GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN / GERMANY

International Max Planck Research School

Molecular Biology

MSc/PhD Program

YEARBOOK 2020 / 2021

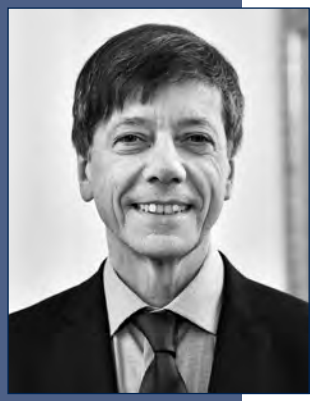
Yearbook 2020/2021

MSc/PhD Molecular Biology Program

at the University of Göttingen

International Max Planck Research School

Index



Letter from the President

The University of Göttingen is committed to the education of the next-generation scientists. Firmly rooted in excellent science, our goals are to train competent and critical young academics that are able to meet the challenges of the future. Within the Göttingen Campus, the cooperation between our university, the local Max-Planck Institutes and the German Primate Center fosters a dynamic and vibrant research environment in which the free exchange of ideas leads to top science in a true manifestation of the famous “Göttingen Spirit”.

The two international MSc/PhD programs in Molecular Biology and Neurosciences are highly acclaimed role models in graduate training that almost 20 years after their foundation continue to be enormously successful. Embedded in the Göttingen Campus they integrate faculty members across institutional borders and provide junior faculty members with full rights as thesis supervisors. The programs offer not only scientific training of outstanding quality but also a comprehensive range of services including training in professional skills, career counseling, and practical support for dealing with daily life, greatly facilitating integration of students from abroad. Due to their success, these programs served as blueprints for the creation of additional PhD training programs that are united under the roof of the Göttingen Graduate Center for Neurosciences, Biophysics and Molecular Biosciences (GGNB). The GGNB was supported by the Federal Excellence Initiative until the expiration of its Graduate School program and is now stably financed by the university in cooperation with its partners on the Göttingen Campus.

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 almost two decades, these international programs have been particularly successful in attracting large numbers of high quality applicants from all around the world, allowing for the selection of the very best candidates. The new concepts that were introduced by these programs have recently 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 keep pace with the dynamic change of research areas in the participating institutions. Accordingly, 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 maintain close links with the relevant industries to enhance the opportunities of the graduates for a successful professional career in the private sector.

As founding member and former speaker of the international MSc/PhD program in Molecular Biology I am very proud of what we all have achieved, and I remain on board as an active faculty member despite the many obligations in my new office. Most importantly, I would like to thank all colleagues and institutions for their unwavering commitment to 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 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. Reinhard Jahn

(President of the University of Göttingen)

Letter from the Max Planck Society

The mission of the Max Planck Society is to conduct top-level basic research in science and the humanities. Because this is only possible with bright young minds, the Max Planck Society funds graduate education nationwide - including the International Max Planck Research School for Molecular Biology in Göttingen.

Currently, over 80 Max Planck Institutes are located on scientific campuses across Germany, most of them close to universities. To strengthen the scientific ties with universities, the Max Planck Society, together with the German University Rectors' Conference, launched the International Max Planck Research Schools (IMPRSs) as a new joint program - during celebrations in Göttingen on the occasion of the 50th anniversary of the Max Planck Society.

The goals of the International Max Planck Research Schools are

- to attract excellent students from all around the world to intensive PhD training programs in Germany, preparing them for careers in science,
- to integrate internationally renowned Max Planck researchers into top-level scientific training programs for junior scientists, 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, 64 International Max Planck Research Schools have been established involving 81 Max Planck Institutes, 35 German universities, and 26 universities abroad. Over 3,100 PhD students from 123 countries are presently enrolled.

Since their foundation in 2000, the Göttingen IMPRSs in Molecular Biology and Neurosciences have met with particular - and extraordinary - success. This is due to multiple factors. Most notably, both programs are the result of a true synergism between the local Max Planck Institutes, the University of Göttingen, the University Medical Center and the German Primate Center, which allowed to completely reform local graduate education in the course of their establishment. Moreover, all of the respective IMPRS funds are invested into excellent training conditions, comprehensive services and financial support of the students, which is a major attraction for the best students worldwide. Accordingly, most former students of our programs moved on to prestigious international institutions and continued their successful careers.

Over the past two decades, the IMPRS-funded graduate programs in Molecular Biology and Neurosciences have 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 Center 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 our IMPRS students will continue to be successful in their professional careers - and that they will remember their training period in Göttingen as an exciting, stimulating, and formative phase of their lives.

Marina Rodnina
Spokesperson of the IMPRS
for 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 2020/21 class, the faculty members, the program committee and the coordination team.

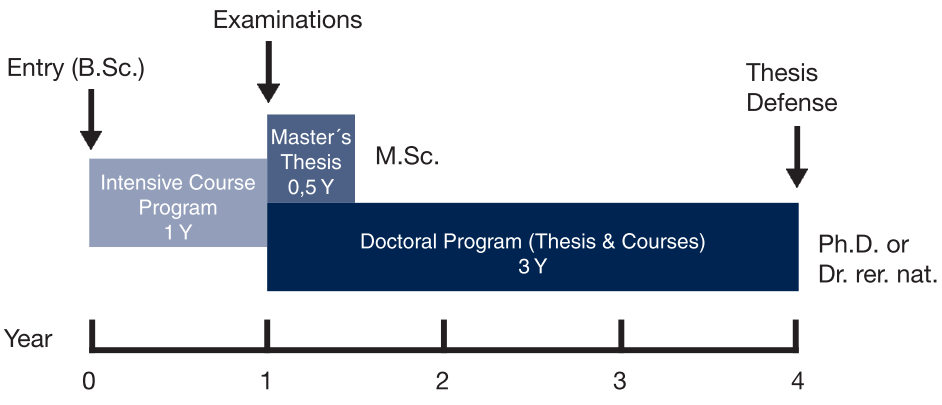
The program is a member of the Göttingen Graduate Center for Neurosciences, Biophysics, and Molecular Biosciences (GGNB), which was supported by the Excellence Initiative of the German Federal and State Governments until the expiration of its funding line for graduate schools. The GGNB is now stably financed by the University in cooperation with its partners on te Göttingen Campus. 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 20-24 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.) orthe 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. The continuation in the PhD Program is possible and desired.



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

- Fundamental of biophysical chemistry
- Architecture of the cell
- DNA and chromatin structure, epigenetics, genomics
- DNA replication and repair
- 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
- 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 system, sensory systems
- Developmental biology

Module M.MolBio.14: Model Systems / Biotechnology

- Stem cells
- Fungi, *Arabidopsis, Drosophila*
- Regeneration, organoids, oocyte development, mouse
- Primate, non-human primate models, use in virus 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)

- Programming in R, basic statistics
- Next generation sequencing, NGS analysis with R
- Protein bioinformatics
- Comparative sequence analysis, phylogeny
- Gene ontologies & biological networks

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

- Protein-nucleic acid 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 2020

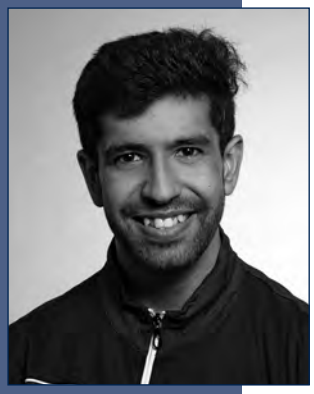
Applicants must hold a Bachelor's degree or equivalent in biology, biochemistry, chemistry, medicine, or related fields. Applicants who are not native speakers of English should demonstrate adequate competence of the English language by acceptable results in an internationally recognized test.

In the year 2020, the Molecular Biology Program received 612 applications from 75 countries.

Continent	Applications	Admissions
Europe (total)	**93**	**12**
Germany	10	3
other West Europe	18	1
East Europe	65	8
America (total)	**34**	**4**
North America	11	1
Central/South America	23	3
Africa (total)	**128**	**1**
North Africa	51	1
Central/South Africa	77	0
Asia (total)	**357**	**7**
Near East	43	0
Central Asia/ Far East	314	7

Students 2020 / 2021

Name		Home Country
Gantavya	Arora	India
Luis	Camacho	Costa Rica
Eduardo	Cienfuegos Pecina	Mexico
Nilanjan	Ghosh Dastidar	India
Monica Yasser	Gobran	Egypt
Béla	Goertz	Germany
Paulius	Greicius	Lithuania
Milena	Ivanišević	Serbia
Oğuz Can	Koç	Turkey
Alexandra	Kolodyazhnaya	Russian Federation
Priya	Kumar	India
Sumeru	Panta	Nepal
Kimberly	Quililan	Philippines
Rahul	Shaha	India
Nikola	Todorov	Bulgaria
Juan Camilo	Torres Bonilla	Colombia
Josefa	Torres Llanos	Chile
Dimitra	Tsouraki	Greece
Lidiia	Tynianskaia	Russian Federation
Çağıl	Urhan	Turkey
Malena	von Elling-Tammen	Germany
Zehra	Vural	Turkey
Lucia	Winkler	Germany
Yumeng	Zhan	P.R. China



India

Gantavya Arora

EDUCATION

College / University

Sri Venkateswara College, University of Delhi

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry, Genetics, Molecular Biology, Advanced Cell Biology, Membrane Biology, Metabolism, Physiology & Endocrinology, Immunology

Lab Experience

UV-visible spectrophotometry, enzyme assays, protein purification techniques, chromatography, gel electrophoresis, Isolation and purification of total nucleic acid, PCR, transforming *E. coli* cultures with recombinant plasmid, sub-cellular fractionation, visualization of biological samples under microscope, *Drosophila* husbandry, basic immunological techniques, basic bioinformatics.

Projects / Research

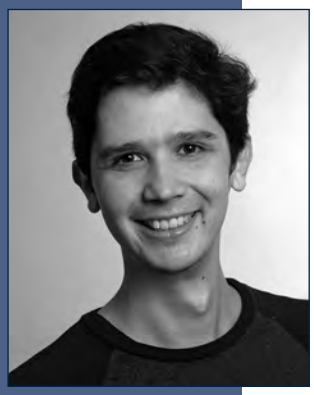
2019: Molecular biology of *Mycobacterium tuberculosis* with the aim to sub-clone the promoter region of Rv3134c gene in *Mycobacterium tuberculosis* using pGEM T-easy vector, and understand the functions and properties of Rv3134c gene in stress conditions. Supervisor: Dr Vandana Malhotra, Sri Venkateswara College, University of Delhi

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018 – 2019: College Rank Holder (2nd), Sri Venkateswara College, University of Delhi (South Campus).

2017: 2nd position in class XII - Higher secondary education of my school affiliated to CBSE Board, India



Costa Rica

Luis Camacho

EDUCATION

College / University

University of Costa Rica

Highest Degree

Bachelor of Science

Major Subjects

Microbiology and Clinical Chemistry

Lab Experience

Recombinant protein expression (*E.coli*), bacteria cell culture, SDS-PAGE, immobilized metal affinity chromatography, HPLC, ELISA, enzyme assays, blotting, immunization, PCR and RT-PCR, DNA/RNA extraction, handling of clinical samples.

Projects / Research

2018 – 2019: *Escherichia coli* expression and purification of a hemolytic and nonhemolytic A2 phospholipase from the venom of *Micrurus fulvius*. Bachelor's thesis, supervisor - Prof. Dr. Bruno Lomonte, Clodomiro Picado Institute, Costa Rica

2017: Intravascular hemolysis induced by phospholipases A2 from the venom of the Eastern coral snake, *Micrurus fulvius*: Functional profiles of hemolytic and non-hemolytic isoforms. Lic. Maria Laura Fernandez, Prof. Dr. Bruno Lomonte, Clodomiro Picado Institute, Costa Rica

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2017: Summer program Biomembranes & Cellular Microcompartments by Costa Rica Zentrum at Osnabrück University

Mexico

Eduardo Cienfuegos Pecina

EDUCATION

College / University

Universidad Autónoma de Nuevo León

Highest Degree

Bachelor of Science

Major Subjects

Clinical Chemistry, Biochemistry, Hepatology, Organic Chemistry, Molecular Biology

Lab Experience

In vivo surgical models of ischemia-reperfusion injury in rats, ELISA, Western blot, total protein, DNA and RNA extraction, purification, and quantification, gel electrophoresis, PCR, RT-qPCR, organic synthesis, column and thin-layer chromatography, structural elucidation by NMR, 1H-NMR-based metabolomics, polarimetry, clinical laboratory routine techniques, basics of mammalian cell culture.

Projects / Research

2018 – 2020: Effect of inhibitors of the EGLN family of prolyl-4-hydroxylases against hepatic and renal ischemia-reperfusion injury.Universidad Autónoma de Nuevo León

2020: Effect of sodium (S)-2-hydroxyglutarate in male, and succinic acid in female Wistar rats against renal ischemia-reperfusion injury, suggesting a role of the HIF-1 pathway. PeerJ 2020, 8:e9438

2018: Nephroprotective effect of *Sonchus oleraceus* extract against kidney injury induced by ischemia-reperfusion in Wistar rats. Oxid Med Cell Longev, 2018; ID 9572803

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: Academic Merit Award by the Universidad Autónoma de Nuevo León

2018: Academic exchange at the University of Buenos Aires, Argentina

India

Nilanjan Ghosh Dastidar

EDUCATION

College / University

University of Hyderabad

Highest Degree

Master of Science

Major Subjects

Molecular Biology, Cell Biology, Genetics, Intermediary Metabolism, Bioinformatics

Lab Experience

Microscopy, live cell Imaging, yeast handling, genome-wide yeast two-hybrid screens, protein-protein interaction studies, Western blot, protein extraction and purification, RNA based techniques, chromatography techniques, spectroscopy techniques, immunology techniques, ELISA, SRID, enzymology and clinical biochemistry assays, bioinformatics tools, PYMOL and COOT analysis.

Projects / Research

2019 – 2020: Analysis of the function of Uip4, a novel protein of the Endoplasmic Reticulum. Master's thesis, University of Hyderabad. Awarded A+ (highest grade).

