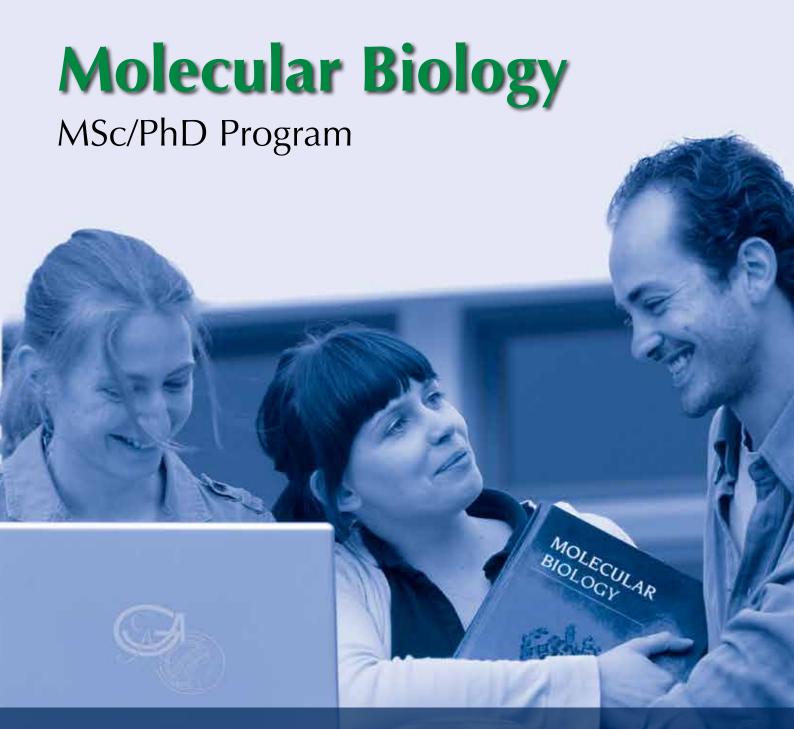


International Max Planck Research School



YEARBOOK 2016 / 2017

# MSc/PhD Molecular Biology Program

at the University of Göttingen

International Max Planck Research School

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#### **Letter from the President**

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

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

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

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

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

Prof. Dr. Ulrike Beisiegel

(President of the Georg-August University of Göttingen)





### **Letter from the Max Planck Society**

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

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

The goals of the International Max Planck Research Schools are

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

By now, 64 International Max Planck Research Schools have been established involving 72 Max Planck Institutes, 32 German universities and 26 universities abroad. About 3,050 PhD students from 120 countries are presently enrolled.

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

Martin Stratmann President Max Planck Society Marina Rodnina Dean of the IMPRS Molecular Biology

#### **Overview**

This yearbook is intended to provide information on the international MSc/PhD Molecular Biology Program in Göttingen, Germany, which was established in the year 2000 as a joint venture of the University of Göttingen and its non-university partners. It is also supported by the Max Planck Society as an International Max Planck Research School (IMPRS). In addition to general information on the program, the yearbook introduces the MSc students of the 2016/17 class, the faculty members, the program committee and the coordination team.

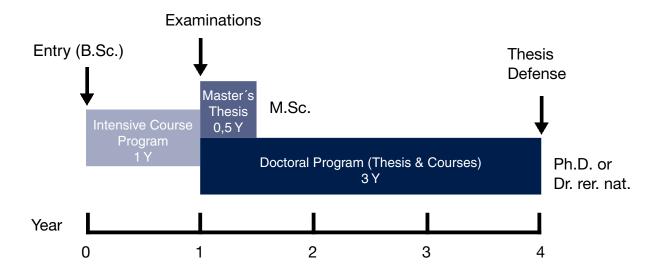
The program belongs to the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences (GGNB), which is funded by the Excellence Initiative of the German Federal and State Governments. It is offered by the Göttingen Center for Molecular Biosciences (GZMB), the Max Planck Institute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

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

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

Subsequently, two separate segments are offered:

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



## **Intensive Course Program (First Year)**

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

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

#### **Lectures and Tutorials**

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

#### Module M.MolBio.11: DNA and Gene Expression

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

#### Module M.MolBio.12: Metabolic and Genetic Networks

- basic metabolism, metabolic networks
- biological membranes
- photosynthesis
- signal transduction
- genomics, 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
- meiosis
- immunology, infectious diseases, principles of pathogenicity
- cell cycle, apoptosis, cancer
- neurons, synapses, synaptic transmission
- glial cells and brain vasculature
- nervous systems, sensory systems
- developmental biology

#### Module M.MolBio.14: Model Systems / Biotechnology

- stem cells
- fungi, Arabidopsis, Drosophila
- C. elegans, Xenopus, zebrafish, mouse
- primates, viral systems in primate research
- biotechnology (bacteria, fungi, plants, insects)

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

#### **Methods Courses**

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

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

- proteins
- DNA

#### **Bioinformatics courses (week 3-4)**

- next generation sequencing, data analysis
- protein structure & bioinformatics databases
- comparative sequence analysis, phylogeny
- gene ontologies & biological networks
- advanced biological networks

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

- analysis or protein-protein and nucleic acid-protein interaction
- chemical and enzymatic analysis of RNA structure
- 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

### **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 2016**

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 2016, the Molecular Biology Program received 747 applications from 77 countries.

Continent	Applications	Admissions
Europe (total)	101	12
Germany	23	4
other West Europe	22	1
East Europe	56	7
America (total)	46	2
North America	25	2
Central/South America	21	0
Africa (total)	169	0
North Africa	72	0
Central/South Africa	97	0
Asia (total)	430	12
Near East	96	1
Central Asia/ Far East	334	11
Australia	1	0

## **Students 2016 / 2017**

Name		Home Country
Gerrit	Altmeppen	Germany
Oleksandr	Dovgusha	Ukraine
Jakob	El Kholtei	Germany
Jose Loreno	Ferrer	Philippines
Gaurika	Garg	India
Alberto	Hernández Armendáriz	Mexico
Ida	Jentoft	Norway
Anubhav	Kaphle	Nepal
Ana	Kutschat	Brazil
Kseniia	Lysakovskaia	Russian Federation
Vitalii	Mudryi	Ukraine
Dilantha	Perera	Sri Lanka
Panagiotis	Poulis	Greece
Martin Daniel	Qui	Philippines
Damir	Sakhapov	Russian Federation
Ninadini	Sharma	India
Anuruti	Swarnkar	India
Liezel	Tamon	Philippines
Cole	Townsend	USA
Taras	Velychko	Ukraine
Gabriel Jose	Villamil	Philippines
Meike	Wiegand	Germany
Roya	Yousefi	Iran
Xizhou	Zhang	P.R. China
Zhenwei	Zhang	P.R. China
Valentyna	Zinchenko	Ukraine



Germany

### **Gerrit Altmeppen**

#### **EDUCATION**

College / University

University of Heidelberg

**Highest Degree** 

**Bachelor of Science** 

**Major Subjects** 

Biochemistry

#### Lab Experience

Mouse models, cell/ tissue culture (generation and culture of primary mouse embryonic fibroblasts and culture of NIH 3T3 cells, fetal thymus organ culture), transfection of mammalian cells, flow cytometry and cell sorting, basic techniques in molecular biology (Western blot, PCR, *in situ* hybridization), genetic engineering and genome editing, cloning and preparation of DNA, protein purification, immunoprecipitation, analytical techniques such as NMR and HPLC/MS

#### Projects / Research

1/2016 – 3/2016 "Methylation optimization for sphingolipids using TMSD and analysis using MS", Prof. Brügger, Biochemistry Center Heidelberg, University of Heidelberg

4/2016 – 9/2016 "In vitro reconstitution of FoxN1 in the nude mouse thymus", Prof. Rodewald, German Cancer Research Center (DKFZ) Heidelberg

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School



Ukraine

### **Oleksandr Dovgusha**

#### **EDUCATION**

#### College / University

Taras Shevchenko National University of Kyiv

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Biology (Minor: Biochemistry)

#### Lab Experience

Various techniques in molecular biology and biochemistry, basic bioinformatics tools, analysis of transcriptomic data, familiar with Python and R programming

#### **Projects / Research**

10/2012 – 5/2015 Effect of aqueous extract from phaseolus vulgaris pods on cytokine profile of streptozotocin-induced diabetic rats.

6/2015 – 5/2016 Integrative analysis of microarray gene expression profiles in human placenta

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2011, 2012, 2013, 2015 The Increased Excellence Stipend of Taras Shevchenko National University of Kyiv



Germany

#### Jakob El Kholtei

#### **EDUCATION**

#### **College / University**

Ruprecht-Karls University Heidelberg

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biosciences

#### Lab Experience

DNA/RNA-Isolation, agarose gel electrophoresis, SDS-PAGE, Southern/Northern/Western blot, PCR/RT-qPCR, mammalian cell culture, transformation/cloning, restriction analysis, transfection (plasmid-DNA/siRNA), luciferase assay, metabolite assays (NEFA, blood glucose, ketone bodies), immunoprecipitation (IP,Co-IP, ChIP), *in vitro* antibody staining

#### **Projects / Research**

7/2015 – 9/2015 "Assessing micro RNA ability to supress the expression of target genes", Laboratory of Evolution and Development, Jerome Hui, Chinese University of Hong Kong

5/2015 – 7/2015 "The Role of CITED4 in adipocyte differentiation", Research Group "Metabolic regulation and stem cell plasticity", A. Vegiopoulos, German Cancer Research Center (DKFZ), Heidelberg, Germany

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2015 German Academic Exchange Service (DAAD) RISE Stipend



Philippines

#### Jose Lorenzo Ferrer

#### **EDUCATION**

#### College / University

University of the Philippines Diliman

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Molecular Biology and Biotechnology

#### Lab Experience

Gene cloning and manipulation, cell culture, cancer assays (proliferation, scratch wound, focus formation & apoptosis assays), semi-/qRT-PCR, immuno/cytochemistry, Western blotting, exosome isolation (RNA/protein content), microscopy, dual-luciferase assay, bioinformatics (CRISPR gRNA, RNA secondary structure, protein-protein interactions)

#### **Projects / Research**

10/2015 – 8/2016 Science research specialist: Confirmatory and orthogonal assays to eliminate artefactual drug bioactivities. Tumor-released exosomes. Detection and differential sorting of CRNDE and other CRC-associated IncRNAs. Functionalization of CRNDE IncRNA *via* overexpression and knockdown. Functional characterization of LUCAT1 IncRNA. Functional characterization of novel NRAS mutations.

2/2014 – 6/2015 Undergraduate thesis student: Functional Sequelae of CRNDE.

