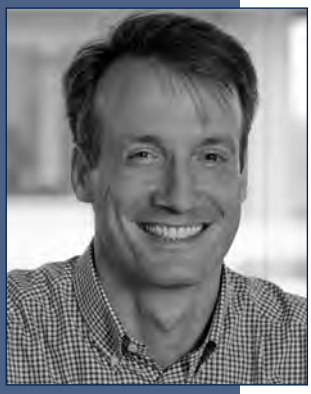
Söding J (2017) Big-data approaches to protein structure prediction. Science (perspective) 355: 248-249

Siebert M, Söding J (2016) Markov models consistently outperform PWMs at-predicting regulatory motifs in nucleotide sequences. Nucleic Acids Res 44: 6055-6069

Baejen C, Andreani J, Torkler P, Battaglia S, Schwalb B, Lidschreiber M, Maier KC, Boltendahl A, Rus P, Esslinger S, Söding J, Cramer P (2017) Genome-wide analysis of RNA polymerase II termination at protein-coding genes. Mol Cell 66: 38-49.e6

Meier A, Söding J (2015) Automatic prediction of protein 3D Structures by probabilistic multi-template homology modeling. PLoS Comput Biol 11: e1004343

Siebert M, Söding J (2014) Universality of core promoter motifs? Nature 511: E11–E12



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Holger Stark

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1996 Dr. rer. nat. (Biochemistry) Free University of Berlin
- 1997 – 1998 Postdoc (Laboratory of Marin van Heel, Imperial College, London)
- 1998 – 1999 Junior group leader, University of Marburg
- 2000 – 2004 Junior group leader, MPI for Biophysical Chemistry
- 2005 – BioFuture group leader, MP for Biophysical Chemistry
- 2005 – 2007 BioFuture group leader
- since 2007 Professor for Molecular Electron Cryomicroscopy, University Göttingen and group leader, MPI for Biophysical Chemistry
- since 2015 Director, Dept. Structural Dynamics, MPI for Biophysical Chemistry

Major Research Interests

The work in our group is focused on 3D structure determination of large macromolecular complexes by single particle electron cryomicroscopy (cryo-EM). In cryo-EM, thousands of electron microscopical images of a macromolecular complex are taken at low temperature in the electron microscope and are used to calculate a 3D reconstruction of the object by computational image processing. Electron microscopical images can be considered as almost ideal two-dimensional projection images, similar to images obtained by computer tomography in medical applications. However, in cryo-EM the relative orientation of the molecules is a priori unknown and must be determined by computational means prior to calculating the 3D structure.

Cryo-EM is the method of choice for 3D structure determination of macromolecular complexes that are difficult to purify in the amounts and quality that is required for crystallization (X-ray crystallography). Due to the low copy number of many functionally important macromolecular complexes in the cell, cryo-EM is very often the only available method to study the 3D structure of these large macromolecules. Work in our group concentrates on macromolecular complexes related to pre-mRNA splicing, translation and cell cycle regulation and on the development of new methods to improve sample preparation, imaging and computational image processing techniques

Selected Recent Publications

Bertram K, Agafonov DE, Liu WT, Dybkov O, Will CL, Hartmuth K, Urlaub H, Kastner B, Stark H, Lührmann R (2017) Cryo-EM structure of a human spliceosome activated for step 2 of splicing. Nature 542: 318-323

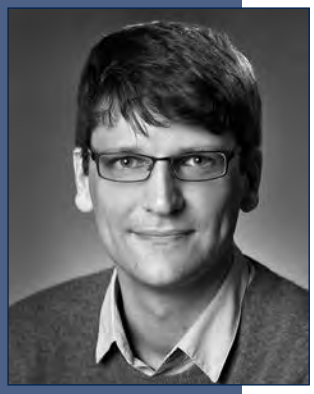
Agafonov DE, Kastner B, Dybkov O, Hofele RV, Liu WT, Urlaub H, Lührmann R, Stark H (2016) Molecular architecture of the human U4/U6.U5 tri-snRNP. Science 351(6280): 1416-20

Fischer N, Neumann P, Bock LV, Maracci C, Wang Z, Paleskava A, Konevega AL, Schröder GF, Grubmüller H, Ficner R, Rodnina M, Stark H (2016) The pathway to GTPase activation of elongation factor SelB on the ribosome. Nature 540, 80-85

Rauhut R, Fabrizio P, Dybkov O, Hartmuth K, Pena V, Chari A, Kumar V, Lee CT, Urlaub H, Kastner B, Lührmann R, Stark H (2016) Molecular architecture of the *Saccharomyces cerevisiae* activated spliceosome. Science 353: 1399-1405