2019: Structural effect of gold nanoparticles on PIMT repair enzyme, Bose Institute, India

2017 – 2018: Development of an indigenous gradient gel electrophoresis system for separation of broad range DNA fragments, Maulana Azad College, Kolkata

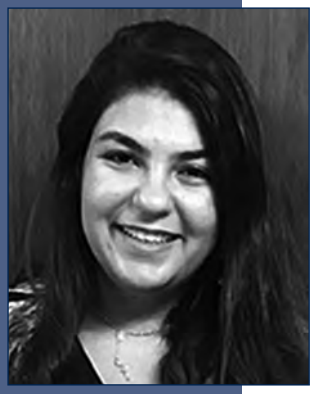
Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: Qualified NET exam for Junior Research Fellowship and Lecturership from CSIR, India

2019: Highest grade and aggregate in class of MSc Biochemistry, University of Hyderabad

2011: 2nd rank holder in National Science Seminar, Government of India



Egypt

Monica Yasser Gobran

EDUCATION

College / University

German University in Cairo

Highest Degree

Bachelor of Science

Major Subjects

Pharmaceutical Sciences and Biotechnology

Lab Experience

Cell isolation and cell culture techniques, DNA and RNA isolation, Real-Time PCR, SDS-PAGE, agarose gel electrophoresis, comet assay, AMES test, bacterial transformation, *in vivo* drug administration, *in vitro* pharmacological assays, spectrophotometry, chromatography including TLC and HPLC, neurobehavioral tests, microbiology techniques including growing bacterial cell cultures, fermentation and growth experiments.

Projects / Research

2019 – 2020: Junior Research Assistant in The Molecular Pathology Research Lab in The German University in Cairo under the supervision of Prof. Dr. Nabila Hamdi

2019: Cognitive Assessment and Neuroinflammatory Gene Analysis in Experimental Mouse Model: Hands-on Training on Real-Time PCR and Neurobehavioral Tests

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: GUC Excellence Award offering a course in Pharmaceutical Engineering in Berlin

2017: GUC Academic Excellence Award offering a course in Pharmaceutical Drug Development and Research in Berlin

2016: DAAD Scholarship offering a German language course in Ulm

2015: GUC Academic Achievement Scholarship for admission

Germany

Béla Goertz

EDUCATION

College / University

Humboldt University of Berlin

Highest Degree

Bachelor of Science

Major Subjects

Biology

Lab Experience

Bacterial culture and transformation, PCR, agarose gel electrophoresis, SDS-PAGE, restriction cloning, recombinant protein expression and purification, microscopy (light, fluorescence, confocal), FRAP, primer design, sequence alignments.

Projects / Research

2020: *In vitro* granule formation by the RNA-binding protein CP29A, Prof. Dr. Schmitz-Linneweber, Molecular Genetics, Humboldt University of Berlin (Bachelor's Thesis)

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2017 – 2021: Scholarship by the German Academic Scholarship Foundation (Studienstiftung des deutschen Volkes)

Lithuania

Paulius Greicius

EDUCATION

College / University

University of York

Highest Degree

Bachelor of Science

Major Subjects

Biology

Lab Experience

Dry lab: coding in R and Python, Bash pipeline development, use of Unix command line tools for analysis of genomic data, version control using GIT, Anaconda, development of R Shiny applications. Wet lab: cell culture and transfection, ELISA, MALDI-TOF MS sample preparation and analysis, enzyme assays using UV-visible spectroscopy, ion exchange chromatography, agarose gel electrophoresis, fluorescent microscopy.

Projects / Research

2019 – 2020: Development of SELEX data analysis pipeline for detection of viral genome packaging signals. Dr. Richard Bingham, University of York

2019: Inference and simulation of gene regulatory networks. Prof. Richard J. Morris, John Innes Centre

2018 – 2019: Development of data analysis applications using R Shiny, Dr James Reid, Oxford Gene Technology

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: Stipend by John Innes Centre Undergraduate Summer School

2018 – 2019: Industrial Placement in Oxford Gene Technology

Serbia

Milena Ivanišević

EDUCATION

College / University

University of Belgrade, Serbia

Highest Degree

Bachelor of Science

Major Subjects

Molecular biology and Physiology

Lab Experience

Human cancer cell culturing, Western Blot analysis, total RNA isolation, reverse transcription reaction, PCR primer designing, PCR, qRT-PCR for mRNA, qRT-PCR for micro RNA, DNA cloning, chromatin extraction, isolation of RNA from bacterial cells, tissue staining with eosin and haematoxylin, spectrophotometry, ion exchange chromatography, SDS PAGE, FACS sorting.

Projects / Research

2019: Unravelling the connection between cell cycle and chromatin-associated meta-bolism. Dr Sara Sdelci and Dr Maria Guirola Tsibulova, Center for Genomic Regulation (CRG)

2018: Mechanism of p53 activation by small molecules inhibiting the de novo pyrimidine synthesis pathway. Dr Gergana Popova, Karolinska Institutet

Scholarships / Awards

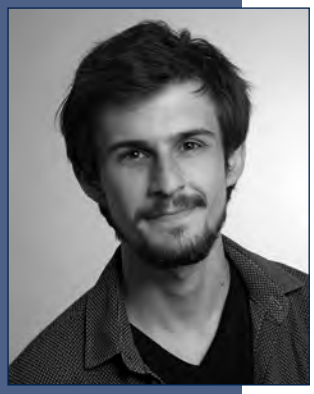
2020 – 2021: Stipend by the International Max Planck Research School

2019: Centre for Genomic Regulation summer internship stipend

2018: Amgen Scholars Program scholarship

2017 – 2020 : Scholarship of the Serbian Government for students with high average grade

Oğuz Can Koç



Turkey

Oğuz Can Koç

EDUCATION

College / University

Boğaziçi University

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Genetics

Lab Experience

PCR, molecular cloning, bacterial transformation, agarose gel electrophoresis, plasmid and genomic DNA isolation, site-directed mutagenesis, mammalian cell culture, transfection (calcium-phosphate method), Lentiviral transduction, immunoprecipitation, His Pull-down, GST Pull-down, SDS-PAGE, Western blotting, immunofluorescence.

Projects / Research

2019 – 2020: Intern/Project student at Laboratory of Post-Translational Modifications, Department of Molecular Biology and Genetics, Boğaziçi University

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018 – 2020: Scholarship by the Boğaziçi University Foundation

Alexandra Kolodyazhnaya

Russian Federation

Alexandra Kolodyazhnaya

EDUCATION

College / University

Novosibirsk State University

Highest Degree

Bachelor of Science (study program Cytology and Genetics)

Major Subjects

Biology, Cytology and Genetics

Lab Experience

Drosophila stocks maintenance, specimen preparation, immunostaining, fluorescence *in situ* hybridisation, PCR, DNA probe labelling, plasmid cloning. Human cell cultivation, bacterial cells cultivation, manipulations with plants and aphids, agrobacterium infiltration, Western blot, plant-mediated RNAi. Python (basic level), Linux (basic).

Projects / Research

2017 – 2020: Effects of mutations in the *Drosophila melanogaster* Rif1 Ggene on the replication and underreplication of pericentromeric heterochromatin in salivary gland polytene chromosomes. Institute of Molecular and Cell Biology SB RAS, Novosibirsk, Russia

2018: Aphid-plant interactions, John Innes Centre, Norwich, UK

2017: Optimizing conditions for the high-throughput screening by sequencing (HiTSeq) experiment. Broad Institute of MIT and Harvard, Cambridge, USA

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2016 – 2017: Grant of the President of Russian Federation for individuals with outstanding abilities

2017: Zimin Foundation SMTB Alumni Summer Research Programme scholarship

India

Priya Kumar

EDUCATION

College / University

Indian Institute of Technology Bombay, India

Highest Degree

Master of Science

Major Subjects

Biotechnology

Lab Experience

Gel electrophoresis, spectrophotometry, CD and fluorescence spectroscopy, microbial identification, DNA isolation, PCR amplification, transformation, protein expression and purification, SDS PAGE, chemotaxis and paralysis assays with *C. elegans*, DPPH assay for antioxidant activity, basics of C-programming, database searches, BLAST and HMM profiling.

Projects / Research

2019 – 2020: Identification of phosphoglycosyltransferases (PGTs) from whole-genome sequences using homology-based functional annotation. MSc Project, IIT Bombay

2019: Studying the effect of cyclotides on the formation of β-amyloid using chemotaxis and paralysis assays on *C. elegans*. Summer Research Internship, NCBS Bangalore

2017 – 2018: Comparison of antioxidant activity and SDS-PAGE profiles of self-cultivated and commerical species of local mushrooms, DBT Star Scheme Project

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2020: Institute Silver Medal, IIT Bombay 58th Convocation Day

2019: Mary Yoshio Translational Hexagon Award, Fujio Cup Quiz, Japan

2018: Academic Excellence Award in BSc Biotechnology, Fergusson College

Nepal

Sumeru Panta

EDUCATION

College / University

Sri Venkateswara College, University of Delhi

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry, Cell Biology, Immunology, Membrane Biology

Lab Experience

Spectrophotometric analysis, microscopy, enzymatic assays, chromatographic techniques, polymerase chain reaction (PCR), electrophoresis (SDS-PAGE, agarose), protein purification, nucleic acids isolation from plants and animal tissues, plasmid DNA isolation from *E. coli* cells, Western blotting, immunological techniques, lab experience with mice and *Drosophila*, basic bioinformatics tools and software, handling EEG.

Projects / Research

2018 – 2020: To evaluate the condition of Delayed Sleep Phase Disorder in urban teens and correlate it with the stress levels. Dr Nandita Narayanasamy, Sri Venkateswara College, University of Delhi

2019: Genotyping of Wild type, Syngap1 and Yfp mice and analysis of the expression of β-ACTIN protein as a control in wild type mice through Western blotting. James Clement Lab, Neuroscience Unit, JNCASR, Bengaluru

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: Stipend by Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), Bengaluru

Kimberly Quililan

Philippines

Kimberly Quililan

EDUCATION

College / University

University of the Philippines Diliman

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Biotechnology

Lab Experience

gDNA/RNA extraction, gene cloning, site-directed mutagenesis, Western blot, qPCR, Hi-C, capture Hi-C, transfection via lipofection and electroporation, immunocytochemistry, cancer assays (wound migration and Caspase 3/7 GLO apoptosis assay).

Projects / Research

2020: 3D chromatin interactions of the immunoglobulin locus in lymphoma. Beekman Group, Center for Genomic Regulation (CRG), Barcelona, Spain.

2019 – 2020: Drug Discovery: Screening synthetic compounds and lead hits for their ADME-Tox properties. National Institute of Molecular Biology and Biotechnology, Philippines.

2019: Investigating promoter preferences of cofactor and viral synthetic activators using STAP-Seq in human cells. Stark Group, IMP, Vienna Biocenter, Vienna, Austria.

2017 – 2018: Reciprocal regulation of the putative ceRNAs PIK3CA and ZNF148 through miR-506. Bachelor's thesis, University of the Philippines Diliman, Philippines

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2014 – 2018: Gerry Roxas Leadership Scholarship

Rahul Shaha

India

Rahul Shaha

EDUCATION

College / University

Indian Institute of Technology Bombay

Highest Degree

Master of Science Biotechnology

Major Subjects

Cell Biology, Biophysics, Biochemistry, Immunology, Enzymology, Molecular Biology

Lab Experience

Wet Lab: Fluorescence, CD and UV-visible spectroscopy, cloning and expression of protein. Dry Lab: Supervised machine learning using Weka Tool, modelling of proteins, protein structure visualization using PyMOL and Coot, molecular docking using AutoDock.

Projects / Research

2019 – 2020: Predication of Donor substrates of glycosyltransferases using *in-silico* approaches

2019: Study of weak interactions in protein and developing a program to predict Pi-Pi interaction between carbonyl residues in PDB file of protein

2016 – 2017: Extraction of microbial enzymes for the preparation of biological detergent

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018 – 2020: DBT scholarship for MSc Biotechnology

2019: MYTH (Mary-Yoshio Translational Hexagon) Award for Fujio-Cup quiz, Japan

2018: Offered Junior Research Fellowship (JRF) award by CSIR India (All India Rank 61)

2016: Awarded Kishore Vaigyanik Protsahan Yojana (KVPY) fellowship by the Department of Science and Technology, India

Bulgaria

Nikola Todorov

EDUCATION

College / University

The University of York

Highest Degree

Bachelor of Science (with an year in industry)

Major Subjects

Molecular Cell Biology

Lab Experience

Molecular Biology: (derived) Cleaved Amplified Polymorphic Sequence molecular marker design and utilization in plants, molecular cloning via restriction/ligation and DNA assembly, single-cell transcriptomics on 10x Genomics. Microbiology: Serial dilutions, Gram staining. Mammalian Cell culture: Chinese hamster ovarian cells. Biochemistry: Enzyme kinetics by spectrophotometry, protein chromatography and nickel-histidine pull-down. Other: Fluorescent microscopy of GFP-tagged proteins in yeast, surface plasmon resonance (of soluble T-cell receptors). Dry Lab: AutoDock Vina for docking small molecules to enzyme active sites.

Projects / Research

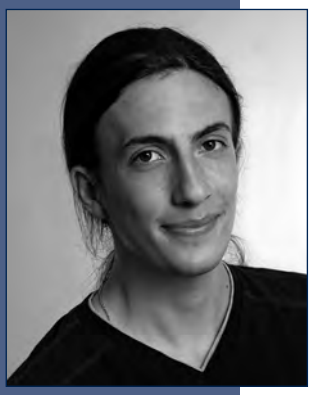
2019 – 2020: Towards functional studies of the barley time for coffee ortholog: Annotation of nucleotide sequence, genotyping and *in silico* characterization of missense mutations, BSc Project at The University of York

2018 – 2019: A streamlined method for expression cloning of paired αβ T-cell receptors from single cells via isothermal DNA assembly, Year in Industry Project, Immunocore Ltd

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018: Best Academic Performance Prize for Stage 2 Biology (University of York)



Colombia

Juan Camilo Torres Bonilla

EDUCATION

College / University

Hochschule Bonn-Rhein-Sieg; Radboud University, Semester abroad

Highest Degree

Bachelor of Science

Major Subjects

Medical biotechnology, Protein and genetic engineering

Lab Experience

Molecular cloning, protein expression, and IMAC purification, ELISA, Cell culture, Gels and standard molecular biology techniques, Computer modelling (COMSOL Multiphysics).