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School



India

Mexico

### **Gaurika Garg**

#### **EDUCATION**

#### College / University

Sri Venkateswara College, University of Delhi

### **Highest Degree**

Bachelor of Science (Honors)

#### **Major Subjects**

Biochemistry, Molecular Biology, Cell Biology, Membrane Biology, Immunology, Recombinant DNA Technology, Genetics, Chemistry

#### Lab Experience

Basic molecular and biochemical techniques: PCR, transformation, spectrometry (including UV and fluorescence), gel electrophoresis, enzyme assays and purification. Chromatography. Immunology: ELISA and double difusion assays. Western Blotting. Genetics: Maintaining *Drosophila* stocks and cross setting

#### **Projects / Research**

DBT-STAR College Project 2014-15: "Structural characterization and protein conformational studies of osmolytes on trypsin"

Summer Internship at the Indian Institute of Technology, Delhi: "Immobilization of glucose-oxidase on egg shell membrane and its application to detect glucose in food and blood"

Inspire Internship Programme organized by the Dept. of Science and Technology, Government of India, held at the Indian Institute of Technology, Delhi, 2012

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2012 – 2013 Shanta Sethi Memorial Scholarship for meritorious performance in Biology

### Alberto Hernández Armendáriz

#### **EDUCATION**

#### College / University

National Polytechnic Institute (2011-2014, 2015-2016), Mexico City KTH Royal Institute of Technology (9/2014-01/2015), Stockholm

#### **Highest Degree**

Bachelor in Biotechnological Engineering

#### **Major Subjects**

Biotechnology, Molecular Biology and Genetics

#### Lab Experience

PCR, RT-qPCR, gel electrophoresis, SDS-PAGE, LPS, DNA, RNA and protein extraction, cell culture, transformation, stereotactic surgery and handling of mice, and optical microscopy

#### **Projects / Research**

6/2015 – 8/2015 "Immunopotentiation of vaccines through molecular species of TLR4/TLR2 agonists". Institute of Pharmacy and Foods, Havana University 2/2015 – 8/2016 "Diminishment or the Warburg effect in cervical cancer cell lines after resveratrol treatment". Center for Research and Advanced Studies (CINVESTAV) of the National Polytechnic Institute (IPN), Mexico City

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2014 – 2015 University Mobility Scholarship in North America, Europe and Asia-Pacific (ANEA), granted by the Mexican government

2012 – 2015 TELMEX Scholarship, granted by the Carlos Slim-Telmex Foundation



Norway

#### **Ida Marie Astad Jentoft**

#### **EDUCATION**

#### College / University

University of Copenhagen
McGill University, Montreal
Université Paul-Valéry (Montpellier III)

#### **Highest Degree**

Bachelor of Science in Molecular Biomedicine

#### **Major Subjects**

Molecular Biology, Cell Biology, Developmental Biology

#### Lab Experience

Cell culture, transfection (sirRNA, plasmids etc), RNA and DNA isolation, PCR, rt-PCR, gel electrophoresis, Western blots, luciferase assays, heat map analysis etc.

#### **Projects / Research**

9/2014 - 4/2015 "Priming the kidney progenitor cell" – Paul Goodyer lab, the Montreal Children's Hospital

9/2014 – 4/2015 "Wilms tumor suppressor, WT1, cooperates with microRNA-26a and microRNA-101 to suppress translation of the Polycomb protein, EZH2, in mesenchymal stem cells" – Paul Goodyer lab, the Montreal Children's Hospital

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School

2016 – 2017 Stipend by the Norwegian Educational State Loan Fund

2014 - 2015 The Internationalization Scholarship from the University of Copenhagen



Nepal

### **Anubhav Kaphle**

#### **EDUCATION**

#### College / University

Siddaganga Institute of Technology/ Visvesvaraya Technological University, Belgaum, India

#### **Highest Degree**

Bachelor of Engineering

#### **Major Subjects**

Biochemistry, Molecular Biology, Bioinformatics, Fermentation Technology, Bio-process Control

#### Lab Experience

Standard molecular biology techniques such as gel electrophoresis, DNA extraction, PCR, chromatography, analysis of transcriptomics and proteomics data, Python programming, Discovery Studio 4.0

#### **Projects / Research**

2015 – 2016 "Mapping protein coding regions in the human genome". Research Internship at the Institute of Bioinformatics, Bengaluru, India

2014 – 2015 "Transcriptomic analysis of the non-model plant *Andrographis paniculata* using RNA-Seq data". Department of Biotechnology, SIT, Tumkur

2014 – 2015 "Evaluating andrographolide as a potent inhibitor of NS3-4A protease and its drug-resistant mutants using *in silico* approaches". Department of Biotechnology, SIT, Tumkur

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School



Brazil

#### Ana Patricia Kutschat

#### **EDUCATION**

#### College / University

University of Michigan, Ann Arbor, USA

### **Highest Degree**

Bachelor of Science (B.Sc.)

#### **Major Subjects**

Biochemistry

#### Lab Experience

Various techniques in basic spectroscopy, molecular biology, and biochemistry

#### **Projects / Research**

1/2015 – 5/2016 Elucidation of the role of PTIP, a chromatin remodeling protein, during kidney damage and regeneration (Prof. Dressler, University of Michigan) 5/2015 – 8/2015 Investigation of the intermitochondrial calcium regulation in Trypanosoma cruzi with a side project for the knockout of MCUb using CRISPR/ Cas9 (Prof. Vercesi, Prof. do Campo, Dr. Manfredi, Dr. Chiurillo, UNICAMP, Brazil) 1/2014 - 12/2014 Development of nanoparticles for a Photodynamic Chemo Dual Therapy for cancer and arrhythmia (Prof. Kopelman, University of Michigan) 6/2014 - 8/2014 Characterization of the expression patterns and virulence of lpg1889, a protein secreted by Legionella pneumophila (Dr. Auraß, Dr. Flieger, Robert Koch Institut, Germany)

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2014 International Institute Individual Fellowship, University of Michigan 2013 Alumni 1st Year Achievement Award in Chemistry, University of Michigan



Russian Federation

### Kseniia Lysakovskaia

#### **EDUCATION**

#### College / University

Lomonosov Moscow State University

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Molecular Biology

#### Lab Experience

Various techniques in biochemistry, molecular and cell biology; microscopybased techniques

#### **Projects / Research**

7/2016 - 8/2016 Analysis of signaling pathways involved in blood vessel formation, MPI for Molecular Biomedicine, Münster, Germany. Summer internship

7/2015 - 9/2015 Vimentin silencing: influence on phenotypic properties of MDA-MB-231 breast cancer cell line, DKFZ, Heidelberg, Germany. Summer internship

9/2014 - 6/2015 Native alpha and beta T-cell receptor chain pairs: identification and quantification by digital droplet PCR, Lomonosov Moscow State University, Moscow, Russia. Bachelor's thesis

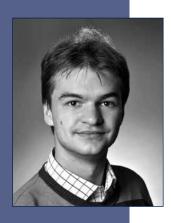
#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School

7/2016 - 8/2016 CiM Summer School Fellowship, Münster, Germany

7/2015 - 9/2015 CellNetworks Summer School Fellowship, Heidelberg, Germany

9/2013 - 9/2015 Increased State Academic Scholarship, Moscow, Russia



Ukraine

### Vitalii Mudryi

#### **EDUCATION**

#### College / University

Taras Shevchenko National University of Kyiv

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biology (Minor: Biochemistry)

#### Lab Experience

SDS-PAGE, enzyme electrophoresis, spectrophotometric analysis, creating recombinant DNA, DNA gel electrophoresis, bacterial transformation with recombinant DNA, DNA extraction, genomic PCR, homology modeling, docking and virtual screening, molecular dynamics simulation

#### **Projects / Research**

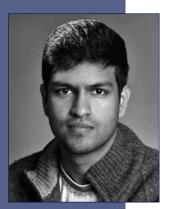
8/2015 - 10/2015 "Investigating structure - phenotype relationship in Apparent Mineralocorticoid Excess Disease". University College London School of Pharmacy, London, UK

9/2013 – 9/2015 "Investigating interaction between PH domain of BCR-ABL oncoprotein and GLG1 protein". Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine, Kyiv, Ukraine

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2015 Biochemical Society Summer Vacation Studentships grant

2012 – 2016 Ukrainian governmental enhanced scholarship for academic excellence



Sri Lanka

#### Dilantha Perera

#### **EDUCATION**

#### College / University

Jacobs University Bremen

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biochemistry and Cell Biology

#### Lab Experience

Techniques in biochemistry and cell biology including 2D PAGE, MALDI-TOF, different types of microscopy and cell staining, and conventional molecular biology techniques such as PCR (conventional and colony) and qPCR

#### **Projects / Research**

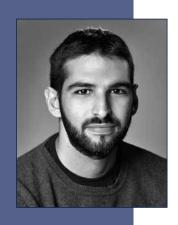
9/2015 - 5/2016 "Investigating the proteome of cocoa beans during a lab-scale fermentation", Molecular Microbiology Laboratory – Prof. Dr. Matthias Ullrich, Jacobs University Bremen, Bremen, Germany

6/2015 – 8/2015 "Underway sampling for marine molecular observation *via* an automated module for sampling, filtration and preservation of marine protists", Planktosens Group – Dr. Katja Metfies, Alfred-Wegener-Institut Helmholtz-Zentrum für Polar- und Meeresforschung, Bremerhaven, Germany

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School

2013 – 2016 Merit Scholarship by Jacobs University Bremen



Greece

### **Panagiotis Poulis**

#### **EDUCATION**

#### College / University

National & Kapodistrian University of Athens

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Biology

#### Lab Experience

Bacterial cell culture & transformation, bacterial mutagenesis with MMS, chromosomal & plasmid DNA extraction, DNA restriction digestion & cloning, DNA gel electrophoresis, gene expression assays (reporter gene assays), *in silico* gene promoter analysis

#### **Projects / Research**

9/2014 – 9/2015 "Transcriptional regulation of SOS genes in the ethanologenic bacterium *Zymomonas mobilis*", Prof. K. M. Pappas, Department of Genetics & Biotechnology, Faculty of Biology, National & Kapodistrian University of Athens

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2016 – 2018 Alexander S. Onassis Public Benefit Foundation Partial Scholarship for Master studies



Philippines

#### **Martin Daniel Qui**

#### **EDUCATION**

#### College / University

University of the Philippines Diliman

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Molecular Biology and Biotechnology