Fischer N, Neumann P, Konevega AL, Bock LV, Ficner R, Rodnina MV, Stark H (2015) Structure of the *E. coli* ribosome-EF-Tu complex at <3 Å resolution by Cs-corrected cryo-EM. Nature 520(7548): 567-70

Chari A, Haselbach D, Kirves JM, Ohmer J, Paknia E, Fischer N, Ganichkin O, Möller V, Frye JJ, Petzold G, Jarvis M, Tietzel M, Grimm C, Peters JM, Schulman BA, Tittmann K, Markl J, Fischer U, Stark H (2015) ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nat Methods 12(9): 859-65



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Alexander Stein

Group Leader at the Max Planck Institute for Biophysical Chemistry

- 2008 Dr. rer. nat, Free University of Berlin and MPI for Biophysical Chemistry
- 2008 – 09 Postdoctoral Fellow at the MPI for Biophysical Chemistry
- 2010 – 14 Postdoctoral Fellow at Harvard Medical School (Boston, USA)
- since 2014 Otto Hahn Group Leader

Major Research Interests

The removal of misfolded proteins is an essential process in all cells. Failure to discard such proteins often results in disease. A particularly intriguing process serves to discard misfolded proteins from the endoplasmic reticulum (ER). The ER does not itself degrade proteins, so a machinery has evolved that moves misfolded proteins into the cytosol where they can be degraded by the proteasome. This retro-translocation process is called ERAD (for ER-associated protein degradation) and is conserved in all eukaryotes. Besides its function in the removal of misfolded proteins, it plays an important role in the controlled degradation of metabolic enzymes, like the ones involved in sterol biosynthesis. The ERAD pathway is also co-opted by certain viruses (e.g. Human cytomegalovirus) and bacterial toxins (e.g. cholera toxin).
Compared to other membrane translocation processes, the mechanism of ERAD is still poorly understood. How are misfolded proteins distinguished from folding intermediates? How are proteins moved across the membrane? How are they extracted from the membrane? How is the energy for membrane translocation provided? The aim of our research is to provide answers to these fundamental questions. To study the mechanism of ERAD we use the budding yeast *Saccharomyces cerevisiae* as a model organism. We take a bottom-up approach and try to understand the mechanism of ERAD by reconstituting the entire process with purified individual components. These experiments will be complemented by studies in intact yeast cells.
In a second project, we investigate an ERAD-like process that moves proteins into the apicoplast, a plastid-like organell in unicellular parasites, like the malaria parasite *Plasmodium falciparum*. The apicoplast performs metabolic reactions essential for the parasite's survival, which include the synthesis of lipid precursors, heme and iron-sulfur clusters. The apicoplast is the target of many antimalarial drugs. We hope that a better understanding of its cell biology will facilitate the development of new drugs against malaria.

Selected Recent Publications

Stein A, Ruggiano A, Carvalho P, Rapoport TA, (2014) Key Steps in ERAD of Luminal ER Proteins Reconstituted with Purified Components. Cell 158(6): 1375-88

Hernandez JM, Stein A, Behrmann E, Riedel D, Cypionka A, Farsi Z, Walla PJ, Raunser S, Jahn R (2012) Membrane fusion intermediates via directional and full assembly of the SNARE complex. Science 336(6088): 1581-1584

Stein A, Weber G, Wahl MC, Jahn R (2009) Helical extension of the neuronal SNARE complex into the membrane. Nature 460(7254): 525-U105.

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Claudia Steinem

Professor of Biomolecular Chemistry

- 1987 – 1989 Studies of Biology at the University of Münster
- 1989 – 1994 Studies of Chemistry at the University of Münster
- 1994 – 1997 PhD thesis under supervision of Prof. Dr. H.-J. Galla
- 1997 – 1998 Postdoctoral Researcher at the Scripps Research Institute (La Jolla, California, USA)
- 1999 – 2001 Habilitation in Biochemistry at the University of Münster
- 2001 – 2006 Associate professor (C3) for Bioanalytics and Biosensors at the University of Regensburg
- 2006 Full professor (W3) for Biomolecular Chemistry at the University of Göttingen

Major Research Interests

Development and application of new artificial membrane systems based on highly ordered porous substrates; transport processes across membranes; protein-membrane and protein-cytoskeleton interactions; membrane fusion and –fission; membrane-confined silica formation in diatoms.