Projects / Research

2020: Rewiring cancer cell signaling through a toxin-inspired system for cytosolic protein delivery. “A computational investigation of *in-vivo* cytosolic protein delivery for cancer therapy” - soon to be submitted for publication, first author. Biochemistry Dept. at the Radboud Institute for Molecular Life Sciences, Nijmegen (NL)

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019 – 2020: Erasmus+ Scholarship

2018 – 2019: Deutschlandstipendium

Chile

Josefa Torres

EDUCATION

College / University

University of Concepción

Highest Degree

Biochemist

Major Subjects

Biochemistry, Cell Biology, Clinical Chemistry

Lab Experience

Immunocytochemistry, fluorescence microscopy, Western blot, proton NMR, UV/Vis spectroscopy, bacterial culture and transformation, molecular cloning, PCR, DNA purification, agarose gel electrophoresis, transfections, ELISA, mouse hippocampal neuron culture, rotarod performance test and clinical biochemistry.

Projects / Research

2019: Stereospecific Inhibition of Ethanol Potentiation on Glycine Receptor by M554 stereoisomers

2017 – 2019: Internalization of folate-conjugated dendrimers mediated by folate-receptor

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018: Production Development Corporation (CORFO) funding for thesis research

Greece

Dimitra Tsouraki

EDUCATION

College / University

National and Kapodistrian University of Athens (N.K.U.A.)

Highest Degree

Bachelor of Science

Major Subjects

Biology

Lab Experience

Lentivirus production, transduction, FastFUCCI system, immunocytochemistry, microscopy, electrophoresis, hematoxylin eosin staining, Maxi prep, polymerase chain reaction, 3´ Rapid Amplification of cDNA Ends (3´ RACE).

Projects / Research

2019 – 2020: Visiting student, Department of Biochemistry and Molecular Biology, Faculty of Biology, School of Sciences, N.K.U.A.

2018 – 2020: Study of epigenetic modifications in cancer cells that are related to chemoresistance. Faculty of Biology, School of Sciences, N.K.U.A. and Biomedical Research Foundation, Academy of Athens (BRFAA)

2019: Tsouraki D. and Kontos CK. CEACAM19 (carcinoembryonic antigen related cell adhesion molecule 19). Atlas Genet Cytogenet Oncol Haematol, 2019

2017: The significant contribution of immunotherapy in cancer treatment - applications and expectations in Greece. 3rd Symposium on Advances in Cancer Immunology and Immunotherapy, 2-4 November 2017 Athens, Greece

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

Russian Federation

Lidiia Tynianskaia

EDUCATION

College / University

Ruprecht Karl University of Heidelberg

Highest Degree

Bachelor of Science

Major Subjects

Cell Biology, Biochemistry, Molecular Biology, Genetics, Neurobiology, Developmental Biology

Lab Experience

Protein purification and analysis methods, PCR-based techniques, Western blot, Immunostaining, fluorescence microscopy, confocal imaging, preparation and handling of primary neuronal cultures, The International Zebrafish and Medaka Course (IZMC), agarose gel electrophoresis, *in ovo* electroporation, retinal wholemount, genome editing using the CRISPR-Cas system.

Projects / Research

2020: Time- and size-dependent changes in protein distribution under conditions of excitotoxicity-mediated nuclear permeability breakdown in mouse cortical neurons. Department of Neurobiology, Interdisciplinary Center for Neuroscience, Heidelberg

2019: Optogenetic inhibition of astrocytic PKA signaling. Department of Neurobiology, Interdisciplinary Center for Neuroscience, Heidelberg

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

Turkey

Çağıl Urhan

EDUCATION

College / University

Middle East Technical University

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Genetics

Lab Experience

Nucleic acid isolation, bacterial and yeast transformation, cDNA synthesis, PCR, electrophoresis (agarose, SDS-PAGE and urea PAGE), BCA assay, RNase H activity assay, nucleotide incorporation assay, ^{32}P labeling of RNA and DNA, chromatography (TLC and column), *Drosophila melanogaster* husbandry.

Projects / Research

2019: Inhibition of the RNase H and Polymerase Activity of HIV Reverse Transcriptases, Department of Virology and Microbiology, Centro de Biología Molecular Severo Ochoa

2018: Analysis of Immunohistochemistry Results for Diagnosis of Breast Cancer, Department of Pathology, Ufuk University Dr. Rıdvan Ege Hospital

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: ERASMUS + Traineeship Grant

Malena von Elling-Tammen

Germany

Malena von Elling-Tammen

EDUCATION

College / University

Georg-August-Universität Göttingen

Highest Degree

Master of Science

Major Subjects

Molecular Medicine

Lab Experience

Cell culture, DNA and RNA isolation, immunohistochemistry, FISH, ELISA, Western blot, chorioallantoic membrane assay, multi electrode array, STED microscopy.

Projects / Research

2019 – 2020: Internship, Dr. Manuel Nietert and Dr. Jürgen Dönitz, Department of Medical Bioinformatics, University Medical Center Göttingen

2019: The Effects of Biological Rhythms on Synaptic Activity in Dissociated Hippocampal Neurons. Prof. Dr. Silvio O. Rizzoli, Institute for Neuro and Sensory Physiology, University Medical Center Göttingen

2018 – 2019: Investigating Nanoscale Dendritic Spine Architecture Using Super-Resolution Microscopy. Dr. Martin Helm, Institute for Neuro and Sensory Physiology, University Medical Center Göttingen

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018 – 2019: Deutschlandstipendium

2016: Niedersachsenstipendium

Zehra Vural

Turkey

Zehra Vural

EDUCATION

College / University

Izmir Institute of Technology

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Genetics

Lab Experience

Total DNA and RNA isolation, agarose gel electrophoresis, SDS-PAGE, Western blot, PCR, RT-qPCR, cloning techniques, mammalian cell culture, BrdU Assay, MTT assay, soft agar colony formation assay, siRNA and cDNA transfections, immunofluorescence assays, CRISPR with D10A nickase, confocal microscopy, Image J analysis.

Projects / Research

2019 – 2020: Generation of cell lines with fluorescently-tagged endogenous proteins implicated in cholesterol metabolism by CRISPR. Dr. Rainer Pepperkok, Cell Biology and Biophysics, EMBL

2017 – 2019: Examination of Connexin32 protein overexpression in normal breast MCF10A and breast cancer MDA-MB-231 cells in terms of cell proliferation and regulation of cell cycle. Assistant Professor Gülistan Meşe Özçivici, Department of Molecular Biology and Genetics, IZTECH

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2018 and 2019 – 2020: Erasmus Scholarship

2019: Highest Ranked Student among all Students, IZTECH

Germany

Lucia Winkler

EDUCATION

College / University

Georg-August-Universität Göttingen

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry

Lab Experience

Membrane model systems: solid supported bilayers, proteoliposomes, Langmuir-Blodgett-films. DNA techniques: purification, Gateway cloning, double enzyme digestion. Protein techniques: recombinant expression in *E.coli*, purification through affinity chromatography, Western blot. Other: Cultivation of anaerobic bacteria, confocal microscopy.

Projects / Research

2020: Analysis of the diatom protein Silicanin-1 in a model membrane system (Bachelor thesis, supervisor: Prof. Dr. Claudia Steinem, Institute of Organic and Biomolecular Chemistry, Göttingen)

2019: Metagenomic characterization of microbial consortia involved in the sulfur cycle (Students' research project, supervisor: PD Dr. Michael Hoppert, Institute of Microbiology and Genetics, Göttingen)

2015: Role of MYB transcription factors in heat stress in *Arabidopsis thaliana* (Research internship, supervisor: Dr. Yariv Brotman, MPI of Molecular Plant Physiology, Golm)

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

Since 2017: German Academic Scholarship Foundation

2015: Scholarship by the German Life Science Association (VBIO) for a research internship

P. R. China

Yumeng Zhan

EDUCATION

College / University

China Agricultural University

Highest Degree

Bachelor of Science

Major Subjects

Biological Sciences, Mathematics and Applied Mathematics (Double Degree)

Lab Experience

Molecular cloning, protein expression in bacteria and insect cells, protein purification (affinity chromatography, ion-exchange chromatography, SEC, SEC-MALS, etc.), protein-protein interaction analysis (pull-down assays, ITC, MST, etc.), enzyme assays.

Projects / Research

2019 – 2020: Reconstitution of synaptic plasticity *in vitro*. The Hong Kong University of Science and Technology

2017 – 2019: Expression, purification and protein-protein interaction analysis of Dengue virus nonstructural protein NS3 and NS4B. China Agricultural University

Scholarships / Awards

2020 – 2021: Stipend by the International Max Planck Research School

2019: The Hundred Excellent Undergraduate Theses of China Agricultural University

2017, 2018, 2019: The Second Prize Scholarship of China Agricultural University

Faculty

Name		Group / Institution	
Sarah	Adio	Single Molecule Biochemistry	U Göttingen
Mathias	Bähr	Neurology	UMG
Holger	Bastians	Cellular Oncology	UMG
Rüdiger	Behr	Degenerative Diseases	DPZ
Tim	Beißbarth	Statistical Bioinformatics	UMG
Markus	Bohnsack	Molecular Biology	UMG
Gerhard H.	Braus	Molecular Microbiology and Genetics	U Göttingen
Bertram	Brenig	Molecular Biology of Livestock	U Göttingen
Nils	Brose	Molecular Neurobiology	MPI em
Patrick	Cramer	Molecular Biology	MPI bpc
Rolf	Daniel	Genomic and Applied Microbiology	U Göttingen
Matthias	Dobbelstein	Molecular Oncology	UMG
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	UMG
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	UMG
Helmut	Grubmüller	Theoretical and Computational Biophysics	MPI bpc
Ufuk	Günesdogan	Developmental Biology	U Göttingen
Heidi	Hahn	Human Genetics	UMG
Kai	Heimel	Microbial Cell Biology	U Göttingen
Stefan	Hell	NanoBiophotonics	MPI bpc
Till	Ischebeck	Plant Biochemistry	U Göttingen
Reinhard	Jahn	Neurobiology	MPI bpc
Andreas	Janshoff	Biophysical Chemistry	U Göttingen
Stefan	Jakobs	Mitochondrial Structure and Dynamics	MPI bpc
Dieter	Klopfenstein	Biophysics	U Göttingen

U Göttingen = University of Göttingen, UMG = University Medical Center Göttigen, MPI bpc = Max Planck Institute for Biophysical Chemistry, MPI em = Max Planck Institute for Experimental Medicine, DPZ = German Primate Center

Name		Group / Institution	
Wilfried	Kramer	Molecular Genetics	U Göttingen
Heike	Krebber	Molecular Genetics	U Göttingen
Péter	Lénárt	Live-cell Imaging Facility	MPI bpc
Volker	Lipka	Plant Cell Biology	U Göttingen
Reinhard	Lührmann	Cellular Biochemistry	MPI bpc
Michael	Meinecke	Molecular Membrane Biology	UMG
Burkhard	Morgenstern	Bioinformatics	U Göttingen
Tobias	Moser	Auditory Neuroscience	UMG
Klaus-Armin	Nave	Neurogenetics	MPI em
Argyris	Papantonis	Translational Epigenetics	UMG
Stefanie	Pöggeler	Genetics of Eukaryotic Organisms	U Göttingen
Stefan	Pöhlmann	Infection Biology	DPZ
Peter	Rehling	Biochemistry	UMG
Jochen	Rink	Tissue Dynamics and Regeneration	MPI bpc
Silvio	Rizzoli	Neuro- and Sensory Physiology	UMG
Marina	Rodnina	Physical Biochemistry	MPI bpc
Melina	Schuh	Meiosis	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	UMG
Kai	Tittmann	Molecular Enzymology	U Göttingen
Henning	Urlaub	Bioanalytical Mass Spectrometry	MPI bpc
Lutz	Walter	Primate Genetics	DPZ
Jürgen	Wienands	Cellular and Molecular Immunology	UMG
Marcel	Wiermer	Molecular Biology of Plant-Microbe Interactions	U Göttingen
Ernst	Wimmer	Developmental Biology	U Göttingen

U Göttingen = University of Göttingen, UMG = University Medical Center Göttigen, MPI bpc = Max Planck Institute for Biophysical Chemistry, MPI em = Max Planck Institute for Experimental Medicine, DPZ = German Primate Center

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e-mail: sadio@gwdg.de

Further Information

http://www.uni-goettingen.de/en/579309.html

Sarah Adio

GZMB Research Group Leader

- PhD thesis at the Ludwig-Maximilians University of München, 2003 – 2007
- Post-doctoral fellow at the National Institute for Medical Research (NIMR), London, United Kingdom, 2007 – 2008
- Post-doctoral researcher at the Max-Planck Institute for Biophysical Chemistry Göttingen, 2008 – 2017
- Research Group Leader at the Göttingen Center for Molecular Biology (GZMB) of the University of Göttingen, since 2017

Major Research Interests

Molecular machines are enzymes that generate directed motion within cells. Their action is required in virtually all vital processes. Prime examples for molecular machines are ribosomes, which read the messenger RNA in order to translate it into proteins. My research centers on the understanding of how ribosomes generate motion along the mRNA and how the internal motions of the ribosome translate into its function in protein synthesis. To this end, my group employs a multidisciplinary approach bridging state-of-the-art single-molecule fluorescence microscopy with classic molecular biology and biochemistry techniques. Our work aims to visualize the multitude of small-scale intermolecular movements on individual ribosome complexes as well as the large scale displacement of single ribosomes on the mRNA. On single molecule level, we establish methods to address fundamental questions on the mechanisms of ribosome motility:

1. How fast and processive does the ribosome transit along the mRNA
2. How does the ribosome negotiate obstacles imposed by RNA secondary structure or RNA binding proteins?
3. How is ribosome motion regulated?