#### Lab Experience

Molecular and cellular biology: nucleic acid/protein extraction (cells/whole tissue), site-directed mutagenesis, PCR/qRT-PCR, transformation, restriction enzyme digestion, Western blot, light and fluorescence microscopy, transient transfection, clonal selection, luciferase/proliferation/migration assays, shRNA design

#### **Projects / Research**

2014 – 2016 Regulatory and functional consequences on tumor suppression of MEG3 SNP variants

2016 Mutational analysis and functional characterization of novel mutations in downstream effectors of the EGFR-signalling pathway among Filipino colorectal cancer patients

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School



Russian Federation

### **Damir Sakhapov**

#### **EDUCATION**

#### College / University

Kazan (Volga region) Federal University

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Biology (Minor: Genetics)

#### Lab Experience

Molecular biology methods: DNA/RNA isolation, cDNA synthesis, PCR and Real-Time PCR, protein extraction, SDS-PAGE, Western blotting. Histology: Immunohistochemical and immunofluorescent staining methods, deriving tissues and organs from laboratory rats, histology samples preparation (paraffin processing of tissues, cutting tissues on microtome or cryotome)

#### **Projects / Research**

6/2014 - 8/2016 "Vegf165 and fgf2 recombinant genes expression analysis after gene & cell therapy on rats' lower limb ischemia model." Institute of Fundamental Medicine and Biology, Kazan (Volga Region) Federal University

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2012, 2014 Academic scholarship, based on excellent academic performance



India

### Ninadini Sharma

#### **EDUCATION**

#### College / University

Miranda House, University of Delhi

#### **Highest Degree**

Bachelor of Science (Honors) Botany

#### **Major Subjects**

Molecular and Cell Biology, Biochemistry, Genetics and Biotechnology

#### Lab Experience

Various biochemical techniques, enzymatic assays, behavioral assays and dissections with *Drosophila*, plant tissue culture, nanoparticles synthesis

#### Projects / Research

5/2016 – 7/2016 "Temporal study of breakdown of nuclear envelope during cell division in *C. neoformans* using fluorescent protein markers" at JNCASR

5/2015 – 7/2015 "In vivo chromosome visualization using tetO array/ tetR-GFP system in *C. neoformans*" at JNCASR

11/2013 – 3/2015 "Nanoparticles and plant systems: *in vitro* and *in silico* studies". University of Delhi Innovation Project

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 2016 First rank holder in B.Sc. (Hons.) Botany, University of Delhi

2014 – 2016 Diploma in Biology with stipend for POBE at JNCASR, Bangalore 2013 – 2016 INSPIRE Scholarship for Higher Education by DST Government of India to top 1% students in India



India

**Philippines** 

#### **Anuruti Swarnkar**

#### **EDUCATION**

#### College / University

Institute of Home Economics, University of Delhi

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biochemistry, Molecular Biology, Genetics, Recombinant DNA Technology, Immunology, Membrane Biology and Bioenergetics, Chemistry

#### Lab Experience

Cell and Molecular Biology: Expression of recombinant protein, RNA and plasmid DNA isolation, PCR, gel electrophoresis, Western blotting, sub-cellular fractionation, haemocytometry. Biochemistry: Enzyme assays and inhibition studies, protein chromatography spectrophotometry, immunodiffusion, agglutination assays and ELISA. Genetics: Drosophila handling and cross-setting

#### **Projects / Research**

5/2015 - 7/2015 'Alternative targets against tuberculosis: Molecular cloning of Rv0114 from Mycobacterium tuberculosis'. Summer Research Fellowship program under Indian Academy of Science (IAS) at National Institute of Immunology, New Delhi with Dr. Bichitra K. Biswal

1/2015 - 3/2015 'Evaluation of herbal extracts as potential anti-hyperglycemic agents', Institute of Home Economics, University of Delhi

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School 2015 Stipend by the Indian Academy of Sciences for Summer Research Fellowship program

#### **Liezel Tamon**

#### **EDUCATION**

#### College / University

University of the Philippines Diliman

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Molecular Biology and Biotechnology

#### Lab Experience

Molecular cloning, semi-quantitative RT-PCR, DNA, RNA and protein extraction, Western blot, Bradford assay, luciferase assay, transient transfection of mammalian cells, light and fluorescence microscopy, testing CRISPR/Cas9 system efficiency through surveyor assay, basic microbiology techniques, sub-sampling (i.e. coning and quartering)

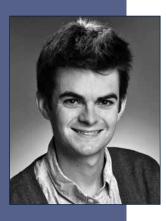
#### **Projects / Research**

4/2014 - 5/2015 "Co-regulation of KRAS and ONECUT2 Oncogenes by Shared MicroRNAs, hsa-miR-181a-5p and hsa-miR-15a-3p" (Unpublished)

5/2010 - 1/2011 "Isolation and Characterization of Actinomycetes with Antimicrobial Activity from Sediments in Barangay San Jose, Puerto Princesa City, Palawan, Philippines" (Unpublished)

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School 2015 Winner, Sanger Institute Prize Competition



USA

#### Cole Townsend

#### **EDUCATION**

#### College / University

University of Oklahoma

#### **Highest Degree**

Bachelor of Science in Biochemistry

#### **Major Subjects**

Biochemistry, Molecular Biology, Chemistry

#### Lab Experience

Western blotting, bacterial and animal cell culture, cloning, immunofluorescence microscopy, RT-PCR, IR spectroscopy, agarose gel electrophoresis, DNA/RNA isolation, flow cytometry, UV spectrophotometry

#### **Projects / Research**

7/2014 – 5/2016 "Single-cell mass spectrometry reveals a possible mechanism of sphingolipid-driven apoptosis." University of Oklahoma, Norman, OK

6/2015 – 8/2015 "The tumor microenvironment and phenotypic plasticity." Cold Spring Harbor, NY

5/2014 – 7/2014 "MicroRNA-200c restores chemo- and radiosensitivity to triple-negative breast cancer." Stephenson Cancer Center, Oklahoma City, OK

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School

2016 Carl Albert Award from the University of Oklahoma (highest award given to one student in the College of Arts and Sciences)

2015 Outstanding Senior Award at the University of Oklahoma



Ukraine

### **Taras Velychko**

#### **EDUCATION**

#### College / University

Taras Shevchenko National University of Kyiv, Ukraine

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biochemistry and Molecular Biology

#### Lab Experience

Mammalian cell culture; reprogramming to iPS cells and quantification of reprogramming efficiency; basic molecular cloning methods; RNA and DNA purification; retrovirus production, titration and transduction; enzyme immobilization; enzyme inhibition; evaluation of biosensor characteristics.

#### **Projects / Research**

7/2015 – 9/2015 Dissecting reprogramming determinants of Sox2 and Sox17. MPI for Molecular Biomedicine, Münster, Germany

9/2014 – 11/2014 Elaboration of a novel conductometric biosensor based on zeolite immobilized recombinant urease. METU Central Laboratory, Ankara, Turkey 9/2012 – 6/2016 Development of enzyme conductometric biosensors for medical, research and ecological purposes. Laboratory of Biomolecular Electronics, Kyiv

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School 7/2016 – 9/2016 FEBS Summer Fellowship

2012 – 2016 (5/8 semesters) Ukrainian State Scholarship for students with excellent studying achievements



**Philippines** 

### **Gabriel Jose Villamil**

#### **EDUCATION**

#### College / University

University of the Philippines Diliman

### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Molecular Biology and Biotechnology

#### Lab Experience

Molecular cloning and expression, next generation sequencing, bioinformatics, molecular docking and dynamics

#### **Projects / Research**

6/2013 – 8/2016 "Whole genome shotgun sequencing identifies five bacterial isolates from outbreaks of luminous vibriosis." Philippine Genome Center, University of the Philippines

9/2012 – 1/2013 "Computational analysis of integrin subunit glycosylation: Investigations on its role in orienting ligand receptor interaction." National Institute of Molecular Biology and Biotechnology, University of the Philippines Diliman

6/2009 – 3/2010 "A survey of integrin subunit expression profiles in cell lines representing different tissue types." National Institute of Molecular Biology and Biotechnology, University of the Philippines Diliman

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School

2006 – 2010 Philippine Department of Science and Technology Science Education Institute Merit Scholarship

### **Meike Wiegand**

#### **EDUCATION**

#### College / University

Technische Universität Darmstadt

#### **Highest Degree**

Bachelor of Science (Biology)

#### **Major Subjects**

Genetics, Molecular Biology of Plants, Biochemistry, Developmental Biology

#### Lab Experience

Various techniques in molecular biology, genetics and biochemistry, including PCR, electrophoresis, basic cell culture of *E. coli* and *Trypanosoma brucei brucei*, recombinant protein expression, affinity chromatography, Thermal Shift Assay, spectrophotometry, densitometric analysis of protein expression, plasmid isolation, DNA sequencing, etc.

#### **Projects / Research**

1/2016 - 4/2016 Heterologous expression of the N-terminal domain of the trypanosomal SRA-protein. Bachelor's thesis at the Department of Molecular Genetics, Technische Universität Darmstadt

4/2015 – 6/2015 Research internship at the Department of Molecular Genetics, Technische Universität Darmstadt

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School



Germany



Iran

# Roya Yousefi

College / University

College of Science, University of Tehran

**Highest Degree** 

Bachelor of Science

**Major Subjects** 

Biotechnology

#### Lab Experience

Molecular techniques including DNA extraction, PCR, electrophoresis, blotting, real-time PCR, routine microbial techniques, primer and shRNA designing, gene cloning, mammalian cell culture, gene transfection to animal cells, virus packaging and gene transduction

#### **Projects / Research**

9/2015 – present "Evaluation of Hsf1 silencing on sensitivity of prostate cancer cell line (PC-3) to anti-cancer drugs in 2D cultures" (Master's Thesis), Department of Biotechnology, University of Tehran

2014 "Isolation and identification of heat-stable lipases of native strains of thermal-springs-living microorganisms" (Bachelor's Thesis), Department of Biotechnology, University of Tehran

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School

2011 - 2016 Iran's National Elites Foundation Scholarship

2011 - 2016 University of Tehran Fellowship for Exceptional Talents

2011 – 2016 Ministry of Science, Research and Technology Scholarship for Biotechnology Students, Iran

### Xizhou Zhang

#### **EDUCATION**

#### College / University

Jacobs University Bremen

#### **Highest Degree**

Bachelor of Science

#### **Major Subjects**

Biochemistry and Cell Biology

#### Lab Experience

General molecular biology and microbiology techniques; laser scanning microscopy; protein crystallization and over-expression; protein structural refinement

#### **Projects / Research**

9/2015 – 6/2016 Antibiotics response of ToIC multi-drug resistance transporter (Bachelor Thesis), Jacobs University Bremen