Selected Recent Publications

Gerdes B, Rixen RM, Kramer K, Forbrig E, Hildebrandt P, Steinem C (2018) Quantification of Hv1-induced proton translocation by a lipid-coupled Oregon Green 488-based assay. Anal Bioanal Chem 410: 6497–6505

Nöding H, Schön M, Reinermann C, Dörrer N, Kürschner A, Geil B, Mey I, Heussinger C, Janshoff A, Steinem C (2018) Rheology of membrane-attached minimal actin cortices. J Phys Chem B 122: 4537-4545

Schütte OM, Mey I, Enderlein J, Savic F, Geil B, Janshoff A, Steinem C (2017) Size and mobility of lipid domains tuned by geometrical constraints. Proc Natl Acad Sci U S A 114: E6064-E6071

Schwamborn M, Schumacher J, Sibold J, Teiwes NK, Steinem C (2017) Monitoring ATPase induced pH changes in single proteoliposomes with the lipid-coupled fluorophore Oregon Green 488. Analyst 14: 2670-2677

Kuhlmann JW, Junius M, Diederichsen U, Steinem C (2017) SNARE-mediated single-vesicle fusion events with supported and freestanding lipid membranes. Biophys J 112: 2348-2356

Gleisner M, Kroppen B, Fricke C, Teske N, Kliesch TT, Janshoff A, Meinecke M, Steinem C (2016) Epsin N-terminal homology domain (ENTH) activity as a function of membrane tension. J Biol Chem 291: 19953-19961

Rost U, Steinem C, Diederichsen U (2016) Beta-Glutamine-mediated self-association of transmembrane beta-peptides within lipid bilayers. Chem Sci 7: 5900-5907

Ludolphs M, Schneeberger D, Soykan T, Schäfer J, Papadopoulos T, Brose N, Schindelin H, Steinem C (2016) Specificity of collybistin-phosphoinositide interactions: Impact of the individual protein domains. J Biol Chem 291: 244-254

Schwenen LLG, Hubrich R, Milovanovic D, Geil B, Yang J, Kros A, Jahn R, Steinem C (2015) Resolving single membrane fusion events on planar pore-spanning membranes. Sci Rep 5: 12006

Schütte OM, Ries A, Orth A, Patalag LK, Römer W, Steinem C, Werz DB (2014) Influence of Gb3 glycosphingolipids differing in their fatty acid chain on the phase behavior of solid supported membranes: Chemical syntheses and impact of Shiga toxin binding. Chem Sci 5: 3104-3114

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- 1990 Diploma (Biology), Ernst-Moritz-Arndt-Universität Greifswald
- 1994 Dissertation (Dr. rer. nat.), Ernst-Moritz-Arndt-Universität Greifswald
- 1994 – 1996 Postdoctoral Fellow at the Institut Pasteur, Paris
- 1996 – 2003 Group leader at the Chair of Microbiology, University Erlangen-Nürnberg
- 2000 Habilitation (Microbiology), University Erlangen-Nürnberg
- Since 2003 Professor of General Microbiology, Head of the Department of General Microbiology at the Institute of Microbiology and Genetics, University of Göttingen

Major Research Interests

Our group studies the regulation of metabolism in the pathogenic bacterium *Mycoplasma pneumoniae* and the model organism *Bacillus subtilis*. We are following global ("post-genomic") and gene-specific approaches. In *Mycoplasma pneumoniae*, we study the regulation of gene expression in this pathogenic bacterium and its relation to pathogenicity. This is highly interesting because this bacterium is an important cause of pneumonia. Moreover, *M. pneumoniae* is one of the organisms with the smallest genetic equipment that is capable of independent life. Understanding *M. pneumoniae* means understanding life! Specifically, we are analysing protein phosphorylation and mechanisms of transcription regulation in *M. pneumoniae*. We have shown, that protein phosphorylation of is of key importance for pathogenicity of *M. pneumoniae*. Metabolism in *Bacillus subtilis* is studied by transcriptomics, metabolome and fluxome analyses. Our specific interests are focussed on two key pathways: glycolysis and glutamate biosynthesis, the decisive link between carbon and nitrogen metabolism. The regulation of glycolysis is studied at the level of a controlled protein-RNA interaction. Regulation through RNA has become widely recognized in the past few years. Our studies revealed that glycolytic enzymes themselves are part of a protein complex that is required for mRNA processing and degradation. Finally, we are interested in systems biology approaches to the analysis of *B. subtilis* and develop web interfaces for the functional annotation.