Selected Recent Publications

Adio S, Sharma H, Senyushkina T, Karki P, Maracci C, Wolgemuth I, Holtkamp W, Peske F, Rodnina MV (2018) Dynamics of ribosomes and release factors during translation termination in *E.coli*. eLife: e34252

Sharma H, Adio S, Senyushkina T, Belardinelli R, Peske F, Rodnina MV (2016) Kinetics of spontaneous and EF-G-accelerated rotation of ribosomal subunits. Cell Rep 16(8): 2187-2196

Adio S, Senyushkina T, Peske F, Fischer N, Wintermeyer W, Rodnina M (2015) Fluctuations between multiple EF-G-induced chimeric tRNA states during translocation on the ribosome. Nat Commun 6: 7442

Adio S, Jaud J, Ebbing B, Rief M, Woehlke G (2009) Dissection of kinesin's processivity. PLoS One 4(2): e4612

Mayr MI , Hümmer S, Bormann J, Grüner T, Adio S, Woehlke G, Mayer TU (2007) The human kinesin Kif18A is a motile microtubule depolymerase essential for chromosome congression. Curr Biol 17(6): 488-98

Adio S, Bloemink M, Hartel M, Leier S, Geeves MA, Woehlke G (2006) Kinetic and mechanistic basis of the nonprocessive Kinesin-3 motor NcKin3. J Biol Chem 281(49): 37782-93

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e-mail: mbaehr@gwdg.de

Further Information

http://www.baehrlab.med.uni-goettingen.de/

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

http://www.moloncol.med.uni-goettingen.de/de/content/researchgroups/101.html
and: http//www.for2800.de

Holger Bastians

Professor for Cellular Oncology

- Speaker of the DFG Research Unit 2800 (FOR2800) "Chromosome Instability: Cross-talk of DNA replication stress and mitotic dysfunction", since 2019
- Professor for Cellular Oncology, University Medical Center, Göttingen (UMG), since 2013
- Heisenberg-Professor for 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

A hallmark of human cancer is genome instability. A major form of genome instability is chromosomal instability (CIN), which is defined as the perpetual gain or loss of whole chromosomes leading to aneuploidy. Evolving aneuploidy results in massive changes in gene expression and drives adaptation and the aquirement of new tumor phenotypes including metastasis and therapy resistance, a process now known as tumor evolution. Since chromosome missegregation takes place during mitosis it is pivotal to identify the mitotic defects underlying CIN. In fact, our lab discovered that abnormal microtubule dynamics during mitosis acts as a major trigger for CIN in human cancer cells. Moreover, we identified several oncogenes and tumor suppressor genes including BRCA1 and p53/p73 as well as Wnt signaling as important regulators of CIN. Most recently, we surprisingly found that also defects during DNA replication, so-called replication stress, can contribute to mitotic dysfunction and CIN. These cross-talks between DNA replication and mitosis are subject of our newly established DFG-Research Unit (FOR2800), in which we collaborate with seven laboratories in Göttingen and in Germany to address this important question regarding the origin of genome instability (see: www.for2800.de). Current work in our lab focuses on the following research questions:

1. How do oncogenes and tumor suppressors (e.g. BRCA1) and other cancer-relevant signaling pathways (e.g. Wnt signaling) (de)regulate mitosis to trigger CIN?
2. What are the molecular mechanisms of mitotic chromosome missegregation in response to deregulated microtubule dynamics?
3. What are the cross-talk mechanisms between DNA replication stress and mitotic chromosome missegregation?

Selected Recent Publications

Böhly N, Kistner M, Bastians H (2019) Mild replication stress causes aneuploidy by deregulating microtubule dynamics in mitosis. Cell Cycle Aug: 1-14

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 micro-tubule 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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Rüdiger Behr

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- 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 ofGenetics, 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 pluripotent stem cells (ESCs and iPSCs) from different primate species including humans. We use these stem cells for basic and translational (preclinical) projects. For instance, we differentiate iPSCs into cardiomyocytes. As gene editing technologies we apply different CRISPR/Cas approaches and for gene expression reversible transposon, episomal and self-replicating RNA constructs. Based on our reproductive biology expertise, we are also aiming at the genetic modification of monkeys in order to establish human disease models. They will be used for testing of novel cell and / or gene-based therapies. Finally, we investigate germ cell development in primates.

Selected Recent Publications

Stauske M, Rodriguez Polo I, Haas W, Knorr DY, Borchert T, Streckfuss-Bömeke K, Dressel R, Bartels I, Tiburcy M, Zimmermann WH, Behr R (2020) Non-Human Primate iPSC Generation, Cultivation, and Cardiac Differentiation under Chemically Defined Conditions. Cells 9(6):1349

Wahab F, Drummer C, Mätz-Rensing K, Fuchs E, Behr R (2020) Irisin is expressed by undifferentiated spermatogonia and modulates gene expression in organotypic primate testis cultures. Mol Cell Endocrinol 504:110670

Cardoso-Moreira M, Halbert J, Valloton D, Velten B, Chen C, Shao Y, Liechti A, Ascenção K, Rummel C, Ovchinnikova S, Mazin PV, Xenarios I, Harshman K, Mort M, Cooper DN, Sandi C, Soares MJ, Ferreira PG, Afonso S, Carneiro M, Turner JMA, VandeBerg JL, Fallahshahroudi A, Jensen P, Behr R, Lisgo S, Lindsay S, Khaitovich P, Huber W, Baker J, Anders S, Zhang YE, Kaessmann H (2019) Gene expression across mammalian organ development. Nature 571(7766): 505-509

Wahab F, Drummer C, Schlatt S, Behr R (2017) 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

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

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- 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

Chereda H, Bleckmann A, Kramer F, Leha A, Beißbarth T (2019) Utilizing Molecular Network Information via Graph Convolutional Neural Networks to Predict Metastatic Event in Breast Cancer. Stud Health Technol Inform 267:181-186

Sitte M, Menck K, Wachter A, Reinz E, Korf U, Wiemann S, Bleckmann A, Beißbarth T (2019) Reconstruction of Different Modes of WNT Dependent Protein Networks from Time Series Protein Quantification. Stud Health Technol Inform 267:175-180

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

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

Bohnsack KE, Bohnsack MT (2019) Uncovering the assembly pathway of human ribosomes and its emerging links to disease. EMBO J 38: e100278

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

Warda AS*, Kretschmer J*, Hackert P, Lenz C, Urlaub H, Höbartner C, Sloan KE, Bohnsack MT (2017) Human METTL16 is a N6-methyladenosine (m6A) methyltransferase that targets pre-mRNAs and various non-coding RNAs. EMBO Rep 18: 2004-2014

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

Köhler AM, Harting R, Langeneckert AE, Valerius O, Gerke J, Meister C, Braus GH (2019) Integration of fungal specific CandA-C1 into a trimeric CandA complex allowed splitting of the gene for the conserved receptor exchange factor of CullinA E3 ubiquitin ligases in Aspergilli. mBio 10: e01094-19

Bui TT, Harting R, Braus-Stromeyer SA, Tran VT, Leonard M, Höfer A, Abelmann A, Bakti F, Valerius O, Schlüter R, Stanley CE, Ambrósio A, Braus GH (2019) Verticillium dahliae transcription factors Som1 and Vta3 control microsclerotia formation and sequential steps of plant root penetration and colonisation to induce disease. New Phytol 221: 2138-2159

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

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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 in different species:
Bos taurus
Leg and feet disease (digital dermatitis)
Early embryonal death (lethal haplotypes)
Male infertility
Bovine spastic paresis
Congenital hypotrichosis
Canis familiaris
Hemophilia A
Deafness
Honey bee
Hygienic behaviour
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

Kwiatkowski M, Asif AR, Schumacher J, Brenig B, Zischler H, Herlyn H (2020) Intra-Protein Coevolution Is Increasingly Functional with Greater Proximity to Fertilization. Cytogenet Genome Res 160: 295-308

Leidenfrost RM, Bansch S, Prudnikow L, Brenig B, Westphal C, Wunschiers R (2020) Analyzing the Dietary Diary of Bumble Bee. Front Plant Sci 11: 287

Liu W, Sender S, Kong W, Beck J, Sekora A, Bornemann-Kolatzki K, Schuetz E, Junghanss C, Brenig B, Nolte I, Murua Escobar H (2020) Establishment and characterization of stable red, far-red (fR) and near infra-red (NIR) transfected canine prostate cancer cell lines. Cancer Cell Int 20: 139

Shan S, Xu F, Bleyer M, Becker S, Melbaum T, Wemheuer W, Hirschfeld M, Wacker C, Zhao S, Schutz E, Brenig B (2020) Association of alpha/beta-Hydrolase D16B with Bovine Conception Rate and Sperm Plasma Membrane Lipid Composition. Int J Mol Sci 21(2): 627

Viesser JA, de Melo Pereira GV, de Carvalho Neto DP, Vandenberghe LPS, Azevedo V, Brenig B, Rogez H, Goes-Neto A, Soccol CR (2020) Exploring the contribution of fructophilic lactic acid bacteria to cocoa beans fermentation: Isolation, selection and evaluation. Food Res Int 136: 109478

Zhang X, Hirschfeld M, Beck J, Kupke A, Kohler K, Schutz E, Brenig B (2020) Osteogenesis imperfecta in a male holstein calf associated with a possible oligogenic origin. Vet Q 40: 58-67

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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

Imig C, López-Murcia FJ, Maus L, Hojas Garcia-Plaza I, Mortensen LS, Schwark M, Schwarze V, Angibaud J, Nägerl UV, Taschenberger H, Brose N*, Cooper BH* (2020) Ultrastructural imaging of activity-dependent synaptic membrane-trafficking events in cultured brain slices. Neuron, in press. (*joint corresponding authors)

Lopez-Murcia FJ, Reim K, Jahn O, Taschenberger H*, Brose N* (2019) Acute Complexin knock-out abates spontaneous and evoked transmitter release. Cell Rep 26: 2521-2530 (*joint corresponding authors)

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)

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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Patrick Cramer

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- 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

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 structural biology, in particular cryo-electron microscopy, and complementary functional studies to unravel the three-dimensional structure of large macromolecular complexes involved in transcription. We also develop functional genomics and sequencing methods and computational approaches to unravel the cellular mechanisms of genomic regulation. These efforts led to molecular movies of transcription and provided insights into gene-regulatory cellular networks. Our aim is to understand the functional genome as a regulatory network based on the underlying structural and molecular mechanisms. In the future we will concentrate on transcription regulation within a chromatin context by combining biochemistry, structural biology, functional genomics, and bioinformatics.

Selected Recent Publications

O'Reilly FJ et al (2020) In-cell architecture of an actively transcribing-translating expressome. Science 369(6503): 554-557

Hillen HS, Kokic G, Farnung L, Dienemann C, Tegunov D, Cramer P (2020) Structure of replicating SARS-CoV-2 polymerase. Nature 584(7819): 154-156

Dodonova SO, Zhu F, Dienemann C, Taipale J, Cramer P (2020) Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. Nature 580(7805): 669-672

Wagner FR, Dienemann C, Wang H, Stützer A, Tegunov D, Urlaub H, Cramer P (2020) Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. Nature 579(7799): 448-451

Cramer P (2019) Organization and regulation of gene transcription. Nature 573(7772): 45-54

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, oxido-reductases, 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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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

Wohlberedt K, Klusmann I, Derevyanko PK, Henningsen K, Choo JAMY, Manzini V, Magerhans A, Giansanti C, Eischen CM, Jochemsen AG, Dobbelstein M (2020) Mdm4 supports DNA replication in a p53-independent fashion. Oncogene 39(25):4828-4843

Klusmann I, Wohlberedt K, Magerhans A, Teloni F, Korbel JO, Altmeyer M, Dobbelstein M (2018) Chromatin modifiers Mdm2 and RNF2 prevent RNA:DNA hybrids that impair DNA replication. Proc Natl Acad Sci U S A 115(48): E11311-E11320

Schulz-Heddergott R, Stark N, Edmunds SJ, Li J, Conradi LC, Bohnenberger H, Ceteci F, Greten FR, Dobbelstein M*, Moll UM* (2018) Therapeutic Ablation of Gain-of-Function Mutant p53 in Colorectal Cancer Inhibits Stat3-Mediated Tumor Growth and Invasion. Cancer Cell 34(2): 298-314

Sriraman A, Dickmanns A, Najafova Z, Johnsen SA, Dobbelstein M (2018) CDK4 inhibition diminishes p53 activation by MDM2 antagonists. Cell Death Dis 9(9): 918

Li Y, Köpper F, Dobbelstein M (2018) Inhibition of MAPKAPK2/MK2 facilitates DNA replication upon cancer cell treatment with gemcitabine but not cisplatin. Cancer Lett. Apr 25

Wienken M, Moll UM, Dobbelstein M (2017) Mdm2 as a chromatin modifier. J Mol Cell Biol 9(1): 74-80

Kramer D, Stark N, Schulz-Heddergott R, Erytch N, Edmunds S, Roßmann L, Bastians H, Concin N, Moll UM*, Dobbelstein M* (2017) Strong antitumor synergy between DNA crosslinking and HSP90 inhibition causes massive premitotic DNA fragmentation in ovarian cancer cells. Cell Death Differ 24(2): 300-316

Klusmann I, Rodewald S, Müller 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

Sriraman A, Li Y, Dobbelstein M (2016) Fortifying p53 - beyond Mdm2 inhibitors. Aging (Albany NY) 8(9): 1836-1837

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

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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

Alex Faesen

Research Group Leader, Max-Planck Institute of Biophysical Chemistry

- 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 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 537 (7619): 249-253

Faesen AC, Luna-Vargas MPA, Sixma TK (2012) The role of UBL domains in Ubiquitin-Specific Proteases. Biochemical Society Transactions 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 18(12): 1550-61

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

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Ivo Feußner

Professor of Biochemistry

- 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 ad-dition 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

Rekhter D, Lüdke D, Ding Y, Feussner K, Zienkiewicz K, Lipka V, Wiermer M, Zhang Y, and Feussner I (2019) Isochorismate-derived biosynthesis of the plant stress hormone salicylic acid. Science 365: 498-502

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)
- Honorary Professor for physical chemistry at University of Göttingen

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, enzymes, intrinsically disordered proteins that some times form phase separated state (liquid liquid phase separation) and drug/target complexes using NMR as well as X-ray crystallography to characterize structure and dynamics. A major project is the investigation of proteins involved in neurodegenerative diseases that are studied in the context of the MBExC and involve NMR and other biophysical methods as well as chemical synthesis and are translated to animal experiments in collaboration. 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. We are specifically interested in the determination of oligomer and fibril structures formed from proteins involved in neurodegenerative diseases that interact with therapeutically or diagnostically interesting small molecules.