6/2015 – 8/2015 Structural analysis of BaiCD and BaiH protein in *C. scindens*, Vanderbilt University

1/2015 - 6/2015 DAAD Award for Excellent Extracurricular Engagement

7/2014 – 8/2014 Splicing of human and yeast pre-mRNA, particularly the transition stage between B to complex, Max Planck Institute for Biophysical Chemistry

#### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School

2013 - 2016 DAAD Award for Excellent Extracurricular Engagement

2013 – 2016 Merit scholarship from Jacobs University Bremen



P.R. China



P.R. China

### **Zhenwei Zhang**

#### **EDUCATION**

#### College / University

University of Electronic Science and Technology of China (UESTC)

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Molecular Biology, Cell Biology, Biochemistry, Genetics

#### Lab Experience

Cell culture (human tumor cell line, MDA-MB-231), techniques in molecular biology research (PCR, Real-time PCR, SDS-PAGE, Western and Southern blotting, immunofluorescence technique, RNAi), wound healing experiment, cell adhesion assay

#### **Projects / Research**

2014 – 2016 A Study on the Roles and Molecular Mechanism of Caveolin-1/ Caveolae in the Cell Polarity Formation and the Expression of MT1-MMP under Shear Stress

2014 - 2016 Prediction of Stress Responsive IncRNAs in Plants

#### Scholarships / Awards

2016 - 2017 Stipend by the International Max Planck Research School

2016 Award for Outstanding Graduates, UESTC

2012 - 2015 First Class People's Scholarship, UESTC



Ukraine

### Valentyna Zinchenko

#### **EDUCATION**

#### College / University

Taras Shevchenko National University of Kyiv

#### **Highest Degree**

**Bachelor of Science** 

#### **Major Subjects**

Biology (Minor - Biophysics)

#### Lab Experience

Spectroscopy, amperometry, patch-clamp. RNA isolation, PCR, electrophoresis. Modelling, MD simulations, Python, R for data analysis

#### **Projects / Research**

7/2016 – 8/2016 "Computational modeling of 3'-phosphoadenosine 5'-phosphosulfate Synthase PAPSS2". CNSB AS CR, Nove Hrady, Czech Republic

10/2015 – 6/2016 "Computational modelling of AIMP1 structure and molecular dynamics simulations". IMBG NASU, Kyiv, Ukraine

3/2015 – 10/2015 "Analysis of transcription factor binding sites for genes Pick1, Grin3a and GABRA2". IMBG NASU, Kyiv, Ukraine

1/2014 – 3/2015 "Development of a biosensor for lactate concentration determination based on lactate oxidase". IMBG NASU, Kyiv, Ukraine

### Scholarships / Awards

2016 – 2017 Stipend by the International Max Planck Research School

2013 - 2016 Ukrainian governmental enhanced scholarship for academic excellence

2012 - 2013 Scholarship president of Ukraine for National Olympiad winners

2011 – 2012 Donetsk regional scholarship for National Ukrainian Olympiad winners

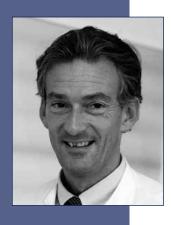
# Faculty

Name		Group / Institution	
Mathias	Bähr	Neurology	U Göttingen
Holger	Bastians	Cellular Oncology	U Göttingen
Rüdiger	Behr	Degenerative Diseases	DPZ
Tim	Beißbarth	Statistical Bioinformatics	U Göttingen
Markus	Bohnsack	Molecular Biology	U Göttingen
Gerhard H.	Braus	Molecular Microbiology and Genetics	U Göttingen
Bertram	Brenig	Molecular Biology of Livestock	U Göttingen
Henrik	Bringmann	Sleep and Waking	MPI bpc
Nils	Brose	Molecular Neurobiology	MPI em
Patrick	Cramer	Molecular Biology	MPI bpc
Rolf	Daniel	Genomic and Applied Microbiology	U Göttingen
Matthias	Dobbelstein	Molecular Oncology	U Göttingen
Roland	Dosch	Molecular Control of Zebrafish Oogenesis	U Göttingen
Jörg	Enderlein	Biophysics	U Göttingen
Ivo	Feußner	Plant Biochemistry	U Göttingen
Ralf	Ficner	Molecular Structural Biology	U Göttingen
Wolfgang	Fischle	Chromatin Biochemistry	MPI bpc
Christiane	Gatz	Plant Molecular Biology and Physiology	U Göttingen
Dirk	Görlich	Cellular Logistics	MPI bpc
Christian	Griesinger	NMR-based Structural Biology	MPI bpc
Uwe	Groß	Medical Microbiology	U Göttingen
Jörg	Großhans	Developmental Biochemistry	U Göttingen
Helmut	Grubmüller	Theoretical and Computational Biophysics	MPI bpc
Heidi	Hahn	Human Genetics	U Göttingen
Kai	Heimel	Microbial Cell Biology	U Göttingen
Stefan	Hell	NanoBiophotonics	MPI bpc
Claudia	Höbartner	Nucleic Acid Chemistry	MPI bpc
Herbert	Jäckle	Molecular Developmental Biology	MPI bpc
Reinhard	Jahn	Neurobiology	MPI bpc
Stefan	Jakobs	Mitochondrial Structure and Dynamics	MPI bpc
Andreas	Janshoff	Biophysical Chemistry	U Göttingen
Steven	Johnsen	Translational Cancer Research	U Göttingen

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

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

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



Department of Neurology University Medical Center Göttingen Robert-Koch-Str. 40

37075 Göttingen Germany

phone: + 49-551-39 66603 fax: + 49-551-39 9348 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**

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

Ribas VT, Schnepf B, Challagundla M, Koch JC, Bähr M, Lingor P (2015) Early and sustained activation of autophagy in degenerating axons after spinal cord injury. Brain Pathol. 25(2): 157-70

Tereshchenko J, Maddalena A, Bähr M, Kügler S (2014) Pharmacologically controlled, discontinuous GDNF gene therapy restores motor function in a rat model of Parkinson's disease. Neurobiol Dis 65: 35-42

Kretzschmar B, Hein K, Moinfar Z, Könnecke B, Sättler MB, Hess H, Weissert R, Bähr M (2014) Treatment with atacicept enhances neuronal cell death in a rat model of optic neuritis. J Neuroimmunol. Mar 15;268(1-2): 58-63

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

Koch JC, Knöferle J, Tönges L, Michel U, Bähr M, Lingor P (2011) Imaging of rat optic nerve axons *in vivo*. Nat Protoc. 3;6(12): 1887-96

Knöferle J, Koch JC, Ostendorf T, Michel U, Planchamp V, Vutova P, Tönges L, Stadelmann C, Brück W, Bähr M, Lingor P (2010) Mechanisms of acute axonal degeneration in the optic nerve *in vivo*. Proc Natl Acad Sci USA 107(13): 6064-9



Institute for Molecular Oncology University Medical Center Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: + 49-551-39 33823 fax: + 49-551-39 9320 e-mail: holger.bastians@ uni-goettingen.de

#### **Further Information**

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

### **Holger Bastians**

#### **Professor of Cellular Oncology**

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

#### **Major Research Interests**

Mitosis represents the key event during the eukaryotic cell cycle during which the DNA is equally distributed onto the two daughter cells. Defects in mitotic signaling pathways are often detected in human cancer and are directly associated with the missegregation of sister chromatids resulting in chromosomal instability (CIN) and aneuploidy. In fact, this is directly linked to tumorigenesis and represents a major characteristic of human cancer. However, the molecular mechanisms underlying CIN and the genetic lesions causing aneuploidy in human cancer are largely unknown.

In addition to its fundamental role for the maintenance of chromosomal stability, mitosis represents an important target for anti-cancer therapy and many anti-mitotic drugs including taxanes and Vinca alkaloids are frequently used in the clinic to treat various malignancies. However, it is still unclear how the interference with the mitotic progression is linked to tumor cell death, the desired outcome of therapy. A knowledge of this cross-talk is required for the development of future therapy concepts.

Based on these key points of cancer research our lab is focusing on the following main questions:

- 1. What are the molecular mechanisms of chromosome segregation during mitosis and what are genetic lesions in human cancer responsible for chromosomal instability?
- 2. What are the molecular mechanisms of mitosis associated cell death after chemotherapeutic treatment and waht are the routes of chemotherapy resistance in human cancer?
- 3. Based on our investigations of mitotic signaling pathways we are aiming to identify novel mitotic drug targets in order to improve current therapies and to develop novel therapeutic concepts.

#### **Selected Recent Publications**

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

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

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

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

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



Degenerative Diseases German Primate Center Kellnerweg 4

37077 Göttingen Germany

phone: +49-551-3851 132 fax: +49-551-3851 431 e-mail: rbehr@dpz.eu

#### **Further Information**

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

### Rüdiger Behr

#### Head of Platform Degenerative Diseases, German Primate Center

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

#### **Major Research Interests**

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

#### **Selected Recent Publications**

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

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

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

Debowski K, Warthemann R, Lentes J, Salinas-Riester G, Dressel R, Langenstroth D, Gromoll J, Sasaki E, Behr R (2015) Non-viral generation of marmoset monkey iPS cells by a six-factor-in-one-vector approach. PLoS One. 2015 Mar 18;10(3): e0118424

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

Eildermann K, Gromoll J, Behr R (2012) Misleading and reliable markers to differentiate between primate testis-derived multipotent stromal cells and spermatogonia in culture. Hum Reprod 27: 1754-67

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



Dept. of Medical Statistics University Medical Center Göttingen Humboldtallee 32

37073 Göttingen Germany

phone: + 49-551-39 14099 fax: + 49-551-39 4995 e-mail: tim.beissbarth@ med.unigoettingen.de

#### **Further Information**

http://www.ams.med.unigoettingen.de/beissb.shtml

#### Tim Beißbarth

#### **Associate Professor of Biostatistics**

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

#### **Major Research Interests**

The Statistical Bioinformatics group of the department of Medical Statistics is developing statistical applications at methods for biomedical research. We are closely working together with other biostatisticians/bioinformaticists as well as clinical and biological researchers. The focus of the group is the development of methods and tools to analyse biomedical data and to reconstruct biological networks. These methods are implemented mostly in the statistical computing environment of R.