Selected Recent Publications

Gundlach J, Herzberg C, Kaever V, Gunka K, Hoffmann T, Weiß M, Gibhardt J, Thürmer A, Hertel D, Daniel R, Bremer E, Commichau FM, Stülke J (2017) Control of potassium homeostasis is an essential function of the second messenger cyclic di-AMP in *Bacillus subtilis*. Science Signal 10: eaal3011

Reuß DR, Altenbuchner J, Mäder U, Rath H, Ischebeck T, Sappa PK, Thürmer A, Guérin C, Nicolas P, Steil L, Zhu B, Feussner I, Klumpp S, Daniel R, Commichau FM, Völker U, Stülke J (2017) Large-scale reduction of the *Bacillus subtilis* genome: consequences for the transcriptional network, resource allocation, and metabolism. Genome Res 27: 289-299

Michna RH, Zhu B, Mäder U, Stülke J (2016) SubtiWiki 2.0-an integrated database for the model organism *Bacillus subtilis*. Nucleic Acids Res 44: D654-D662

Großhennig S, Ischebeck T, Gibhardt J, Busse J, Feussner I, Stülke J (2016) Hydrogen sulfide is a novel virulence factor of *Mycoplasma pneumoniae*: characterization of the unusual cysteine desulfurase/ desulfhydrase HapE. Mol Microbiol 100: 42-54

Commichau FM, Dickmanns A, Gundlach J, Ficner R, Stülke J (2015) A jack of all trades: the multiple roles of the unique essential second messenger cyclic di-AMP. Mol Microbiol 97: 189-204

Schmidl SR, Otto A, Lluch-Senar M, Pinol J, Busse J, Becher D, Stülke J (2011) A trigger enzyme in *Mycoplasma pneumoniae*: Impact of the glycerophosphodiesterase GlpQ on virulence and gene expression. PLOS Pathogens 7: e1002263

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- Center of Biochemistry and Molecular Cell Biology, University of Göttingen
- 1987 Dr. rer. nat., University of Stuttgart
- 1997 Habilitation (Biochemistry), University of Stuttgart

Major Research Interests

We are studying the molecular mechanism of autophagy in the yeast *Saccharomyces cerevisiae*. Autophagy is a starvation induced transport pathway, which delivers cytosolic material for degradation to the lysosome (vacuole). It is highly conserved in all eukaryotes from yeast to human and helps the cells to survive periods of nutrient limitation.

Autophagy further plays an important role in ageing, the development of breast cancer and cardiomyopathy and it was linked to neurodegenerative diseases like Alzheimer´s, Huntington´s and Parkinson´s disease. Autophagy is mechanistically unique, since its transport intermediates, the autophagosomes, are surrounded by two individual membranes. It starts at the newly-discovered preautophagosomal structure, where autophagosomes are formed. Autophagosomes unspecifically enclose parts of the cytoplasm including organelles like mitochondria, peroxisomes and parts of the ER.

When the autophagosomes reach the vacuole, their outer membrane-layer fuses with the vacuolar membrane and a still membrane-enclosed autophagic body is released into the vacuolar lumen. In the vacuole autophagic bodies are lysed and broken down together with their cytosolic content. The intravacuolar breakdown of autophagic bodies requires the selective lysis of their limiting membrane. Due to the use of two limiting membranes the biogenesis of autophagosomes is a very unique process. Molecular dissection of this process is one of our main areas of research.

Selected Recent Publications

Juris L, Montino M, Rube P, Schlotterhose P, Thumm M*, Krick R (2015) PI3P binding by Atg21 organizes Atg8 lipidation. EMBO J 34: 955–973 *corresponding author

Thumm M, Simons M (2015) Myelinophagy: Schwann cells dine in. The Journal of Cell Biology 210(1): 9–10

Busse RA, Scacioc A, Hernandez JM, Krick R, Stephan M, Janshoff A, Thumm M, Kühnel K (2013) Qualitative and quantitative characterization of protein-phosphoinositide interactions with liposome-based methods. Autophagy 9: 770-777

Thumm M, Busse RA, Scacioc A, Stephan M, Janshoff A, Kühnel K, Krick R (2013) It takes two to tango: PROPPINs use two phosphoinositide-binding sites. Autophagy 9: 106-107

Roswitha Krick, Ricarda A Busse, Andreea Scacioc, Milena Stephan, Andreas Janshoff, Michael Thumm*, Karin Kühnel* (2012) Structural and functional characterization of the two phosphoinositide binding sites of PROPPINs, a β-propeller protein family. PNAS 109(30): E2042-9 *corresponding author

Usha Nair, Michael Thumm*, Daniel J Klionsky*, and Roswitha Krick (2011) GFP-Atg8 protease protection as a tool to monitor autophagosome biogenesis. AUTOPHAGY 7 (12): 1546-1550 *corresponding author