Selected Recent Publications

Nath N, Fuentes-Monteverde JC, Pech-Puch D, Rodríguez J, Jiménez C, Noll M, Kreiter A, Reggelin M, Navarro-Vázquez A, Griesinger C (2020) Relative configuration of micrograms of natural compounds using proton residual chemical shift anisotropy. Nat Comm 11: 4372

Wong LE, Bhatt A, Erdmann PS, Hou Z, Maier J, Pirkuliyeva S, Engelke M, Becker S, Plitzko J, Wienands J, Griesinger C (2020) Tripartite phase separation of two signal effectors with vesicles priming B cell responsiveness. Nat Comm 11: 848

Reddy JG, Pratihar S, Ban D, Frischkorn S, Becker S, Griesinger C, Lee D (2018) Simultaneous determination of fast and slow dynamics in molecules using extreme CPMG relaxation dispersion experiments. J. Biomol. NMR 70: 1-9

Martinez Hernandez A, Urbanke H, Gillman AL, Lee J, Ryazanov S, Agbemenyah HY, Benito E, Jain G, Kaurani L, Grigorian G, Leonov A, Rezaei-Ghaleh N, Wilken P, Teran Arce F, Wagner J, Fuhrman M, Caruana M, Camilleri A, Vassallo N, Zweckstetter M, Benz R, Giese A, Schneider A, Korte M, Lal R, Griesinger C, Eichele G, Fischer A (2018) The diphenylpyrazole compound anle138b blocks A channels and rescues disease phenotypes in a mouse model for amyloid pathology, EMBO Mol Med 10: 32-47

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

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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 immunocompromised 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

Emele M F, Joppe F M, Riedel T, Overmann J, Rupnik M, Cooper P, Lia Kusumawati R, Laukien F, Zimmermann O, Bohne W, Groß U, Bader O, Zautner A E (2019) Proteotyping of Clostridioides difficile as alternate typing method to ribotyping is able to differentiate the ribotype 027 from other ribotypes. Frontiers Microbiol, in press.

Acar İ E, Saçar Demirci MD, Groß U, Allmer J (2018) The Expressed MicroRNA-mRNA Interactions of *Toxoplasma gondii*. Front Microbiol J 8: 2630

Seugendo M, Janssen I, Lang V, Hasibuan I, Bohne W, Cooper P, Daniel R, Gunka K, Kusumawati R L, Mshana S E, von Müller L, Okamo B, Ortlepp J R, Overmann J, Riedel T, Rupnik M, Zimmermann O, Groß U (2018) Prevalence and strain characterization of Clostridioides (*Clostridium*) difficile in representative regions of Germany, Ghana, Tanzania and Indonesia – a comparative multi-center cross-sectional study. Frontiers Microbiol

Schneider D, Thürmer A, Gollnow K, Lugert R, Gunka K, Groß U, Daniel R (2017) Gut bacterial communities of diarrheic patients with indications of Clostridioides difficile infection. Sci Data 4: 170152

Zautner A E, Bunk B, Pfeifer Y, Spröer C, Reichard U, Eiffert H, Scheithauer S, Groß U, Overmann J, Bohne W (2017) Monitoring microevolution of OXA-48-producing *Klebsiella pneumoniae* ST147 in a hospital setting by SMRT sequencing. J Antimicrob Chemother 72(10): 2737-2744

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

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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)
- Since 2003 - Director at the Max Planck Institute for Biophysical Chemistry, Göttingen, Head of the Theoretical and Computational Biophysics Department
- Since 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. 20.000 processor cores and ca. 1250 GPUs.

Selected Recent Publications

Igaev M, Grubmüller H (2020) Microtubule instability driven by longitudinal and lateral strain propagation. PloS Comput Biol 16(9):e1008132

Dobrev P, Vemulapalli SPB, Nath N, Griesinger C, Grubmüller H (2020) Probing the accuracy of explicit solvent constant pH molecular dynamics simulations for peptides. J Chem Theory Comput 16:2561-2569

Bock LV, Caliskan N, Korniy N, Peske F, Rodnina MV, Grubmüller H (2019) Thermodynamic control of −1 programmed ribosomal frameshifting. Nat Commun 10:4598

Peng B-Z, Bock LV, Belardinelli R, Peske F, Grubmüller H, Rodnina MV (2019) Active role of elongation factor G in maintaining the mRNA reading frame during translation. Science Adv 5:eaax8030

Igaev M, Grubmüller H (2018) Microtubule assembly governed by tubulin allosteric gain in flexibility and lattice induced fit. eLife 7: 21

von Ardenne B, Mechelke M, Grubmüller H (2018) Structure determination from single molecule X-ray scattering with three photons per image. Nat Commun 9: 2375

Huang J, Rauscher S, Nawrocki G, Ran T, Feig M, de Groot BL, Grubmüller H, MacKerell AD (2017) CHARMM36m: An improved force field for folded and intrinsically disordered proteins. Nat Methods 14: 71 - 73

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

Arenz S, Bock LV, Graf M, Innis CA, Beckmann R, Grubmüller H, Vaiana AC, Wilson DN (2016) A combined cryo-EM and molecular dynamics approach reveals the mechanism of ErmBL-mediated translation arrest. Nat Commun 7: 12026

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

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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

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

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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

Becker M, Bauer J, Pyczek J, König S, Müllen A, Rabe H, Schön MP, Uhmann A, Hahn H (2020) Wif1 suppresses the generation of suprabasal cells in acanthotic skin and growth of basal cell carcinomas upon forced overexpression. J Invest Dermatol 2020, Aug;140(8): 1556-1565.e11

Pyczek J, Khizanishvili N, Kuzyakova M, Zabel S, Bauer J, Nitzki F, Emmert S, Schön MP, Boukamp P, Schildhaus HU, Uhmann A, Hahn H (2019) Regulation and role of GLI1 in cSCC pathogenesis. Front Genet, Dec 4: 10:1185

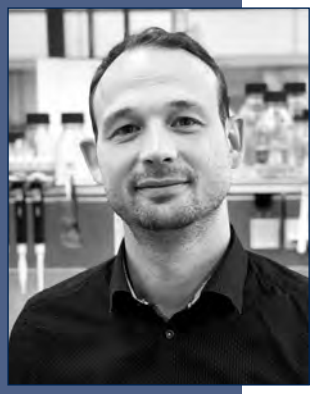
Nitzki F, Cuvelier N, Dräger J, Schneider A, Braun T, Hahn H (2016) Hedgehog/Patched-associated rhabdomyosarcoma formation from Delta1-expressing mesodermal cells. Oncogene 35(22): 2923-31

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, 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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Kai Heimel

apl. Professor of Microbial Cell Biology

- 01/2019 - 03/2019: Guest Professor (invited), University of British Columbia, Vancouver, Canada
- Since 04/2018: apl. Professor for Microbial Cell Biology, Georg-August-University Göttingen
- 04/2012 - 03/2018: 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

Our lab investigates how communication between pathogenic fungi and their plant hosts is achieved. Previous studies revealed an intricate regulatory network between highly conserved signaling pathways and development- and lifestyle-specific regulators, leading to mutual modulation and adaptation of cellular signaling to changing environments. Of central interest is the unfolded protein response (UPR), which serves as a regulatory hub and dominant regulator of fungal virulence.

Specific research interests are:
Pathogenic development of *Ustilago maydis*
Function and regulation of the unfolded protein response (UPR) pathway
UPR signaling and regulation of plant/fungal communication
UPR-MAPK interactions and quantitative control of virulence potential

Selected Recent Publications

Schmitz L, Schwier MA, Heimel K (2019) The unfolded protein response regulates pathogenic development of *Ustilago maydis* by Rok1-dependent inhibition of mating-type signaling. mBio 10(6):e02756-19

Schmitz L, Kronstad JW, Heimel K (2019) Conditional gene expression reveals stage-specific functions of the unfolded protein response in the *Ustilago maydis*–maize pathosystem. Molecular Plant Pathology 21(2):258-271

Pinter N, Hach CA, Hampel M, Rekhter D, Zienkiewicz K, Feussner I, Poehlein A, Daniel R, Finkernagel F, Heimel K (2019) Signal peptide peptidase activity connects the unfolded protein response to plant defense suppression by *Ustilago maydis*. PLoS Pathog 15(4): e1007734

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

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

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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

Pape JK, Stephan T, Balzarotti F, Büchner, R., Lange, F, Riedel D, Jakobs S, Hell SW (2020) Multicolor 3D MINFLUX nanoscopy of mitochondrial MICOS proteins. Proc Natl Acad Sci USA 117: 20607-20614

Gwosch KC, Pape JK, Balzarotti F, Hoess P, Ellenberg J, Ries J, Hell SW (2020) MINFLUX nanoscopy delivers 3D multicolor nanometer resolution in cells. Nat Methods 17: 217-224

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

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

Till Ischebeck

PD Dr. of Biology

- 2005-2008 Doctoral thesis, Department of Plant Biochemistry, University of Göttingen (Germany)
- 2008-2010 Postdoctoral Fellow, Department of Plant Biochemistry, University of Göttingen (Germany)
- 2010-2013 Postdoctoral Fellow (EMBO-fellowship), University of Vienna (Austria)
- since 2013 Junior group leader, Department of Plant Biochemistry, University of Göttingen (Germany)

Major Research Interests

Lipid droplet synthesis and degradation
Pollen biochemistry and metabolism
Primary metabolite profilin

Selected Recent Publications

Kretzschmar FK, Mengel LF, Müller A, Schmitt K, Blersch KF, Valerius O, Braus G, Ischebeck T (2018) PUX10 is a lipid droplet-localized scaffold protein that interacts with CDC48 and is involved in the degradation of lipid droplet proteins. The Plant Cell 30: 2137-2160

Müller AO, Ischebeck T (2018) Characterization of the enzymatic activity and physiological function of the lipid droplet-associated triacylglycerol lipase AtOBL1. New Phytologist 217: 1062-1076

Fornasiero EF, Mandad S, Wildhagen H, Alevra M, Rammner B, Keihani S, Opazo F, Urban I, Ischebeck T, Sakib MS, Fard MK, Kirli K, Centeno TP, Vidal RO, Rahman R-U, Benito E, Fischer A, Dennerlein S, Rehling P, Feussner I, Bonn S, Simons M, Urlaub H, Rizzoli SO (2018) Precisely measured protein lifetimes in the mouse brain reveal differences across tissues and subcellular fractions. Nature Communications 9: 4230

Rotsch AH, Kopka J, Feussner I, Ischebeck T (2017) Central metabolite and sterol profiling divides tobacco male gametophyte development and pollen tube growth into eight metabolic phases. The Plant Journal 92: 129-146

Müller AO, Blersch KF, Gippert AL, Ischebeck T (2017) Tobacco pollen tubes - a fast and easy tool to study lipid droplet association of plant proteins. The Plant Journal 89: 1055-1064

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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
- 2019 President of the University of 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 of the Cell

- 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

Stephan T, Brüser C, Deckers M, Steyer AM, Balzarotti F, Barbot M, Behr TS, Heim G, Hübner W, Ilgen P, Lange F, Pacheu-Grau D, Pape JK, Stoldt S, Huser T, Hell SW, Möbius W, Rehling P, Riedel D, Jakobs S (2020) MICOS assembly controls mitochondrial inner membrane remodeling and crista junction redistribution to mediate cristae formation. EMBO J 39: e104105

Stoldt S, Stephan T, Jans DC, Brüser C, Lange F, Keller-Findeisen J, Riedel D, Hell SW, Jakobs S (2019) Mic60 exhibits a coordinated clustered distribution along and across yeast and mammalian mitochondria. PNAS 116 (20): 9853-9858

Kamper M, Ta H, Jensen NA, Hell SW, Jakobs S (2018) Near-infrared STED nanoscopy with an engineered bacterial phytochrome. Nat Commun 9: 4762

Stoldt S, Wenzel D, Kehrein K, Riedel D, Ott M, Jakobs S (2018) Spatial orchestration of mitochondrial translation and OXPHOS complex assembly. Nat Cell Biol 20: 528–534

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

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, Reuss M, Brakemann T, Eggeling C, Hell SW, Jakobs S (2012) rsEGFP2 enables fast RESOLFT nanoscopy of living cells. Elife 1: e00248

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. Nat Biotech (2011) 29: 942-947

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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

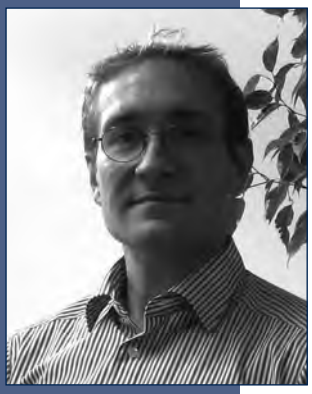
Oelkers M, Witt H, Halder P, Jahn R, Janshoff A (2016) SNARE-mediated membrane fusion trajectories derived from force-clamp experiments. Proceedings of the National Academy of Sciences 113 (46): 13051-13056

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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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

Working in the Department of Molecular Genetics, which is headed by Prof. Dr. H. Krebber, my major scientific interest is focused at present on the interplay of RNA metabolism with other cellular pathways, namely DNA replication/DNA repair and cell cycle/cell division. There is strong genetic evidence that the RNA-binding SR-protein Npl3 from budding yeast, which is involved in many RNA-related cellular processes, also plays an important role in the maintenance of genome stability. We want to further understand the connections between these seemingly unrelated processes. One clue comes from the finding of other labs that RNA-DNA hybrids, so called R-loops, can induce DNA damage and homologous recombination. We try to find out, where in this process Npl3 might be involved, combining genetical and biochemical approaches.

Selected Recent Publications

Zander G, Kramer W, Seel A and Krebber H (2017) *Saccharomyces cerevisiae* Gle2/Rae1 is involved in septin organization, essential for cell cycle progression. Yeast 34: 459-470

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

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

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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

mRNA quality control:
Messenger RNAs are transcribed in the nucleus and translated in the cytoplasm. Thus, it has to be assured that intron containing pre messenger RNAs are retained in the nucleus until processing is completed. RNA quality control allows only fully processed and spliced mRNAs to be transported and translated. Defects lead to diseases such as cancer and neurodegenerative diseases. Our projects functionally study mRNA quality control.

ncRNA functions:
non coding (nc)RNAs make up more than half of all RNAs in cells. However, the knowledge about their cellular functions lack far behind the knowledge of coding mRNAs. In this project we are investigating the function of individual lncRNAs, e.g. those involved in cellular iron metabolism, important to understand iron-related diseases, or the telomerase, important for the unlimited growth of most cancer cells.
We use the eukaryotic model organism *Saccharomyces cerevisiae* that has proven to be pioneer organism for studying fundamental basic scientific questions.