#### **Selected Recent Publications**

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

Wachter A, Beißbarth T (2015) pwOmics: an R package for pathway-based integration of time-series omics data using public database knowledge. Bioinformatics 31(18): 3072-4

von der Hyde S, Bender C, Henjes F, Sonntag J, Korf U, Beißbarth T (2014) Boolean ErbB network reconstructions and perturbation simulations reveal individual drug response in different breast cancer cell lines. BMC Systems Biology, 8: 75

Jung K, Dihazi H, Bibi A, Dihazi GH, Beißbarth T (2014) Adaption of the global test idea to proteomics data with missing values. Bioinformatics 30(10): 1424-30

Kramer F, Bayerlová M, Klemm F, Bleckmann A, Beißbarth T (2013) rBiopax-Parser - an R package to parse, modify and visualize BioPAX data. Bioinformatics 29(4): 520-2

Gade S, Porzelius C, Fälth M, Brase JC, Wuttig D, Kuner R, Binder H, Sültmann H, Beißbarth T (2011) Graph based fusion of miRNA and mRNA expression data improves clinical coutcome prediction in prostate cancer. BMC Bioinformatics 12(1): 488

Bender C, Heyde S, Henjes F, Wiemann S, Korf U, Beißbarth T (2011) Inferring signalling networks from longitudinal data using sampling based approaches in the R-package 'ddepn'. BMC Bioinformatics 2011, 12: 291

Johannes M, Fröhlich H, Sültmann H, Beißbarth T (2011) pathClass: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. Bioinformatics, 2011, 27(10): 1442-3

Jung K, Becker B, Brunner B, Beißbarth T (2011) Comparison of Global Tests for Functional Gene Sets in Two-Group Designs and Selection of Potentially Effect-causing Genes. Bioinformatics, 2011, 27(10): 1377-83



Dept. of Molecular Biology University Medical Center Göttingen Humboldtallee 23

37073 Göttingen Germany

phone: + 49-551-39 5968 fax: + 49-551-39 5960 e-mail: markus.bohnsack@ med.unigoettingen.de

#### **Further Information**

http://www.uni-bc.gwdg.de/index.php?id=671

#### **Markus Bohnsack**

#### **Professor of Molecular Biology**

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

#### **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**

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: e201694885

Heininger AU, Hackert P, Andreou AZ, Boon KL, Memet I, Prior M, Clancy A, Schmidt B, Urlaub H, Schleiff E, Sloan KE, Deckers M, Lührmann R, Enderlein J, Klostermeier D, Rehling P, Bohnsack MT (2016) Protein cofactor competition regulates the action of a multifunctional RNA helicase in different pathways. RNA Biol 13: 320-330

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

Meyer B, Wurm JP, Kötter P, Leisegang MS, Schilling V, Buchhaupt M, Held M, Bahr U, Karas M, Heckel A, Bohnsack MT, Wöhnert J, Entian KD (2011) The protein mutated in Bowen-Conradi Syndrome, Nep1 (Emg1), is required for a unique modification in 18S rRNA. Nucleic Acids Res 39: 1526-1537

Bohnsack MT, Martin R, Granneman S, Ruprecht M, Schleiff E, Tollervey D (2009) Prp43 bound at different sites on the pre-rRNA performs distinct functions in ribosome synthesis. Mol Cell 36: 583-592



Department of Molecular Microbiology and Genetics University of Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: +49-551-39 33771 fax: +49-551-39 33330 e-mail: gbraus@gwdg.de

#### **Further Information**

http://www.unigoettingen.de/molmibio

#### Gerhard H. Braus

#### **Professor of Microbiology and Genetics**

- Diploma (Biology), Albert-Ludwig University, Freiburg i. Br. (Germany), 1983
- Dr.sc.nat., Swiss Federal Institute of Technology (ETH), Zürich (Switzer land), 1987
- Habilitation (Microbiology), Swiss Federal Institute of Technology (ETH), Zürich (Switzerland), 1991
- Associate Professor of Biochemistry, Friedrich Alexander University, Erlangen (Germany), 1993 – 1996
- 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**

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

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

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

Lin CJ, Sasse C, Valerius O, Irmer H, Heinekamp T, Straßburger M, Tran VT, Herzog B, Braus-Stromeyer SA, Braus GH (2015) Transcription factor SomA is required for adhesion, development and virulence of the human pathogen *Aspergillus fumigatus*. PLoS Pathogens 11, e1005205

Sarikaya-Bayram Ö, Bayram Ö, Feussner L, Kim JH, Kim HS, Kaever A, Feussner I, Chae KS, Han DM, Han KH, Braus GH (2014) Membrane-bound methyltransferase complex VapA-VipC-VapB guides epigenetic control of fungal development. Dev. Cell 29, 406-420 [Journal Cover]

Bayram Ö, Krappmann S, Ni M, Bok JW, Helmstaedt K, Valerius O, Braus-Stromeyer S, Kwon NJ, Keller NP, Yu JH, Braus GH (2008) VelB/VeA/LaeA complex coordinates light signal with fungal development and secondary metabolism. Science. 320, 1504-1506. [Comment to the paper in Perspectives: Science. 320, 1430-1431]



Institute of Veterinary Medicine Dept. of Molecular Biology of Livestock University of Göttingen Burckhardtweg 2

37077 Göttingen Germany

phone: +49-551-39 33383 or 39 33380 fax: +49-551-39 33392 e-mail: bbrenig@gwdg.de

#### **Further Information**

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

### **Bertram Brenig**

### **Full Professor of Molecular Biology of Livestock**

- · Director of the Institute of Veterinary Medicine
- · Dr. med. vet., University of Munich, Munich 1987

#### **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

- Molecular genetics of developmental defects of the eye (cataract, iris hypopigmentation) (cattle)
- · Leg and feet disease (digital dermatitis, interdigital hyperplasia) (cattle)
- · Early embryonal death (lethal haplotypes) (cattle)
- Developmental skeletal defects (Osteogenesis imperfecta, osteodystrophy) (cattle)
- Intervertebral disk disease (dog)
- · Hemophilia A and B (dog)
- · Varroa resistance (honey bee)

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**

Schütz E, Wehrhahn C, Wanjek M, Bortfeld R, Wemheuer WE, Beck J, Brenig B (2016) The Holstein Friesian Lethal Haplotype 5 (HH5) Results from a Complete Deletion of TFB1M and Cholesterol Deficiency (CDH) from an ERV-(LTR) Insertion into the Coding Region of APOB. PLoS One 11: e0154602

Menzi F, Keller I, Reber I, Beck J, Brenig B, Schütz E, Leeb T, Drögemüller C (2016) Genomic amplification of the caprine EDNRA locus might lead to a dose dependent loss of pigmentation. Sci Rep 6: 28438

Liu W, Beck J, Schmidt LC, Roolf C, Pews-Davtyan A, Rutgen BC, Hammer S, Willenbrock S, Sekora A, Rolfs A, Beller M, Brenig B, Nolte I, Junghanss C, Schütz E, Escobar HM (2016) Characterization of the novel indolylmaleimides' PDA-66 and PDA-377 effect on canine lymphoma cells. Oncotarget 7: 35379-35389

Brenig B, Schütz E (2016) Recent development of allele frequencies and exclusion probabilities of microsatellites used for parentage control in the German Holstein Friesian cattle population. BMC Genet 17: 18

Schütz E, Brenig B (2015) Analytical and statistical consideration on the use of the ISAG-ICAR-SNP bovine panel for parentage control, using the Illumina BeadChip technology: example on the German Holstein population. Genet Sel Evol 47: 3



Sleep and Waking Group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen <u>Ger</u>many

phone: +49-551-201 1358 fax: +49-551-3899 715 e-mail: henrik.bringmann@ mpibpc.mpg.de

#### **Further Information**

http://www.mpibpc. mpg.de/english/research/ ags/bringmann/

### Henrik Bringmann

### Max Planck Research Group Leader

- · Max Planck Research Group Leader since 2009
- · Postdoctoral fellow at the Laboratory of Molecular Biology, Cambridge, UK
- PhD at the Max Planck Institute for Cell Biology and Genetics, Dresden

#### **Major Research Interests**

Sleep states occur in the life of every animal studied. While the function of waking is obvious, the function of sleep is unknown. Sleep has been suggested to serve a restorative function in the nervous system. Our lab is trying to understand the function and regulation of sleep by studying different model organisms. We have started our studies by looking at sleep in the larva of the nematode *Caenorhabditis elegans*, and are also working with mice.

We are combining behavioral assays with genetics and functional imaging. We recently found a single sleep-inducing neuron in *C. elegans* that is homologous to mammalian sleep neurons. This highly simplified sleep-inducing system in a tractable genetic model provides a great starting point to understand the regulation of sleep and to manipulate sleep in order to study the function of sleep.

#### **Selected Recent Publications**

Besseling J, Bringmann H (2016) Engineered non-Mendelian inheritance of entire parental genomes in *C. elegans*. Nat Biotechnol 34(9): 982-6

Turek M, Besseling J, Spies JP, König S, Bringmann H (2016) Sleep-active neuron specification and sleep induction require FLP-11 neuropeptides to systemically induce sleep. Elife: e12499

Turek M, Besseling J, Bringmann H (2015) Agarose microchambers for long-term calcium imaging of *Caenorhabditis elegans*. J Vis Exp: e52742

Turek M, Lewandrowski IL, Bringmann H (2013) An AP2 transcription factor is required for a sleep-active neuron to induce sleep-like quiescence in *C. elegans*. Current Biology 23 (22): 2215-2223

Schwarz J, Lewandrowski IL, Bringmann H (2011) Reduced activity of a sensory neuron during a sleep-like state in *Caenorhabditis elegans*. Current Biology 21 (24): R983-R984

Redemann S, Schloissnig S, Ernst S, Pozniakowsky A, Ayloo S, Hyman AA, Bringmann H (2011) Codon adaptation-based control of protein expression in *C. elegans*. Nature Methods 8: 250-252



Dept. of Molecular Neurobiology Max Planck Institute for Experimental Medicine Hermann-Rein-Str. 3

37075 Göttingen Germany

phone: +49-551-3899 725 fax: +49-551-3899 715 e-mail: brose@em.mpg.de

#### **Further Information**

http://www.em.mpg.de/

#### **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**

Research in the Department of Molecular Neurobiology focuses on the molecular mechanisms of nerve cell development and synapse formation and function in the vertebrate central nervous system. We combine biochemical, morphological, mouse genetic, behavioral, and physiological methods to elucidate the molecular basis of nerve cell differentiation, synapse formation, transmitter release processes, and postsynaptic transmitter sensing. Our work in the field of nerve cell development focuses on the role of protein ubiqutination and SUMOylation in cell polarity formation, cell migration, and neuritogenesis. The synaptogenesis research in our group concentrates on synaptic cell adhesion proteins, their role in synapse formation and function, and their dysfunction in neuropsychiatric diseases. 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**