Welter E, Thumm M*, Krick R (2010) Quantification of nonselective bulk autophagy in *S. cerevisiae* using Pgk1-GFP. Autophagy 6(6): 794-797 *corresponding author

Krick R*, Bremer S*, Welter E*, Schlotterhose P, Muehe Y, Eskelinen E-L, Thumm M (2010) Cdc48/p97 and Shp1/p47 regulate autophagosome biogenesis in concert with ubiquitin-like Atg8. J Cell Biol 190, 6: 965-973

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- Diploma (Biochemistry), Martin-Luther-University, Halle/Saale (Germany), 1996
- Dr. rer. nat., Martin-Luther-University, Halle/Saale (Germany), 2000
- Postdoc, Institute for Biochemistry, MLU Halle-Wittenberg, Halle/Saale (Germany), 2001 – 2002
- Jun.-Prof. of Molecular Enzymology, Institute for Biochemistry, MLU Halle-Wittenberg, Halle/Saale, (Germany), 2003 – 2008
- Invited Research Scientist at Rutgers University, Newark, NJ, USA, 2003
- Associate Guest Professor, Ben-Gurion-University of the Negev, Beer-Sheva, IL, 2006
- Since 2008 Professor of Bioanalytics, Georg-August-University, Göttingen (Germany)
- Awards: Dorothea-Erxleben-Prize (best doctoral thesis), 2001
- Prize for excellent basic research at Saxony-Anhalt, 2005

Major Research Interests

The central research topic of our department is the analysis of molecular reaction mechanisms of enzymes as nature's chemical catalysts. In this context, we study enzymes with vitamin-derived cofactors, with metal ions, and Schiff base-forming enzymes. A particular focus is laid on the structural and kinetic characterization of enzymatic reaction intermediates by high-resolution X-ray crystallography, steady-state and transient kinetic methods, NMR spectroscopy and theoretical studies. Knowledge about the reaction mechanism is exploited to redesign enzymes for biocatalytic applications and for drug design.

Selected Recent Publications

Schrader J, Henneberg F, Mata RA, Tittmann K, Schneider TR, Stark H, Bourenkov G, Chari A (2016) The inhibition mechanism of human 20S proteasomes enables next-generation inhibitor design. Science 353(6299): 594-8

Pérez-Lara Á, Thapa A, Nyenhuis SB, Nyenhuis DA, Halder P, Tietzel M, Tittmann K, Cafiso DS, Jahn R (2016) PtdInsP(2) and PtdSer cooperate to trap synaptotagmin-1 to the plasma membrane in the presence of calcium. Elife 5: e15886

Sautner V, Friedrich MM, Lehwess-Litzmann A, Tittmann K (2015) Converting Transaldolase into Aldolase through Swapping of the Multifunctional Acid-Base Catalyst: Common and Divergent Catalytic Principles in F6P Aldolase and Transaldolase. Biochemistry 54(29): 4475-86

Brodhun F, Tittmann K (2015) Membrane enzymes: transformers at the interface. Nature Chem Biol 11(2): 102-3

Neumann P, Tittmann K (2014) Marvels of enzyme catalysis at true atomic resolution: distortions, bond elongations, hidden flips, protonation states and atom identities. Curr Opin Struct Biol 29: 122-33

Schröder-Tittmann K, Meyer D, Arens J, Wechsler C, Tietzel M, Golbik R, Tittmann K (2013) Alternating sites reactivity is a common feature of thiamin diphosphate-dependent enzymes as evidenced by isothermal titration calorimetry studies of substrate binding. Biochemistry 52(15): 2505-7

Lüdtke S, Neumann P, Erixon KM, Leeper F, Kluger R, Ficner R, Tittmann K (2013) Sub-Angström resolution crystallography reveals physical distortions that enhance reactivity of a covalent enzymatic intermediate. Nature Chem 5: 762-767

Meyer D, Neumann P, Ficner R, Tittmann K (2013) Observation of a stable carbene at the active site of a thiamin enzyme. Nature Chem Biol 9: 488-490