Selected Recent Publications

Becker D, Hirsch AG, Bender L, Lingner T, Salinas G and Krebber H (2019) Nuclear pre-snRNA export is an essential quality assurance mechanism for functional spliceosomes. Cell Reports 27: 3199-3214

Beissel C, Neumann B, Uhse S, Hampe I, Karki P and Krebber H (2019) Translation termination depends on the sequential ribosomal entry of eRF1 and eRF3. Nucleic Acids Research. 47(9): 4798-4813

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

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

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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Péter Lénárt

Research Group Leader and Head of Live-cell Imaging Facility at the MPI bpc

- since 2018 Research Group Leader and Head of Live-cell Imaging Facility, Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany
- 2011 – 2018 Group Leader, European Molecular Biology Laboratory, Heidelberg, Germany
- 2008 – 2011 Staff Scientist, European Molecular Biology Laboratory, Heidelberg, Germany
- 2005 – 2008 Postdoctoral fellow, Laboratory of Jan-Michael Peters, Institute of Molecular Pathology, Vienna, Austria
- 2000 – 2005 PhD Student, Laboratory of Jan Ellenberg, European Molecular Biology Laboratory, Heidelberg, Germany
- 1995 – 2000 Diploma in Biology, Eötvös Loránd University, Budapest, Hungary

Major Research Interests

Oocyte meiosis is a form of cell division specialized to produce the fertilizable egg. Our main interest is understanding how the cell division machinery, the cytoskeleton in particular, adapted to carry out these specialized divisions. For example, oocytes are exceptionally large cells storing nutrients for the embryo that divide very asymmetrically in order to retain these nutrients in a single egg cell. How does the cytoskeleton support divisions in this extreme geometry? Indeed, we showed that, compared to mitosis of small somatic cells, additional, meiosis-specific mechanisms are required. Interestingly, we found that while in somatic cells microtubules dominate, in the oocyte key functions are taken over by the actin cytoskeleton; for example, an actin net transports chromosomes to the forming spindle and actin is also involved in regulating spindle assembly. To explore the conservation and diversity of these meiosis-specific functions, we are using marine model species such as the oocytes of starfish. These oocytes are highly transparent, exceptionally resistant to light and easy to handle, rendering them an excellent model for live cell microscopy. In our future work we aim to further establish these marine models by developing advanced imaging assays and tools for targeted molecular perturbations. In turn we will use these tools to further dissect mechanisms of meiotic divisions. Studying oocyte meiosis is important, as a euploid egg is at the origin of life of any healthy animal and human individual, while the mechanisms are still poorly understood. In addition, understanding how cell division adapted and diversified to such specialized functions will reveal general principles of cellular organization.

Selected Recent Publications

Wesolowska N, Avilov I, Machado P, Geiss C, Kondo H, Mori M, Lénárt P (2020) Actin assembly ruptures the nuclear envelope by prying the lamina away from nuclear pores and nuclear membranes in starfish oocytes. Elife 9: e49774

Burdyniuk M, Callegari A, Mori M, Nedelec F, Lenart P (2018) F-Actin nucleated on chromosomes coordinates their capture by microtubules in oocyte meiosis. J Cell Biol 217(8): 2661-2674

Bun P, Dmitrieff S, Belmonte JM, Nedelec FJ, Lenart P (2018) A disassembly-driven mechanism explains F-actin-mediated chromosome transport in starfish oocytes. eLife 7, pii. e31469

Bischof J, Brand CA, Somogyi K, Majer I, Thome S, Mori M, Schwarz US, Lenart P (2017) A cdk1 gradient guides surface contraction waves in oocytes. Nat Commun 8(1): 849

Borrego-Pinto J, Somogyi K, Karreman MA, Konig J, Muller-Reichert T, Bettencourt-Dias M, Gonczy P, Schwab Y, Lenart P (2016) Distinct mechanisms eliminate mother and daughter centrioles in meiosis of starfish oocytes. J Cell Biol 212(7): 815-827

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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 department is interested in the molecular analysis of plant innate immunity.
Our research is focused on the
1) molecular dissection of mechanisms that control activation of basal defense in the plant model Arabidopsis thaliana (chitin receptor complex formation & processing; downstream signal transduction; cell death activation and containment) [e.g. Erwig et al., 2017; Petutschnig et al., 2014]
2) analysis of plant defense mechanisms that contribute to resistance against fungal pathogens (pathogen invasion control; pathogen-induced cell polarization; orchestrated organelle relocalization; subcellular compartmentalization; production, transport & discharge of toxic metabolites) [e.g. Fuchs et al., 2016]
3) identification of fungal effector molecules that interfere with the plant defense machinery and allow host plant colonization (effector-mediated reprogramming of host plant development; pathogen-induced drought stress tolerance) [e.g. Reusche et al. , 2012; Reusche et al., 2014].

We combine genetics, cell biology, molecular biology and biochemistry in our experimental strategies to gain novel insights into these complex mechanisms.

Selected Recent Publications

Erwig J, Ghareeb H, Kopischke M, Hacke R, Matei A, Petutschnig EK. Lipka V (2017) Chitin-induced and CHITIN ELICITOR RECEPTOR KINASE1 (CERK1) phosphorylation-dependent endocytosis of *Arabidopsis thaliana* LYSIN MOTIF-CONTAINING RECEPTOR-LIKE KINASE5 (LYK5). New Phytologist 215(1): 382-396

Fuchs R, Kopischke M, Klapprodt C, Hause G, Meyer AJ, Schwarzländer M, Fricker MD, and 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, and 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): 955-967

Reusche M, Truskina J, Thole K, Nagel L, Rindfleisch S, Tran VT, Braus-Stromeyer SA, Braus GH, Teichmann T, Lipka V (2014) Infections with the vascular pathogens *Verticillium longisporum* and *Verticillium dahliae* induce distinct disease symptoms and differentially affect drought stress tolerance of *Arabidopsis thaliana*. Environmental and Experimental Botany 108: 23-37

Reusche M, Thole K, Janz D, Truskina J, Rindfleisch S, Drübert C, Polle A, Lipka V*, and Teichmann T (2012). *Verticillium* Infection triggers VASCULAR-RELATED NAC DOMAIN7-Dependent de novo xylem formation and enhances drought tolerance in *Arabidopsis*. Plant Cell 24: 3823-3837, * corresponding author

Reinhard Lührmann

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 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

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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

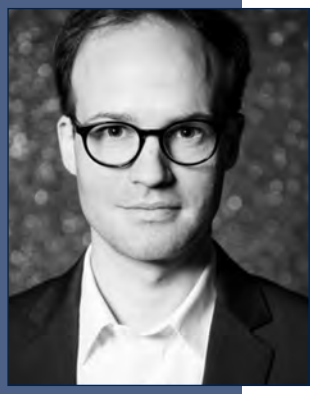
Bao P, Will CL, Urlaub H, Boon KL, Lührmann R (2017) The RES complex is required for efficient transformation of the precatalytic B spliceosome into an activated bact complex. Genes Dev 31: 2416-2429

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

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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- 2007 Dr. rer. nat. University of Osnabrück
- 2008 – 2012 Postdoctoral fellow (with Harvey McMahon, MRC - Laboratory of Molecular Biology, Cambridge, UK
- since 2012 Independent group leader at the Department of Biochemistry II, University Medical Center Göttingen
- 2013 – 2017 Junior Professor of Molecular Membrane Biology at the European Neuroscience Institute Göttingen
- since 2017 Professor of Membranebiochemistry at the Department of Cellular Biochemistry, University Medical Center Göttingen

Major Research Interests

Biological membranes exhibit a wide variety of shapes associated with particular functions. These give rise to the complex and beautiful forms observed within cells and their organelles. Our group is interested in the fundamental molecular principles that lead to these shapes. We study the effects that membrane proteins have on membrane structures. We are also interested in the effects that different membrane morphologies have on the distribution and localization of membrane proteins into clusters and microdomains. Taking a multi-disciplinary approach, we use model membranes to reconstitute the structure and function of organelles *in vitro* and then correlate these results with *in vivo* imaging techniques.
One class of membrane proteins we are particularly interested in are ion-channels. Ion-channels cover a large variety of different molecular functions. Well-studied examples are protein translocases, potassium channels and bacterial pore forming toxins. We use biochemical and biophysical approaches to study the function and regulation of ion-channels on a single molecule level.

Selected Recent Publications

Denkert N, Schendzielorz AB, Barbot M, Versemann L, Richter F, Rehling P, Meinecke M (2017) Cation selectivity of the presequence translocase channel Tim23 is crucial for efficient protein import. ELife pii: e28324

Tarasenko D, Barbot M, Jans DC, Kroppen B, Sadowski B, Heim G, Möbius W, Jakobs S, Meinecke M (2017) The MICOS component Mic60 displays a conserved membrane-bending activity that is necessary for normal cristae morphology. Journal of Cell Biology 216: 889-899

Barbot M, Jans DC, Schulz C, Denkert N, Kroppen B, Hoppert M, Jakobs S, Meinecke M (2015) Mic10 oligomerizes tob end mitochondrial inner membranes at cristae junctions. Cell Metabolism 21: 756-763

Meinecke M, Cizmowski C, Schliebs W, Krüger V, Beck S, Wagner R, Erdmann R (2010) The Peroxisomal Importomer Constitutes a Large and Highly Dynamic Pore. Nature Cell Biology 12: 273-277

Henne WH, Boucrot E, Meinecke M, Evergren E, Vallis Y, Mittal R, McMahon HT (2010) FCHo proteins are nucleators of clathrin-mediated endocytosis. Science 328: 1281-1284

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- 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 “Filtered Spaced Word Matches”, “kmacs”, “Rasbhari”, “Prot-SpaM”, “Multi-SpaM”, “Read-SpaM” and “Slope-SpaM”.
Other areas of research in our department include phylogeny reconstruction, metagenomics, motif discovery and remote homology detection using machine learning methods, and genome annotation for prokaryotes.

Selected Recent Publications

Hosseini M, Pratas D, Morgenstern B, Pinho AJ (2020) Smash++: an alignment-free and memory-efficient tool to find genomic rearrangements. GigaScience 9: giaa048

Röhling S, Linne A, Schellhorn J, Hosseini M, Dencker T, Morgenstern B (2020) The number of k-mer matches between two DNA sequences as a function of k and applications to estimate phylogenetic distances. PLOS ONE 15: e0228070

Dencker T, Leimeister CA, Gerth M, Bleidorn C, Snir S, Morgenstern B (2020) Multi-SpaM: a Maximum-Likelihood approach to Phylogeny reconstruction using Multiple Spaced-word Matches and Quartet Trees. NAR Genomics and Bioinformatics 2: lqz013

Lau AK, Dörrer S, Leimeister C-A, Bleidorn C, Morgenstern B (2019) Read-SpaM: assembly-free and alignment-free comparison of bacterial genomes with low sequencing coverage. BMC Bioinformatics 20, 638

Zielezinski A, Girgis HZ, Bernard G, Leimeister C-A, Tang K, Dencker T, Lau AK, Röhling S, Choi J, Waterman MS, Comin C, Kim S-H, Vinga S, Almeida JS, Chan CX, James B, Sun F, Morgenstern B, Karlowski WM (2019) Benchmarking of alignment-free sequence comparison methods. Genome Biology 20: 144

Leimeister C-A, Dencker T, Morgenstern B (2019) Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. Bioinformatics 35: 211-218

Leimeister C-A, Schellhorn J, Dörrer S, Gerth M, Bleidorn C, Morgenstern B (2019) Prot-SpaM: Fast alignment-free phylogeny reconstruction based on whole-proteome sequences GigaScience 8, giy148

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

Leimeister C-A, Sohrabi-Jahromi S, Morgenstern B (2017) Fast and accurate phylogeny reconstruction using filtered spaced-word matches. Bioinformatics 33: 971-979

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

Morgenstern B, B Zhu B, Horwege S, Leimeister C-A (2015) Estimating evolutionary distances between genomic sequences from spaced-word matches. Algorithms for Molecular Biology 10: 5

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http://www.dpz.eu/en/platforms/optogenetics/auditory-neuroscience.html

http://www.em.mpg.de/index.php?id=373&tx_jppageteaser_pi1%5BbackId%5D=16

https://mbexc.de/

http://www.sfb889.uni-goettingen.de/

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

Keppeler D, Schwaerzle M, Harczos T, Jablonski L, Dieter A, Wolf B, Ayub S, Vogl C, Wrobel C, Hoch G, Abdellatif K, Jeschke M, Rankovic V, Paul O, Ruther P, Moser T (2020) Multichannel optogenetic stimulation of the auditory pathway using microfabricated LED cochlear implants in rodents. Sci Translat Med Vol 12(553): eabb8086

Jean P, Anttonen T, Michanski S, de Diego A, Steyer AM, Neef A, Oestreicher D, Kroll J, Nardis C, Pangršič T, Möbius W, Ashmore J, Wichmann C, Moser T (2020) Macromolecular and electrical coupling between inner hair cells in the rodent cochlea. Nat Commun 11: 3208

Jean P, Demet Özçete Ö, Tarchini B, Moser T (2019) Intrinsic planar polarity mechanisms influence the position-dependent regulation of synapse properties in inner hair cells. PNAS pii: 201818358

Dieter A, Duque-Afonso CJ, Rankovic V, Jeschke M, Moser T (2019) Near physiological spectral selectivity of cochlear optogenetics. Nature Commun 10: 1962

Wrobel C, Dieter A, Huet A, Keppeler D, Duque-Afonso C, Vogl C, Hoch G, Jeschke M, Moser T (2018) Optogenetic stimulation of cochlear neurons activates the auditory pathway and restores auditory-driven behavior in deaf adult gerbils. Sci Transl Med 10(449), pii: eaao0540