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

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

Imig C, Min SW, Krinner S, Arancillo M, Rosenmund C, Südhof TC, Rhee J, Brose N\*, Cooper BH\* (2014) The morphological and molecular nature of synaptic vesicle priming at presynaptic active zones. Neuron 84: 416-431 (\*joint corresponding authors)

Lipstein N, Sakaba T, Cooper BH, Lin K-H, Strenzke N, Ashery U, Rhee J-S, Taschenberger H, Neher E, Brose N (2013) Dynamic control of synaptic vesicle replenishment and short-term plasticity by Ca<sup>2+</sup>-Calmodulin-Munc13-1 signaling. Neuron 79: 82-96

Tirard M, Hsiao H-H, Nikolov M, Urlaub H, Melchior F, Brose N (2012) *In vivo* localization and identification of SUMOylated proteins in the brain of His6-HA-SUMO1 knock-in mice. Proc Natl Acad Sci USA 109: 21122-21127

Jockusch W, Speidel D, Sigler A, Sørensen J, Varoqueaux F, Rhee J-S, Brose N (2007) CAPS-1 and CAPS-2 are essential synaptic vesicle priming proteins. Cell 131: 796-808



Dept. of Molecular Biology Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

e-mail: patrick.cramer@ mpibpc.mpg.de

#### **Further Information**

http://www.mpibpc.mpg.de/cramer

#### **Patrick Cramer**

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

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

#### **Major Research Interests**

Molecular Biology: from molecular movies to regulatory systems

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

#### **Selected Recent Publications**

Schwalb B, Michel M, Zacher B, Frühauf K, Demel C, Tresch A, Gagneur J, Cramer P (2016) TT-Seq maps the human transient transcriptome. Science 352: 1225-1228

Plaschka C, Hantsche M, Dienemann C, Burzinski C, Plitzko J, Cramer P (2016) Transcription initiation complex structures elucidate DNA opening. Nature 533: 353-358

Bernecky C, Herzog F, Baumeister W, Plitzko J, Cramer P (2016) Structure of transcribing mammalian RNA polymerase II. Nature 529: 551-554

Plaschka C, Larivière L, Wenzeck L, Seizl 2, Hemann M, Tegunov D, Petrotchenko EV, Borchers CH, Baumeister W, Herzog F, Villa E, Cramer P (2015) Architecture of the RNA polymerase II-Mediator core initiation complex. Nature 518(7539): 376-80

Cramer. P (2014) A tale of chromatin and transcription in 100 structures. Cell 159: 985-994

Schulz D, Schwalb B, Kiesel A, Baejen C, Torkler P, Gagneur J, Soeding J, Cramer P (2013) Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. Cell 155(5): 1075-87



Dept. of Genomic and Applied Microbiology University of Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: +49-551-39 33827 fax: +49-551-39 12181 e-mail: rdaniel@gwdg.de

#### **Further Information**

http://appmibio.unigoettingen.de

### **Rolf Daniel**

#### **Professor of Genomic and Applied Microbiology**

- 2013 present: Speaker "North German Center of Microbial Genomics" (Norddeutsches Zentrum f

  ür Mikrobielle Genomforschung, NZMG)
- 04/2012 present: 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**

Gardebrecht A, Markert S, Sievert SM, Felbeck H, Thürmer A, Albrecht D, Woll-Djukic M, Brzuszkiewicz E, Fünfhaus A, Voss J, Gollnow K, Poppinga L, Liesegang H, Garcia-Gonzalez E, Genersch E, Daniel R (2014) How to kill the honey bee larva: genomic potential and virulence mechanisms of *Paenibacillus* larvae. PLOS One 9:e90914

Voget S, Wemheuer B, Brinkhoff T, Vollmers J, Dietrich S, Giebel H.-A., Beardsley C, Sardemann C, Bakenhus I, Billerbeck S, Daniel R, Simon M (2014) Adaptation of an abundant *Roseobacter* RCA organism to pelagic systems revealed by genomic and transcriptomic analyses. ISME J doi:10.1038/ismej.2014.134

Wemheuer B, Güllert S, Billerbeck S, Giebel H-A, Voget S, Simon M, Daniel R (2014) Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. FEMS Microbiology Ecology 87: 378-389

Nacke H, Fischer C, Thürmer A, Meinicke P, Daniel R (2014) Land use type significantly affects microbial gene transcription in soil. Microbial Ecology 67: 919-930

Schneider D, Arp G, Reimer A, Reitner J, Daniel R (2013) Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati Atoll, Central Pacific. PLOS ONE 8:e66662



Institute of Molecular Oncology University Medical Center Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 13840 fax: +49-551-39 13713 e-mail: mdobbel@unigoettingen.de

#### **Further Information**

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

## **Matthias Dobbelstein**

#### **Professor of Molecular Oncology**

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

## **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 nongenotoxic 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

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 Cell61(1): 68-83

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

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

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

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

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

Beyer U, Moll-Rocek J, Moll UM, Dobbelstein M (2011) Endogenous retrovirus drives hitherto unknown proapoptotic p63 isoforms in the male germ line of humans and great apes. Proc Natl Acad Sci USA 108(9): 3624-9



Dept. of Developmental Biochemistry University Medical Center Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 14607 fax: +49-551-39 14614 e-mail: roland.dosch@med. uni-goettingen.de

#### **Further Information**

http://www.uni-bc.gwdg.de/index.php?id=583

## **Roland Dosch**

## Group Leader at the Dept. of Developmental Biochemistry

- 1994 1999 PhD Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany
- 1999 2003 Postdoc University of Pennsylvania, Philadelphia, USA
- 2004 2010 Junior group leader, University of Geneva, Switzerland
- since 2010 Group leader at the Dept. of Developmental Biochemistry, Georg August University, Göttingen

#### **Major Research Interests**

A fundamental hallmark of biological systems is their capacity to reproduce. This remarkable phenomenon is not seen in other domains of science such as chemistry or physics. Multicellular organisms use for their reproduction a dedicated cell lineage termed germ cells. In most animals, only differentiated germ cells *i.e.* sperm and egg have the impressive capacity to generate a copy of their parents. Our team focuses therefore on the molecular mechanism, which control the development of the germline in vertebrates. To investigate this fascinating process in an entire vertebrate model organism, we take advantage of the molecular toolbox available in the zebrafish. These technologies include molecular genetics (e.g. CRISPR/Cas9 system for genome editing), *in vivo* imaging of transparent embryos and biochemistry exploiting the large number of progeny. With these outstanding tools, we have focused our research on two process during zebrafish germline development:

- Germ plasm formation
- Vesicle trafficking

Through our research on vesicle trafficking in oocytes, we recently entered into the research area of neurodegenerative disease. More specifically, genes involved in vesicle trafficking in zebrafish oocytes are also involved in Hereditary Spastic Paraplegia (HSP) in humans. Our long-term goal is here to understand the cellular basis of HSP and to establish zebrafish as an animal model to screen for therapeutic drugs.

#### **Selected Recent Publications**

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

Riemer S, Bontems F, Krishnakumar P, Gömann J, Dosch R, (2015) A functional Bucky ball-GFP transgene visualizes germ plasm in living zebrafish. Gene Expr Patterns 18: 44-52

Kanagaraj P, Gautier-Stein A, Riedel D, Schomburg C, Cerda J, Vollack N, Dosch R (2014) Souffle/Spastizin controls secretory vesicle maturation during zebrafish oogenesis. PLoS Genet 10: e1004449

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

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



III. Physical Institute Biophysics / Complex Systems University of Göttingen Friedrich-Hund-Platz 1

37077 Göttingen Germany

phone: +49-551-39 13833 fax: +49-551-39 7720 e-mail: joerg.enderlein@ physik3.gwdg.de

#### **Further Information**

http://www.joergenderlein.de

## 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**

Karedla N, Stein SC, Hahnel D, Gregor I, Chizhik A, Enderlein J (2015) Simultaneous Measurement of the Three-Dimensional Orientation of Excitation and Emission Dipoles. Phys Rev Lett 115(17): 173002

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

Pieper C, Enderlein J (2011) Fluorescence correlation spectroscopy as a tool for measuring the rotational diffusion of macromolecules. Chem Phys Lett 516: 1-11

Chizhik AI, Chizhik AM, Khoptyar D, Bär S, Meixner AJ, Enderlein J (2011) Probing the Radiative Transition of Single Molecules with a Tunable Microresonator. Nano Lett 11: 1700-1703

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

Berndt M, Lorenz M, Enderlein J, Diez S (2010) Axial Nanometer Distances Measured by Fluorescence Lifetime Imaging Microscopy. Nano Lett 10: 1497-1500

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

Chizhik A, Schleifenbaum F, Gutbrod R, Chizhik A, Khoptyar D, Meixner AJ, Enderlein J (2009) Tuning the Fluorescence Emission Spectra of a Single Molecule with a Variable Optical Sub-wavelength Metal Microcavity. Phys Rev Lett 102: 073002-6



Albrecht von Haller Institute for Plant Sciences Dept. of Plant Biochemistry University of Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 5743 fax: +49-551-39 5749 e-mail: ifeussn@gwdg.de

#### **Further Information**

http://www.plant-biochem. uni-goettingen.de

## Ivo Feußner

#### **Professor of Biochemistry**

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

#### **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-offunction") 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 and more specifically by studying the biosynthesis of aldehydes (fruit aromas) and hydroxy fatty acids (plant defence). Other studies deal with the role of oxylipins in plants, mosses and algae. In addition the catalytic mechanism of lipoxygenases and related dioxygenases is analysed.

Biochemistry of the biosynthesis of structural lipids:

Even in plants a huge number of different fatty acids are found. We are interested in enzymes which introduce new functionalities (i.e. double bonds at unusual positions or conjugated double bonds) in the fatty acid backbone in order to obtain new seed oils for biotechnological, nutritional and medical purposes. Moreover 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 and fungi as well as with wax ester forming enzymes. In addition we aim to identify chemical signals by metabolomics approaches that are exchanged during the infection between *Verticillium longisporum* and *Arabidopsis thaliana*.