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Henning Urlaub

Group Leader - Bioanalytical Mass Spectrometry Group

- from 2010: Group leader “Bioanalytical Mass Spectrometry” group at the Max Planck Institute for Biophysical Chemistry, Göttingen and “Bioanalytics” group at University Medical Center Göttingen (UMG) within Institute for Clinical Chemistry
- 2010: Professor at the Faculty of Medicine at Georg August University Göttingen
- 2005: Research group “Bioanalytical Mass Spectrometry Group” at the Max Planck Institute for Biophysical Chemistry
- 2000 – 2001: Guest researcher at the EMBL in Heidelberg, Germany, in the group of Dr. Matthias Wilm
- 1997 – 2004: Post-Doc at the “Institut für Molekularbiologie und Tumorforschung” (IMT) of the Philipps University of Marburg, Germany (Group of Reinhard Lührmann) and at the Max Planck Institute for Biophysical Chemistry in Göttingen (Group of Reinhard Lührmann)
- 1993 – 1996 Ph.D. and Post-Doc in the research group of Prof. Brigitte Wittmann-Liebold at the Max Delbrück Center for Molecular Medicine (MDC) in Berlin
- 1992 – 1993 Diploma thesis in the research group of Prof. Volker A. Erdmann at the Institute of Biochemistry of the Free University of Berlin
- 1987 – 1993 Studied biochemistry at the Free University of Berlin, Germany

Major Research Interests

Modern mass-spectrometric methods have become key technologies in the life sciences. We apply “state-of-the-art” mass spectrometry to elucidate quantitative changes of proteins and their post-translational modifications derived from different samples, including tissue, cells, organelles, and cell compartments. In addition, we apply mass spectrometric (MS) methods to monitor dynamic changes of protein and protein-ligand complexes through use of crosslinking. Following main projects are investigated by the use of MS are: 1. Monitoring protein abundance, modifications and interactions in the non-stimulated and stimulated synapse by MS, 2. Protein-protein cross-linking combined with MS in stimulated and resting B cells, 3. Method development in protein-protein, protein-RNA and protein-DNA cross-linking combined with MS.

Selected Recent Publications

Fornasiero EF, Mandad S, …, Urlaub H, Rizzoli S (2018) Precisely measured protein lifetimes in the mouse brain reveals biologically-significant differences across tissues and subcellular fractions. Nature Communications

Vos SM, Farnung L, Boehning M, Wigge C, Linden A, Urlaub H, Cramer P (2018) Structure of activated transcription complex Pol II-DSIF-PAF-SPT6. Nature 560: 607-612

Schmidt C, Urlaub H (2017) Combining cryo-electron microscopy (cryo-EM) and cross-linking mass spectrometry (CX-MS) for structural elucidation of large protein assemblies. Curr Opin Struct Biol 46: 157-168

Pan KT, Chen CC, Urlaub H*, Khoo KH (2017) Adapting Data-Independent Acquisition for Mass Spectrometry-Based Protein Site-Specific N-Glycosylation Analysis. Anal Chem 89: 4532-4539

Agafonov D, Kastner B, Dybkov O, Hofele R, Liu W, Urlaub H, Lührmann R, Stark H (2016) Molecular architecture of the human U4/U6.U5 tri-snRNP. Science 351(6280): 1416-1420

Corso J, Pan KT, Walter R, Doebele C, Mohr S, Bohnenberger H, Ströbel P, Lenz C, Slabicki M, Hüllein J, Comoglio F, Rieger MA, Zenz T, Wienands J, Engelke M, Serve H, Urlaub H*, Oellerich T* (2016) Elucidation of tonic and activated B-cell receptor signaling in Burkitt’s lymphoma provides insights into regulation of cell survival. Proc Natl Acad Sci USA 113: 5688-5693

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Lutz Walter

Head of Department of Primate Genetics at the German Primate Center

- Dr. rer. nat. (PhD), University of Göttingen, 1994
- Postdoctoral fellow and group leader at the Division of Immunogenetics, University of Göttingen, 1994 – 2004
- Head of Department of Primate Genetics, German Primate Center, Göttingen, since 2004
- Habilitation (Immunology and Immunogenetics), Medical Faculty of the University of Göttingen, 2005
- apl Professor, Medical Faculty of the University of Göttingen, 2009

Major Research Interests

Natural killer (NK) cells belong to the lymphocyte lineage and represent an essential part of the innate immune system. NK cells can kill other cells and secrete substantial amounts of cytokines. Signals from activating and inhibitory NK cell receptors are integrated and regulate the activity of NK cells. Typical targets for NK cell killing are virus-infected or malignant cells, which both frequently reveal changed patterns of ligand expression on their cell surface. Such changes are recognised by NK cells, leading to killing of virally infected or transformed cells. NK cells can also be activated by different stimuli during interaction with dendritic cells, leading to release of pro-inflammatory cytokines and anti-viral substances. Due to these properties, NK cells play also important roles in autoimmune diseases, transplantation, and reproduction. Recently, NK cells were shown to possess immunological memory. Our interests lie in biology and genetics of natural killer (NK) cells, including regulation of NK cell receptor gene transcription, specific interactions of NK cell receptors and MHC class I ligands, regulation of NK cell activation, NK cell transcriptomics and the role of long noncoding RNA in NK cell development.
A further focus of our research is genomics of nonhuman primates with phylogenetic, demographic, evolutionary, and bioinformatic analyses.
Methods: single-cell RNA sequencing, single-cell qRT-PCR, flow cytometry, next-generation sequencing, bioinformatic analysis tools.