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 9(1): 290

Mager T, Lopez de la Morena D, Senn V4,5, Schlotte J, D Errico A, Feldbauer K, Wrobel C, Jung S, Bodensiek K, Rankovic V, Browne L, Huet A, Jüttner J1, Wood PG, Letzkus JJ, Moser T, Bamberg E (2018) High frequency neural spiking and auditory signaling by ultrafast red-shifted optogenetics. Nat Commun 9(1): 1750

Klaus-Armin Nave

Professor of Molecular Biology, Director at the Max Planck Institute of Experimental Medicine

- 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

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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

Quintes S, Brinkmann BG, Ebert M, Fröb F, Kungl T, Arlt FA, Tarabykin V, Huylebroeck D, Meijer D, Suter U, Wegner M, Sereda MW, Nave KA (2016) Zeb2 is essential for Schwann cell differentiation, myelination and nerve repair. Nat Neurosci 19(8):1050-9

Fünfschilling U, Supplie LM, Mahad D, Boretius S, Saab AS, Edgar J, Brinkmann BG, Kassmann CM, Tzvetanova ID, Möbius W, Diaz F, Meijer D, Suter U, Hamprecht B, Sereda MW, Moraes CT, Frahm J, Goebbels S, Nave K-A (2012) Glycolytic oligodendrocytes maintain myelin and long-term axonal integrity. Nature 485: 517-521

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

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Argyris Papantonis

Professor, University Medical Center

- 2002 – 2008 PhD, 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

Mizi A, Zhang S, Papantonis A* (2020) Genome folding and refolding in differentiation and cellular senescence. Curr Opin Cell Biol 67: 56-63

Casa V, Moronta Gines M, Gade Gusmao E, Slotman JA, Zirkel A, Josipovic N, Oole E, van IJcken WFJ, Houtsmuller AB, Papantonis A*, Wendt KS* (2020) Redundant and specific roles of cohesin STAG subunits in chromatin looping and transcriptional control. Genome Res 30: 515-527

Weiterer SS, Meier-Soelch J, Georgomanolis T, Mizi A, Beyerlein A, Weiser H, Brant L, Mayr-Buro C, Jurida L, Beuerlein K, Müller H, Weber A, Tenekeci U, Dittrich-Breiholz O, Bartkuhn M, Nist A, Stiewe T, van IJcken WF, Riedlinger T, Schmitz ML, Papantonis A*, Kracht M* (2020) Distinct IL-1α-responsive enhancers promote acute and coordinated changes in chromatin topology in a hierarchical manner. EMBO J 39:e101533

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, Nikolićć M, Gusmao EG, Zirkel A, Knoch TA, van Ijcken WF, Cook PR, Costa IG, Grosveld FG, Papantonis A (2016) Binding of nuclear factor κB 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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Professor of Genetics of Eukaryotic Microorganisms

- 1993 Dr. rer. nat., Ruhr-Universität Bochum
- 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

Werner A, Herzog B, Valerius O, Braus GH, Pöggeler S (2019) NBR1 is involved in selective pexophagy in filamentous ascomycetes and can be functionally replaced by a tagged version of its human homolog. Autophagy 15: 78-97

Reschka EJ, Nordzieke S, Valerius O, Braus GH, Pöggeler S (2018) A novel STRIPAK complex component mediates hyphal fusion and fruiting-body development in filamentous fungi. Mol Microbiol 110: 513-532

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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Stefan Pöhlmann

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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

Influenza viruses pose a global health threat. These viruses constantly change and therapeutics may thus cease to be effective. Therefore, we seek to develop novel influenza therapies. One focus of our work is on the host cell protease TMPRSS2 since we obtained evidence that influenza viruses depend on this enzyme for acquisition of infectivity. Moreover, we are investigating how defective interfering particles (DIPs) can be developed as novel therapeutics.
Emerging viruses may cause severe disease. Outbreaks frequently occur abroad but the agents can be imported into Germany via infected travelers. We are investigating how emerging viruses interact with host cells and cause disease. Our focus in on lymphocytic choriomeningitis virus, Ebola virus and SARS coronavirus. One aim of our research is to develop cell culture systems that allow predicting transmissibility and thus pandemic potential of emerging viruses.
Another focus of our research is on primate herpesviruses. The transmission of herpes B virus from macaques to humans can cause serve disease while closely related viruses seem to be apathogenic in humans. We are investigating which viral and host factors determine whether infection will result in severe disease. Moreover, we are developing diagnostics for herpesvirus infections of non-human primates.

Selected Recent Publications

Hoffmann M, Mösbauer K, Hofmann-Winkler H, Kaul A, Kleine-Weber H, Krüger N, Gassen NC, Müller MA, Drosten C, Pöhlmann S (2020) Chloroquine does not inhibit SARS-CoV-2 infection of human lung cells. Nature 585: 588-590

Wrapp D, De Vlieger D, Corbett KS, Torres GM, Wang N, Van Breedam W, Roose K, van Schie L, VIB-CMB COVID-19 Response Team, Hoffmann M, Pöhlmann S, Graham BS, Callewaert N, Schepens B, Saelens X, McLellan JS (2020) Structural Basis for Potent Neutralization of Betacoronaviruses by Single-Domain Camelid Antibodies. Cell 181(6):1436-1441

Hoffmann M, Kleine-Weber H, Pöhlmann S (2020) A multibasic cleavage site in the spike protein of SARS-CoV-2 is essential for infection of human lung cells. Molecular Cell 78(4):779-784.e5

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Braun E, Hotter D, Koepke L, Zech F, Groß R, Sparrer KMF, Müller JA, Pfaller CK, Heusinger R, Wombacher R, Sutter K, Dittmer U, Winkler M, Simmons G, Jakobsen MR, Conzelmann KK, Pöhlmann S, Münch J, Fackler OT, Kirchhoff F, Sauter D (2019) Guanylate-Binding Proteins 2 and 5 Exert Broad Antiviral Activity by Inhibiting Furin-Mediated Processing of Viral Envelope Proteins. Cell Rep 27(7): 2092-2104

Nehls J, Businger R, Hoffmann M, Brinkmann C, Fehrenbacher B, Schaller M, Maurer B, Schönfeld C, Kramer D, Hailfinger S, Pöhlmann S, Schindler M (2019) Release of Immunomodulatory Ebola Virus Glycoprotein-Containing Microvesicles Is Suppressed by Tetherin in a Species-Specific Manner. Cell Rep 26(7): 1841-1853

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

Richter F, Dennerlein S, Nikolov M, Jans DC, Naumenko N, Aich A, MacVicar T, Linden A, Jakobs S, Urlaub H, Langer T, Rehling P (2019) ROMO1 is a constituent of the human presequence translocase required for YME1L protease import. J Cell Biol 218: 598-614

Schendzielorz AB, Bragoszewski 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 inner membrane. Nature Commun 9: 4028

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)

Schulz C, Rehling P (2014) Remodeling of the active presequence translocase drives motor-dependent mitochondrial protein translocation. Nature Commun 5: 4349

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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Jochen Rink

Director at the Max Planck Institute for Biophysical Chemistry

- 1997 – 2000 Bachelor of Arts, Christ's College, Cambridge University, Cambridge (UK)
- 2000 – 2006 Dr. rer. nat. with Prof. Marino Zerial at the Max Planck Institute for Molecular Cell Biology and Genetics in Dresden
- 2006 – 2011 Postdoctoral Research with Alejandro Sanchez-Alvarado, Howard Hughes Institute/University of Utah School of Medicine, Salt Lake City, (USA)
- 2011 – 2019 Independent Max Planck Research Group Leader at the Max Planck Institute for Molecular Cell Biology and Genetics in Dresden
- Since 2019 Director at the Max Planck Institute for Biophysical Chemistry in Goettingen

Major Research Interests

Regeneration, the ability of many animal or plant species to re-grow lost body parts, raises many intriguing questions. For example, what defines the shape, size, and proportions of the regenerating body part? After an injury, how can the remaining tissue 'sense' what's missing? Why is that regeneration seemingly the exception rather than the rule? Or why We use planarian flatworms as model system. Thanks to their abundant pluripotent adult stem cells, many planarian species have the fascinating ability to regenerate complete animals from tiny tissue pieces. Moreover, they continuously renew all cell types even in absence of injury and the resulting dynamic tissue architecture manifests for example in the food-supply dependent bi-directional scaling of body size over a > 40-fold range in body length, a >800-fold range in cell numbers or close to a 10,000 fold range in weight1. And some species continuously grow and shrink, while others age and die.
Our department uses a highly interdisciplinary compendium of methods to study these fascinating phenomena. We probe the self-organizing signaling systems that specify the planarian body plan in terms of biochemistry and cell biology2,3. We sequence genomes4 and develop functional genomics approaches in order to understand how patterning signals program stem cell progeny fate choices or how signaling networks form spatial activity patterns. We explore the quantitative basis of pattern formation, scaling, and size specification in close collaborations with physicists and theoreticians1,2,5. And through worldwide field sampling, we maintain a "zoo" of > 50 planarian species to mechanistically compare regenerative abilities6, body sizes and shapes, organismal life spans, or reproductive strategies between species.
In a nutshell: We study fundamental molecular/cell biological mechanisms and how and why they change in evolution.

Selected Recent Publications

Thommen A*, Werner S*, Frank O*, Alt N, Richter J, Philipp J, Knittelfelder O, Quek Y, Fahmy K, Shevchenko A, Friedrich BM, Juelicher F, Rink JC (2019) Body size-dependent energy storage causes Kleiber's law scaling in planarians. eLife 8:e38187

Stueckemann T, Cleland JP, Werner S, Thi-Kim Vu H, Bayersdorf R, Liu SY, Friedrich B, Juelicher F, Rink JC (2017) Antagonistic Self-Organizing Patterning Systems Control Maintenance and Regeneration of the Anteroposterior Axis in Planarians. Dev Cell 40(3): 248-263

Thi-Kim Vu H*, Mansour S*, Blasse C, Kuecken M, Basquin C, Azimzadeh J, Myers G, Brusch L, Rink JC (2019) Multi-scale coordination of planar cell polarity in planarians. Dev Cell, in press

Grohme M, Schloissnig S, Rozanski A, Pippel M, Young G, Winkler S, Brandl H, Henry I, Dahl A, Powell S, Hiller M, Myers E, Rink JC (2018) The genome of S. mediterranea and the evolution of cellular core mechanisms. Nature 554(7690): 56-61

Werner S, Stueckemann T, Amigo MB, Rink JC, Juelicher F, Friedrich B (2015). Scaling and regeneration of self-organized patterns. Phys Rev Lett 114: 138101

Liu SY, Selck C, Friedrich B, Lutz R, Vila-Farre M, Dahl A, Brandl H, Lakshmanaperumal N, Henry I, Rink JC (2013) Reactivating head regrowth in a regeneration-deficient planarian species. Nature 500(7460): 81-4

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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

Klimova M, Senyushkina T, Samatova E, Peng B-Z, Pearson M, Peske F, Rodnina MV (2019). EF-G induced ribosome sliding along the noncoding mRNA. Science Advances 5: e9049

Andreeva I, Belardinelli R, Rodnina MV (2018) Translation initiation in bacterial polysomes: Ribosome loading on a stand-by site of a highly translated mRNA. Proc Natl Acad Sci USA 115: 4411-4416

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

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

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

So C, Seres KB, Steyer Anna M, Mönnich E, Clift D, Pejkovska A, Möbius W, and Schuh M (2019) A liquid-like spindle domain promotes acentrosomal spindle assembly in mammalian oocytes. Science doi: 10.1126/science.aat9557

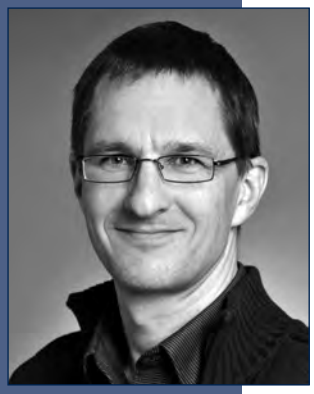
Clift D, McEwan W, Labzin LL, Konieczny V, Mogessie M, James LC, Schuh M1 (2017) A method for the acute and rapid degradation of endogenous proteins. Cell doi: 10.1016

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



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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

Our group develops statistical and computational methods for analyzing data from high-throughput biological experiments. Our work is focussed on protein function and structure prediction, sequence search and assembly in metagenomics, transcription regulation, protein-RNA interactions, gene regulatory networks, and systems medicine.