#### **Selected Recent Publications**

Iven T, Hornung E, Heilmann M, Feussner I (2016) Synthesis of oleyl oleate wax esters in *Arabidopsis thaliana* and *Camelina sativa* seed oil. Plant Biotechnol J 14: 252-259

Tarazona P, Feussner K, Feussner I (2015) An enhanced plant lipidomics method based on multiplexed liquid chromatography-mass spectrometry reveals additional insights into cold- and drought-induced membrane remodeling. Plant J 84: 621-633

Tanaka S, Brefort T, Neidig N, Djamei A, Kahnt J, Vermerris W, Koenig S, Feussner K, Feussner I, Kahmann R (2014) A secreted Ustilago maydis effector promotes virulence by targeting anthocyanin biosynthesis in maize. eLife 3: e01355



Dept. of Molecular Structural Biology Institute for Microbiology and Genetics & GZMB University of Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 14072 fax: +49-551-39 14082 e-mail: rficner@gwdg.de

#### **Further Information**

www.uni-goettingen.de/msb

## **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**

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) elF5B 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, Gorlich 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 β-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



Laboratory of Chromatin Biochemistry Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1340 fax: +49-551-201 1197 e-mail: wfischl@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/research/ags/fischle/

## **Wolfgang Fischle**

## **Group Leader at the MPI for Biophysical Chemistry**

- Dr. rer. nat. (PhD), University of Tübingen, Germany, 2001
- Graduate Research Fellow, The J. David Gladstone Institute (UCSF), San Francisco, CA, USA, 1997 – 2001
- Postdoctoral Fellow, The Rockefeller University, New York, NY, USA, 2001 – 2005
- Damon Runyon Cancer Research Fellow, 2002 2005
- Head of the Chromatin Biochemistry Group, Max Planck Institute for Biophysical Chemistry, Gottingen, Germany, since 2006

#### **Major Research Interests**

To sustain life in different environments cells and organisms must adjust to different conditions and external cues. In contrast to immediate and mostly transient responses to short-term stimuli, processes of long-term adaptation require lasting changes in gene expression patterns. Such epigenetic changes are controlled on the level of chromatin, the packaging form of eukaryotic genomes. Here, different DNA and histone modifications are associated with distinct functional states of chromatin.

Overall, our research aims to gain detailed, fundamental understanding of the processes that read and translate patterns of chromatin marks for mediating biological outcomes. Currently, we are tackling two main questions. A) How do histone modifications in conjunction with DNA methylation establish seemingly stable chromatin structures in response to internal and external cues? B) How do small cellular metabolites and signaling molecules tune the readout of chromatin marks? To address these problems we are constantly expanding our highly interdisciplinary approaches. These include advancing technologies for establishing and analyzing complex chromatin systems *in vitro* (biochemistry and biophysics), molecular and cellular biology for studying essential chromatin components and global analysis of modules of epigenetic regulation.

We strongly believe that by understanding the essential molecular control mechanisms of chromatin regulation we will ultimately be able to develop strategies for intervention of major diseases.

#### Selected Recent Publications

Stützer A, Liokatis S, Kiesel A, Schwarzer D, Sprangers R, Söding J, Selenko P, Fischle W (2016) Modulations of DNA contacts by linker histoens and post-translational modifications determine the mobility and modifiability of nucleosomal H3 tails. Mol Cell 61: 247-259

Hiragami-Hamada K, Soeroes S, Nikolov M, Wilkins B, Kreuz S, Chen C, De La Rosa-Velázquez IA, Zenn HM, Kost N, Pohl W, Chernev A, Schwarzer D, Jenuwein T, Lorincz M, Zimmermann B, Walla PJ, Neumann H, Baubec T,Urlaub H, Fischle W (2015) Dynamic and flexible bridging of H3K9me3 via HP1β-dimerization establishes a plastic state of condensed chromatin. Nat Comm.7: 11310

Kost N, Kaiser S, Ostwal Y, Riedel D, Stützer A, Nikolov M, Rathke C, Renkawitz-Pohl R, Fischle W (2015) Multimerization of *Drosophila* sperm protein Mst77F causes a unique condensed chromatin structure. Nucleic Acids Res 43: 3033-3044

Gelato KG, Tauber M, Ong M, Winter S, Hiragami-Hamada K, Sindlinger J, Lemak A, Bultsma Y, Houliston S, Schwarzer D, Divecha N, Arrowsmith CH, Fischle W (2014) Interaction of UHRF1 with the unmodified or lysine 9 trimethylated H3 tail is allosterically regulated by phosphatidylinositol 5-phosphate. Mol Cell 54: 905-919

Wilkins BJ, Rall NA, Ostwal Y, Kruitwagen T, Hiragami-Hamada K, Winkler M, Barral Y, Fischle W, Neumann H (2014) A cascade of histone modifications induces chromatin condensation in mitosis. Science 343: 77-80



Dept. of General and Developmental Plant Physiology Schwann-Schleiden Research Center University of Göttingen Julia-Lermontowa-Weg 3

37077 Göttingen Germany

phone: +49-551-39 177821 fax.: +49-551-39 177829 e-mail: cgatz@gwdg.de

#### **Further Information**

http://www.uni-goettingen.de/de/311988.html

### **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 (crosstalk). Members of the TGA family of transcription factors have been identified as essential regulators of both responses. These proteins reside in the cell in an inactive state before pathogen infection. We are interested in the SA-mediated mechanisms that activate TGA factors when they function as activators of the SA response (Fode et al., 2008). Moreover, we analyze, how these factors mediate the negative effect of SA on the JA/ET response (Zander et al., 2010; Zander et al 2012). In this context, we have identified the family of plant-specific ROXY-type glutaredoxins, which interact with TGA factors to influence defense responses (Ndamukong et al., 2007; Zander et al., 2012).

We combine genetic (e.g. analysis of mutants and double mutants), 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) 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.

#### **Selected Recent Publications**

Gutsche N, Thurow C, Zachgo S, Gatz C (2015) Plant-specific CC-type glutaredoxins: functions in developmental processes and stress responses. Biol Chem 396(5): 495-509

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



Dept. of Cellular Logistics Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2401 e-mail: dgoerli@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/research/dep/goerlich/

### Dirk Görlich

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

- 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

### **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**

Chug H, Trakhanov S, Hülsmann BB, Pleiner T, Görlich, D (2015) Crystal structure of the metazoan Nup62•Nup58•Nup54 nucleoporin complex. Science 350(6256): 106-10

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

Frey S, Görlich D (2014) A new set of highly efficient, tag-cleaving proteases for purifying recombinant proteins. J Chromatogr A 1337: 95-105

Samwer M, Dehne HJ, Spira F, Kollmar M, Gerlich DW, Urlaub H, Görlich D (2013) The nuclear F-actin interactome of *Xenopus* oocytes reveals an actin-bundling kinesin that is essential for meiotic cytokinesis. EMBO J 32: 1886-1902

Labokha AA, Gradmann S, Frey S, Hülsmann BB, Urlaub H, Baldus M, Görlich D (2013) Systematic analysis of barrier-forming FG hydrogels from *Xenopus* nuclear pore complexes. EMBO J 32: 204-218

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

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. Nat Struct Mol Biol 17: 1367-1376

Frey S, Görlich D (2009) FG/FxFG as well as GLFG repeats form a selective permeability barrier with self-healing properties. EMBO J 28: 2554-2567

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



Dept. of NMB-based Structural Biology Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2201 +49-551-201 2200 fax: +49-551-201 2202 e-mail: cigr@nmr.mpibpc. mpg.de

#### **Further Information**

http://medusa.nmr.mpibpc.mpg.de/

## **Christian Griesinger**

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

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

### **Major Research Interests**

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

#### **Selected Recent Publications**

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

Wagner J, Ryazanov S, Leonov A, Levin J, Shi S, Schmidt F, Prix C, Pan-Montojo F, Bertsch U, Mitteregger-Kretzschmar G, Geissen M, Eiden M, Leidel F, Hirschberger T, Deeg AA, Krauth JJ, Zinth W, Tavan P, Pilger J, Zweckstetter M, Frank T, Bähr M, Weishaupt JH, Uhr M, Urlaub H, Teichmann U, Samwer M, Bötzel K, Groschup M, Kretzschmar H, Griesinger C, Giese A (2013) Anle138b: a novel oligomer modulator for disease-modifying therapy of neurodegenerative diseases such as prion and Parkinson's disease. Acta Neuropathol 125(6): 795-813

Honndorf V, Coudevylle N, Laufer S, Becker S, Griesinger C, Habeck M (2012) Inferential NMR/X-ray-based structure determination of a dibenzo[a,d]cycloheptenone inhibitor-p38a MAP kinase complex in solution. Angew Chem Int Ed 51: 2359-2362

Ban D, Funk M, Gulich R, Egger D, Sabo TM, Walter KFA, Bryn Fenwick R, Giller K, Pichierri F, de Groot BL, Lange OF, Grubmüller H, Salvatella X, Wolf M, Loidl A, Kree R, Becker S, Lakomek NA, Lee D, Lunkenheimer P, Griesinger C (2011) Kinetics of conformational sampling in ubiquitin. Angew Chem Int Ed 50: 11437-11440

Rodriguez-Castaneda F, Maestre-Martinez M. Coudevylle N, Dimova K, Junge H, Lipstein N, Lee D, Becker S, Brose N, Jahn O, Carlomagno T, Griesinger C (2010) Modular architecture of Munc13/calmodulin complexes: dual recognition by Ca<sup>2+</sup> and possible function in short-term synaptic plasticity. EMBO J 29: 680-91

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

Bayrhuber M, Meins T, Habeck M, Becker S, Giller K, Villinger S, Vonrhein C, Griesinger C, Zweckstetter M, Zeth K (2008) Structure of the human voltage-dependent anion channel. Proc Natl Acad Sci USA 105: 15370-15375



Department of Medical Microbiology Medical Faculty of the University of Göttingen Kreuzbergring 57

37075 Göttingen Germany

phone: +49-551-39 5801 +49-551-39 5806 fax: +49-551-39 5861 e-mail: ugross@gwdg.de

#### **Further Information**

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

### **Uwe Groß**

#### **Professor of Medical Microbiology**

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

#### **Major Research Interests**

The Institute of Medical Microbiology is trying to understand infectious diseases by linking applied and basic sciences, e.g. aspects of epidemiology and pathogenesis. In regards to bacteriology, we are focusing on the intestinal pathogens *Campylobacter jejuni* and *Clostridium difficile*, where we use molecular approaches to identify and characterize virulence-associated factors, such as those involved in invasion (*Campylobacter*) or in spore regulation (*Clostridium*). In addition, the epidemiology of both pathogens in different regions and environments is under investigation.

Fungal infections caused by *Candida* and *Aspergillus* is a second major research topic. Like in bacterial infections, antimicrobial resistances are an emerging threat in mycology as well. Therefore, we focus on analyzing the epidemiology and the mechanisms of antifungal resistances, but are also investigating fungal factors and mechanisms that are involved in pathogenesis of mycoses.