Selected Recent Publications

Byrareddy et al. (2016) Sustained virologic control in SIV+ macaques following short term ART and $\alpha 4\beta 7$-mAb treatment. Science 354(6309): 197-202

Walter L, Ansari AA (2015) MHC and KIR Polymorphisms in Rhesus Macaque SIV Infection. Front Immunol 6: 540

Carbone et al. (2014) Gibbon genome and the fast karyotype evolution of small apes. Nature 513: 195-201

Albrecht C, Malzahn D, Brameier M, Hermes M, Ansari AA, Walter L (2014) Progression to AIDS in SIV-infected rhesus macaques is associated with distinct KIR and MHC class I polymorphisms and NK cell dysfunction. Front Immunol 5: 600

Byrareddy SN, Kallam B, Arthos J, Cicala C, Nawaz F, Hiatt J, Kersh EN, McNicholl JM, Hanson D, Reimann KA, Brameier M, Walter L, Rogers K, Mayne AE, Dunbar P, Villinger T, Little D, Parslow TG, Santangelo PJ, Villinger F, Fauci AS, Ansari AA (2014) Blockade of alpha4beta7 integrin, a T-cell gut-homing receptor, reduces mucosal transmission and dissemination of simian immunodeficiency virus infection. Nat Med 20: 1397-1400

Walter L (2014): Immunogenetics of NK cell receptors and MHC class I ligands in non-human primates. In: Ansari AA, Silvestri G (eds) Natural hosts of SIV. Implications in AIDS. Elsevier, pp. 269-285

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Jürgen Wienands

Professor of Cellular and Molecular Immunology

- 1982 – 89 Study of Biology at the University of Cologne; graduated at the Institute of Genetics, Dept. of Immunology
- 1989 – 92 Ph.D. poject at the Max Planck Institute for Immunobiology, Freiburg, Germany
- 1992 – 94 Postdoctoral fellow at the Dept. of Preclinical Research at Sandoz Pharma Ltd., Basel, Switzerland
- 1994 – 96 Postdoctoral fellow at the Max Planck Institute for Immunobiology, Freiburg, Germany
- 1996 – 2001 Group leader at the University of Freiburg, Institute of Biology III
- 2001 “Habilitation” and Venia Legendi in “Molecular Immunology and Biochemistry”
- 2001 – 2004 Full Professor for “Biochemistry and Molecular Immunology” at the University of Bielefeld
- since August 2004 Full Professor for “Molecular and Cellular Immunology” at the University of Göttingen
- 2015 – 2016 President of the German Society for Immunology (DGfI)

Major Research Interests

The signature structure of B lymphocytes is their clonotypic antigen receptor (BCR), which recognizes extracellular pathogens or toxins, and consequently initiates their combating by soluble antibodies. Our research focuses on how the ligated BCR activates intracellular signaling pathways upon primary and secondary antigen encounter. Our studies showed that BCR classes expressed on antigen-experienced, so-called memory B cells, possess a signal amplification mechanism that lowers the BCR signaling threshold compared to newly generated B cells. This finding provides a molecular explanation for immunological memory which is the fundamental basis for successful vaccination strategies. We also identified key effector proteins of the BCR such as SLP-65 or CIN85. They function as adaptor proteins which nucleate the formation of multi-molecular protein complexes to integrate and amplify BCR signals. Interference with expression or function of these effectors cause severe immunodeficiencies in mouse and man. To investigate these processes we apply cutting edge technologies of biochemistry and genetics including protein interaction studies, flow cytometry, targeted gene disruption in cell culture and embryonic stem cells followed by reconstitution experiments using electroporation techniques or retroviral gene transfer

Selected Recent Publications

Keller B, Shoukier M, Schulz K, Bhatt A, Heine I, Strohmeier V, Speckmann C, Engels N, Warnatz K, Wienands J (2018) Germline deletion of CIN85 in humans with X chromosome-linked antibody deficiency. J Exp Med 215(5): 1327-1336