Selected Recent Publications

Levi Karin E, Mirdita M, Söding J (2020) MetaEuk – sensitive, high- throughput gene discovery and annotation for eukaryotic metagenomics. Microbiome 8(48)

Erijman A, Kozlowski L, Sohrabi-Jahromi S, Fishburn J, Warfield L, Schreiber J, Noble WS, Söding J*, Hahn S* (2020) A high-throughput screen for transcription activation domains reveals their sequence characteristics and permits reliable prediction by deep learning. Mol Cell 78: 890–902

Sohrabi-Jahromi S#, Hofmann KB#, Boltendahl A, Roth C, Gressel S, Baejen C, Söding J*, Cramer P* (2019) Transcriptome maps of general eukaryotic RNA degradation factors. eLife 8:e47040 (#Equal contributions *Corresponding authors)

Söding J, Zwicker D, Sohrabi-Jahromi S, Boehning M, Kirschbaum J (2019) Mechanisms of active regulation of biomolecular condensates. bioRxiv: doi: https://doi org/10.1101/694406

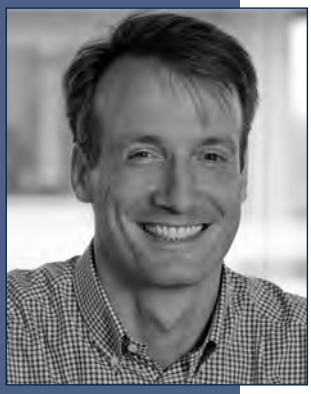
Steinegger M, Mirdita M, and Söding J (2019) Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. Nature Methods 16: 603–606

Banerjee S, Zeng L, Schunkert H, and Söding J (2018) Bayesian multiple logistic regression for GWAS analysis. PloS Genetics 14: e1007856

Vorberg S, Seemayer S and Söding J (2018) Synthetic protein alignments by CCMgen quantify noise in residue-residue contact prediction. PLoS Comput Biol 14: e1006526

Steinegger M, Söding J (2018) Clustering huge protein sequence sets in linear time. Nature Commun 9: 2542

Steinegger M, Söding J (2017) MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. Nature Biotechnol 35: 1026–1028



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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

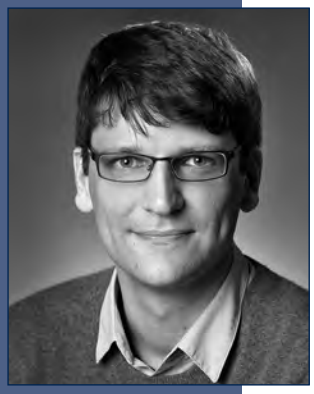
Agafonov DE, Kastner B, Dybkov O, Hofele RV, Liu WT, Urlaub H, Lührmann R, Stark H (2016) Molecular architecture of the human U4/U6.U5 tri-snRNP. Science 351(6280): 1416-20

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

Protein quality control processes are important to maintain cellular homeostasis. In each organelle of the eukaryotic cell, different pathways detect and remove misfolded and missorted proteins. Failure to discard such proteins often results in protein aggregation and eventually disease. A particularly intriguing process serves to discard misfolded proteins from the endoplasmic reticulum (ER). The ER does not itself degrade proteins, but a machinery has evolved that moves misfolded proteins from the membrane and lumen of the ER back into the cytosol. Here, chains of ubiquitin are attached to misfolded substrates lead to their degradation by the proteasome. This process is called ER associated protein degradation, or short ERAD.
We are interested in understanding the molecular mechanism of ERAD. How are misfolded proteins recognized? How can the ERAD machinery distinguish misfolded proteins from folding intermediates? How is a protein transported form the lumen of the ER into the cytosol, or a membrane protein extracted from the ER membrane? To understand these processes in detail we try to rebuild them in a bottom-up approach. We purify individual factors and study them in different model membranes. This is particularly challenging, because most events in ERAD take place at a membrane, and the proteins involved are membrane proteins. We also aim to determine structures of proteins involved in ERAD.
ERAD not only degrades misfolded proteins, but also proteins that the cell no longer needs, e.g. because of changes in metabolic demand. In this case, the protein becomes an ERAD substrate or is stabilized under specific condition. We aim to understand the mechanisms behind this poorly understood phenomenon.

Selected Recent Publications

Schmidt CC, Vasic V, Stein A (2020) Doa10 is a membrane protein retrotranslocase in ER-associated protein degradation. Elife 9:e56945

Vasic V, Denkert N, Schmidt CC, Riedel D, Stein A, Meinecke M (2020) Hrd1 forms the retrotranslocation pore regulated by auto-ubiquitination and binding of misfolded proteins. Nat Cell Biol 22:274-281

Natarajan N, Foresti O, Wendrich K, Stein A, Carvalho P (2020) Quality Control of Protein Complex Assembly by a Transmembrane Recognition Factor. Mol Cell 77:108-119 e109

Schoebel S, Mi W, Stein A, Ovchinnikov S, Pavlovicz R, DiMaio F, Baker D, Chambers MG, Su H, Li D, Rapoport TA, Liao M (2017) Cryo-EM structure of the protein-conducting ERAD channel Hrd1 in complex with Hrd3. Nature 548:352-355

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

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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

Mühlenbrock P, Herwig K, Vuong L, Mey I, Steinem C (2020) Fusion pore formation observed during SNARE-mediated vesicle fusion with pore-spanning membranes. Biophys J 119: 151-161

Sibold J, Kettelhoit K, Vuong L, Liu F, Werz DB, Steinem C (2019) Synthesis of head group labeled Gb3 glycosphingolipids and their distribution in phase-separated giant unilamellar vesicles. Angew Chem 131: 17969-17977; Angew Chem Int Ed 58: 17805-17813

Hubrich R, Park Y, Mey IP, Jahn R, Steinem C (2019) SNARE-mediated fusion of single chromaffin granules with pore-spanning membranes. Biophys J 116: 308–318

Spindler S, Sibold J, Mahmoodabadi RG, Steinem C, Sandoghdar V (2018) High-speed microscopy of diffusion in pore-spanning lipid membranes. Nano Lett 18: 5262–5271

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

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

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

Braunger JA, Brückner BR, Nehls S, Pietuch A, Gerke V, Mey I, Janshoff A, Steinem C (2014) Phosphatidylinositol 4,5-bisphosphate alters the number of attachment sites between ezrin and actin filaments: a colloidal probe study. J Biol Chem 289: 9833-9843

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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Jörg Stülke

Professor of Microbiology

- 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

O'Reilly FJ, Xue L, Graziadei A, Sinn L, Lenz S, Tegunov D, Blötz C, Hagen WJH, Cramer P, Stülke J, Mahamid J, Rappsilber J (2020) In-cell architecture of an actively transcribing-translating expressome. Science 369: 554-557

Reuß DR, Faßhauer P, Mroch PJ, Ul-Haq I, Koo BM, Pöhlein A, Gross CA, Daniel R, Brantl S, & Stülke J (2019) Topoisomerase IV can functionally replace all type 1A topoisomerases in *Bacillus subtilis*. Nucleic Acids Res 47: 5231-5242

Zhu B, & Stülke J (2018) SubtiWiki in 2018: From genes and proteins to functional network annotation of the model organism *Bacillus subtilis*. Nucleic Acids Res 46: D743-D748

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

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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Michael Thumm

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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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Kai Tittmann

Professor of Bioanalytics

- 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
- Peter Yates Lecture, University of Toronto, 2014

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

Rabe von Pappenheim F, Aldeghi M, Shome B, Begley T, de Groot BL, Tittmann K (2020) Structural basis for antibiotic action of the B1 antivitamin 2'-methoxy-thiamine. Nature Chem Biol, in press

Singh K, Graf B, Linden A, Sautner V, Urlaub H, Tittmann K, Stark H, Chari A (2020) Discovery of a regulatory subunit of the yeast fatty acid synthase. Cell 180: 1130-1143

Dai S, Funk LM, von Pappenheim FR, Sautner V, Paulikat M, Schröder B, Uranga J, Mata RA, Tittmann K (2019) Low-barrier hydrogen bonds in enzyme cooperativity. Nature 573: 609–613

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

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

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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

Fang P, Ji Y, Silbern I, Doebele C, Ninov M, Lenz C, Oellerich T, Pan KT, Urlaub H (2020) A streamlined pipeline for multiplexed quantitative site-specific Nglycoproteomics. Nat Commun 11: 5268

Stützer A, Welp LM, Raabe M, Sachsenberg T, Kappert C, Wulf A, Lau A, David SS, Chernev A, Kramer K, Politis A, Kohlbacher O, Fischle W, Urlaub H (2020) Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. Nat Commun 11: 5250

Linden A, Deckers M, Parfentev I, Pflanz R, Homberg B, Neumann P, Ficner R, Rehling P, Urlaub H (2020) A Cross-linking Mass Spectrometry Approach Defines Protein Interactions in Yeast Mitochondria. Mol Cell Proteomics 19: 1161-1178

Parfentev I, Schilbach S, Cramer P, Urlaub H (2020) An experimentally generated peptide database increases the sensitivity of XL-MS with complex samples. J Proteomics 220: 103754

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

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

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Lutz Walter

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- 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 proinflammatory cytokines and anti-viral substances. Due to these properties, NK cells play also important roles in autoimmune diseases, transplantation, and reproduction. Certain NK cells were shown to possess immunological memory and are called adaptive NK cells. Our interests lie in biology and genetics of natural killer (NK) cells, including molecular biology and function of NK cell receptors, specific interactions of NK cell receptors and MHC class I ligands, regulation of NK cell activation, NK cell transcriptomics and the therapeutic use of NK cells.
A further focus of our research is genomics of nonhuman primates with phylogenetic, demographic, evolutionary, and bioinformatic analyses.
Methods: flow cytometry, cell culture and protein methods, next generation sequencing, various bioinformatic analysis tools.

Selected Recent Publications

Bennstein SB, Weinhold S, Manser AR, Scherenschlich N, Noll A, Raba K, Kögler G, Walter L, Uhrberg M (2020) Umbilical cord blood-derived ILC1-like cells constitute a novel precursor for mature KIR+NKG2A- NK cells. eLife 9:e55232

Rogers J et al. (2019) The comparative genomics and complex population history of Papio baboons. Sci Adv 5(1): eaau6947

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

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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
- 2012 – 2016: Member of the DFG Review Panel Section 201 (Basic Research in Biology and Medicine) of the German Research Foundation DFG (Deutsche Forschungsgemeinschaft)
- 2015 – 2016 President of the German Society for Immunology (DGfI)
- since 2016: Member of the DFG Review Panel Section 204 (Microbiology, Virology, Immunology) of the German Research Foundation DFG (Deutsche Forschungsgemeinschaft)
- since 04/2020: Dean of Research of the University Medical Center Göttingen

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 immuno-deficiencies 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

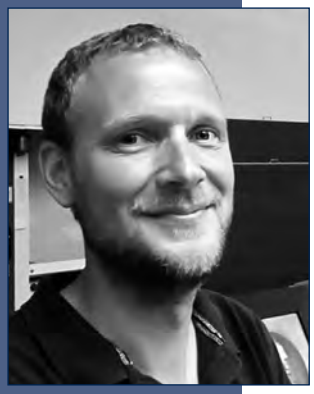
Selected Recent Publications

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



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Marcel Wiermer

Group Leader

- 2018 Habilitation in Botany, Faculty of Biology and Psychology, Georg-August-University Göttingen
- 2016 Group leader of the independent research group 'Molecular Biology of Plant-Microbe Interactions' Georg-August-University Göttingen, Germany
- 2011-2016 Junior research group leader, Department of Plant Cell Biology, Georg-August-University Göttingen, Germany
- 2010 Feodor Lynen postdoctoral return fellow, Department of Plant Cell Biology, Georg-August-University Göttingen, Germany
- 2006-2009 Feodor Lynen postdoctoral fellow, Michael Smith Laboratories, University of British Columbia, Vancouver, Canada
- 2005-2006 Postdoctoral fellow, Max-Planck Institute for Plant Breeding Research, Cologne, Germany
- 2002-2005 PhD, Max-Planck Institute for Plant Breeding Research, Cologne, Germany
- 2001 Diploma (Biology), University of Münster, Germany

Major Research Interests

Research efforts in our laboratory are directed towards understanding the molecular mechanisms that regulate spatial communication between the cytoplasm and the nucleus in plant cellular immunity to pathogenic microbes, using *Arabidopsis* as model organism. We employ biochemical, cell biological, genetic and molecular approaches to study the functions of nuclear transport receptors (NTRs) and nuclear pore complex proteins (Nucleoporins) that are essential for plant disease resistance and control nucleocytoplasmic trafficking of proteins and RNAs. Our studies further include affinity purification approaches coupled with mass spectrometry, forward and reverse genetics to identify novel biochemical and genetic interactors required for plant defense. Another line of research is aimed at exploring molecular functions of secreted fungal effector proteins that are targeted into host cell nuclei during infection and at identifying respective host cell NTRs that mediate nuclear effector translocation.

Selected Recent Publications

Rekhter D, Lüdke D, Ding Y, Feussner K, Zienkiewicz K, Lipka V, Wiermer M, Zhang Y, Feussner I (2019) Isochorismate-derived biosynthesis of the plant stress hormone salicylic acid. Science 365: 498-502

Roth C, Lüdke D, Klenke M, Quathamer A, Valerius O, Braus G, Wiermer M (2017) The truncated NLR protein TIR-NBS13 is a MOS6/IMPORTIN-α3 interaction partner required for plant immunity. Plant J 92: 808-821

Genenncher B, Wirthmueller L, Roth C, Klenke M, Ma L, Sharon A, Wiermer M (2016) Nucleoporin-regulated MAP kinase signaling in immunity to a necrotrophic fungal pathogen. Plant Physiol 172: 1293-1305

Wirthmueller L, Roth C, Fabro G, Caillaud MC, Rallapalli G, Asai S, Sklenar J, Jones AME, Wiermer M, Jones JDG, Banfield MJ (2015) Probing formation of cargo/importin-alpha transport complexes in plant cells using a pathogen effector. Plant J 81: 40-52

Wirthmueller L, Roth C, Banfield MJ, Wiermer M (2013) Hop-on hop-off: importin-alpha-guided tours to the nucleus in innate immune signaling. Front Plant Sci 4: 149

Roth C, Wiermer M (2012) Nucleoporins Nup160 and Seh1 are required for disease resistance in *Arabidopsis.* Plant Signal Behav 7: 1212-1214

Wiermer M, Cheng YT, Imkampe J, Li M, Wang D, Lipka V, Li X (2012) Putative members of the *Arabidopsis* Nup107-160 nuclear pore sub-complex contribute to pathogen defense. Plant J 70: 796-808

Cheng YT, Germain H, Wiermer M, Bi D, García AV, Wirthmueller L, Després C, Parker JE, Zhang Y, Li X (2009) Nuclear Pore Complex Component MOS7/Nup88 Is Required for Innate Immunity and Nuclear Accumulation of Defense Regulators in *Arabidopsis*. Plant Cell 21: 2503-2516

Ernst Wimmer

Professor of Developmental Biology

- 1991 Diplom (Biology), Ludwig Maximilians University, Munich (Germany)
- 1995 Dr. rer. nat., Max-Planck-Institute for Biophysical Chemistry, Göttingen (Germany) and Howard Hughes Medical Institute, Baylor College of Medicine, Houston (USA)
- 1995 – 1998 Postdoctoral Fellow and Associate, Howard Hughes Medical Institute, The Rockefeller University, New York (USA)
- 1998 – 2003 Assistant Professor and Robert Bosch Foundation 'Junior Professor' Department of Genetics, University of Bayreuth, Bayreuth (Germany)
- Since 2003 Professor of Developmental Biology at the Johann Friedrich Blumenbach Institute of Zoology and Anthropology, Georg August University, Göttingen (Germany)

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

Ahmed HMM, Hildebrand L, Wimmer EA (2019) Improvement and Use of CRISPR/Cas9 to Engineer a Sperm-marking Strain for the Invasive Fruit Pest *Drosophila suzukii*. BMC Biotechnology 19:85

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

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