Kühn J, Wong LE, Pirkuliyeva S, Schulz K, Schwiegk C, Fünfgeld KG, Keppler S, Batista FD, Urlaub H, Habeck M, Becker S, Griesinger C, Wienands J (2016) The adaptor protein CIN85 assembles intracellular signaling clusters for B cell activation. Sci Signal 9(434): ra66

Lutz J, Dittmann K, Bösl MR, Winkler TH, Wienands J, Engels N (2015) Reactivation of IgG-switched memory B cells by BCR-intrinsic signal amplification promotes IgG antibody production. Nat Commun 6: 8575

Engels N, König LM, Schulze W, Radtke D, Vanshylla K, Lutz J, Winkler TH, Nitschke L, Wienands J (2014) The immunoglobulin tail tyrosine motif upgrades memory-type BCRs by incorporating a Grb2-Btk signalling module. Nat Commun 5: 5456

for review see:

Wienands J, Engels N (2016) The Memory Function of the B Cell Antigen Receptor. Curr Top Microbiol Immunol 393: 107-21

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- 1995 Dr. rer. nat., Max-Planck-Institute for Biophysical Chemistry, Göttingen (Germany) and Howard Hughes Medical Institute, Baylor College of Medicine, Houston (USA)
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Major Research Interests

Phylogenetic Variance and Plasticity of Developmental Processes. A key question in evolutionary developmental biology is how diverse animal body plans are specified. To identify the plasticity in developmental processes, we study their conservation and divergence in different arthropod species by transgenesis and functional genomics approaches. This will help us to understand how animal evolution is based on changes in gene regulation governing pattern formation and sex determination processes.
Smelling Beetles: Stink Glands and Odour Detection the Red Flour Beetle *Tribolium castaneum*. Beetles are prolific producers of repellent and/or toxic compounds. Defensive substances are usually multifunctional: as repellents, toxicants, insecticides, or antimicrobics, they are directed against a large array of potential target organisms or may function for boiling bombardment or as surfactants. We are interested both in the development of these glands as well as their biochemical composition and biological function. The red flour beetle also offers a great system to address olfaction from the odour recognition and discrimination at the periphery to the analysis of the plasticity of the central olfactory pathway.
Applied Developmental Biology: Biotechnological improvements on the Sterile Insect Technique (SIT). SIT is a successful genetic pest management strategy to prevent, control, suppress, or even eradicate invasive insect pest species from islands, large agricultural production areas, or even complete continents. SIT is a species-specific and eco-friendly insect birth control measure involving mass production, sterilization, and sustained area-wide release of large quantities of sterilized insects. This leads to unproductive matings, which shrinks the population. Our current biotechnological efforts, which include transposon-based germ line transformation and CRISPR/Cas9-based genome editing improve on transgenic female-specific lethality systems to enable more efficient male-only releases, on reproductive sterility systems to overcome the problem of radiation-reduced fitness, and on transgenic markers to better monitor the efficacy of SIT applications.

Selected Recent Publications

KaramiNejadRanjbar M, Eckermann KN, Ahmed HMM, Sánchez C, Dippel S, HM, Marshall JM, Wimmer EA (2018) Consequences of resistance evolution in a Cas9-based sex conversion suppression gene drive for insect pest management. Proc. Natl. Acad. Sci. 115, 6189–6194

Sharma A, Heinze SD, Wu Y, Kohlbrenner T, Morilla I, Brunner C, Wimmer EA, van de Zande L, Robinson MD, Beukeboom LW, Daniel Bopp D (2017) Male sex in houseflies is determined by Mdmd, a paralog of the generic splice factor gene CWC22. Science 356: 642–645

Dippel S, Kollmann M, Oberhofer G, Montino A, Knoll C, Krala M, Rexer KH, Frank S, Kumpf R, Schachtner J, Wimmer EA (2016) Morphological and Transcriptomic Analysis of a Beetle Chemosensory System Reveals a Gnathal Olfactory Center. BMC Biology 14: 90

Schmitt-Engel C, et al. (2015) The iBeetle large scale RNAi screen reveals novel gene functions for insect development and physiology. Nat Commun 6: 7822

Li J, Lehmann S, Weißbecker B, Ojeda-Naharros I, Schütz S, Joop G, Wimmer EA (2013) Odoriferous defensive stink gland transcriptome to identify novel genes for quinone synthesis in the red flour beetle, *Tribolium castaneum*. PLoS Genet 9: e1003596

Schetelig MF, Caceres C, Zacharopoulou A, Franz G, Wimmer EA (2009) Conditional embryonic lethality to improve the sterile insect technique in *Ceratitis capitata* (Wiedemann; Diptera: Tephritidae). BMC Biology 7: 4

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In memory of our dear colleague
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