The protozoan parasite *Toxoplasma gondii* usually causes asymptomatic infections in immunocompetent adults leading to lifelong persistence especially in the brain and in muscle tissue. Infections are especially dangerous during pregnancy and in immuno-compromised individuals (i.e. patients suffering from AIDS). We are interested in the epidemiology of toxoplasmosis as well as in the cross-talk between the parasite and its host cell on a molecular level. Here, we investigate how the parasite (i) modulates the host cell capacity for MHC-restricted antigen presentation and (ii) inhibits apoptosis of the infected cell. Both mechanisms allow intracellular persistence.

Recently, we also started to develop the theme Global Health in regards to infectious diseases and cooperate with scientists from Ghana, Kenya, and Tanzania

#### **Selected Recent Publications**

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

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

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

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

Bader O, Weig M, Reichard U, Lugert R, Kuhns M, Christner M, Held J, Peter S, Schumacher U, Buchheidt D, Tintelnot K, Groß U, MykoLabNet-D Partners (2013) Cyp51A-based mechanisms of *Aspergillus fumigatus* azole drug resistance present in clinical samples from Germany. Antimicrobial Agents Chemother 57: 3513-357



Dept. of Developmental Biochemistry University Medical Center Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 14613 fax: +49-551-39 14614 e-mail: Joerg.grosshans@ medizin.uni-goettin-

gen.de

#### **Further Information**

http://www.gwdg.de/ ~jgrossh/ http://www.uni-goettingen. de/en/105241.html

## Jörg Großhans

## **Professor of Developmental Biochemistry**

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

## **Major Research Interests**

Biological structure formation and ageing.

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

#### **Selected Recent Publications**

Winkler F, Gummalla M, Künneke L, Lv Z, Zippelius A, Aspelmeier T, Großhans J (2015) Fluctuation analysis of centrosomes reveals a cortical function of Kinesin-1. Biophysical Journal 109(5): 856-68

Wessel AD, Gummalla M, Grosshans J, Schmidt CF (2015) The mechanical properties of early *Drosophila* embryos measured by high-speed video microrheology. Biophysical Journal 108: 1899-1907

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

Acharya S, Laupsien P, Wenzl C, Yan S, Großhans J (2014) Function and dynamics of slam in furrow formation in early *Drosophila* embryo. Dev Biol 386: 371-384

Schulz O, Pieper C, Hähnel D, Clever M, Pfaff J, 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.

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

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

Albrecht SC, Barata A, Grosshans J, Teleman AA, Dick TP (2011). *In vivo* mapping of hydrogen peroxide and oxidaized glutathione reveals chemical and regional specificity of redox homeostasis. Cell Metab 14: 819-29



Dept. of Theoretical and Computational Biophysics Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2300 +49-551-201 2301 fax: +49-551-201 2302 e-mail: hgrubmu@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/home/grubmueller/index.html

## **Helmut Grubmüller**

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

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

## **Major Research Interests**

The question 'How do proteins work?' is our driving force. We study biomolecular dynamics and function by atomistic molecular dynamics and qm/mm simulations. Emphasis is on protein function, as well as on protein/DNA/RNA interactions.

Available projects address nuclear pore transport, the ribosome, molecular motors such as F-ATPase, protein unfolding as well as the interaction with radiation with a focus at single molecules, typically in close collaboration with experimental groups. The simulation of single molecule AFM experiments by force probe techniques helps us to reveal mechanisms of proteins 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 post-docs 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. 3000 processor cores.

## **Selected Recent Publications**

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

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

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

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

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

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

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



Department of Human Genetics Section of Developmental Genetics University Medical Center Göttingen Heinrich-Düker-Weg 12

37073 Göttingen Germany

phone: +49-551-39 14010 fax: +49-551-39 6580 e-mail: hhahn@gwdg.de

#### **Further Information**

http://www.uni-goettingen.de/en/57976.html

### Heidi Hahn

## **Professor of Molecular Developmental Genetics**

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

### **Major Research Interests**

Cancer is a disease that results from inappropriate cell division induced by hyperproliferation. In many cases, the development of cancer is associated with genes or signaling pathways important for patterning during embryogenesis.

We investigate the role of the Hedgehog/Patched (Hh/Ptch) signaling cascade in the development of solid tumors. The focus is on rhabdomyosarcoma and basal cell carcinoma. In addition, we are investigating the role of Hh/Ptch signaling in cutaneous squamous cell carcinoma and adenoma of the pituitary gland.

The first aim is the discovery of molecular and cellular events that trigger the initiation of Ptch associated tumors. The second aim is to elucidate the function of Hh signaling during tumor progression. The current focus is on the interaction between Hh/Ptch and Wnt signaling, and on Hh/Ptch and Ras signaling during formation and progression of basal cell carcinoma and rhabdomyosarcoma. The third goal is the identification of drugs that target Hh/Ptch-associated solid tumors. Currently we are analyzing the anti-tumoral effects of several Hh inhibitors in combination with drugs targeting the Ras/Mek/Erk and PI3K/Akt/mTor signaling cascades. To test the anti-tumor activity of the drugs we use tumor-bearing Ptch mutant mice.

#### **Selected Recent Publications**

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

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

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

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

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

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

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



Dept. of NanoBiophotonics Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2501 fax: +49-551-201 2505 e-mail: shell@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/groups/hell/

## **Stefan Hell**

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

- 1987 Diploma in Physics, University of Heidelberg (1.0)
- 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
- since 12/2003 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
- 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**

Hoyer P, de Medeiros G, Balázs B, Norlin N, Besir C, Hanne J, Kräusslich H-G, Engelhardt J, Sahl SJ, Hell SW, Hufnagel L (2016) Breaking the diffraction limit of light-sheet fluorescence microscopy by RESOLFT. Proc Natl Acad Sci USA 113: 3442-3446

Danzl JG, Sidenstein SC, Gregor C, Urban NT, Ilgen P, Jakobs S, Hell SW (2016) Coordinate-targeted fluorescence nanoscopy with multiple off states. Nature Photonics 10: 122-128

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

Hanne J, Falk HJ, Görlitz F, Hoyer P, Engelhardt J, Sahl SJ, Hell SW (2015) STED nanoscopy with fluorescent quantum dots. Nat Commun 6: 7127

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

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

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

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



Dept. of Molecular Microbiology and Genetics University of Göttingen Grisebachstraße 8

37077 Göttingen <u>Ger</u>many

phone: +49-551-39 3815 fax: +49-551-39 3330 e-mail: kheimel@gwdg.de

#### **Further Information**

http://www.uni-goettingen.de/de/434133.html

## Kai Heimel

#### **Professor of Microbial Cell Biology**

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

### **Major Research Interests**

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

#### **Selected Recent Publications**

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

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

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

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

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

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

Zahiri A\*, Heimel K\*, Wahl R, Rath M, Kämper J (2010) The Ustilago maydis Forkhead Transcription Factor Fox1 Is Involved in the Regulation of Genes Required for the Attenuation of Plant Defenses During Pathogenic Development. Mol Plant Microbe Interact 18(9): 1118-29 (\*equal contribution)



Institute for Organic and Biomolecular Chemistry University of Göttingen Tammannstr. 2

37077 Göttingen Germany

phone: +49-551-39 20906 e-mail: claudia.hoebartner @chemie.unigoettingen.de

#### **Further Information**

https://www.uni-goettingen.de/en/507570.html

## Claudia Höbartner

## **Professor, Institute for Organic and Biomolecular Chemistry**

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

### **Major Research Interests**

Our research is focused on the chemistry and biochemistry of natural and artificial nucleic acids.

Functional nucleic acids with new properties can be identified in the laboratory by *in vitro* selection. We use this method to develop catalytic DNA and RNA for labeling and ligation reactions of biomolecules, and we explore functional and structural properties of deoxyribozymes and fluorogenic aptamers. Recently we reported the first crystal structure of a catalytic DNA which allowed mechanistic insights into the regioselectivity of DNA-catalyzed RNA ligation and enabled engineering of DNA enzymes for substrates that could previously not be used in DNA-catalyzed ligations.

In addition, we investigate natural modifications of DNA and RNA and develop labeling methods for their biochemical and spectroscopic detection, with particular emphasis on the emerging field of posttranscriptional RNA modification.

#### **Selected Recent Publications**

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

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

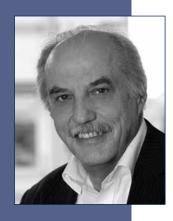
Javadi-Zarnaghi F, Höbartner C (2016) Functional hallmarks of a catalytic DNA that makes lariat RNA. Chem Eur J 22: 3720-3728

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

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

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

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



Dept. of Molecular Developmental Biology Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1482 fax: +49-551-201 1755 e-mail: hjaeckl@gwdg.de

### **Further Information**

http://www.mpibpc.mpg.de/groups/jaeckle

## Herbert Jäckle

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

- Faculty member at the EMBL, Heidelberg (1980 1982)
- Head of the group (associate professor), Max Planck Institute for Develop mental Biology, Tübingen (1982 – 1988)
- Professor and Chairman, Dept. of Genetics and Microbiology, Univ. of Munich (1988 – 1991)
- Director, Dept. of Molecular Developmental Biology, Max Planck Institute for Biophysical Chemistry, Göttingen
- Vice-President of the Max Planck Society

#### **Major Research Interests**

Our research interest is focused on molecular processes and the mechanisms involved in the phenonenon of biological pattern formation during Drosophila embryogenesis. Aim of my studies is a better understanding of the biochemical pathways and the molecular characterization of the regulatory networks leading to the establishment of the segmental organization of the embryo, organ formation and cell behaviour underlying morphogenesis. Recent work concerns the genetic basis for energy homeostasis in cells.

#### **Selected Recent Publications**

Pengelly AR, Copur O, Jäckle H, Herzig A, Mueller J (2013) A histone mutant reproduces the phenotype caused by loss of histone-modifying factor Polycomb. Science 339(6120): 698-699

Thiel K, Heier C, Haberl V, Thul PJ, Oberer M, Lass A, Jäckle H, Beller M (2013) The evolutionarily conserved protein CG9186 is associated with lipid droplets, required for their positioning and for fat storage. Journal of Cell Science 126(10): 2198-2212

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

Herzig B, Yakulov T, Klinge K, Günesdogan U, Jäckle H, Herzig A (2014) Bällchen is required for self-renewal of germline stem cells in *Drosophila melanogaster*. Biology Open 3(6): 510-521

Pflanz R, Voigt A, Yakulov T, Jäckle H (2015) *Drosophila* gene tao-1 encodes proteins with and without a Ste20 kinase domain that affect cytoskeletal architecture and cell migration differently. Open Biology 5(1): 140161



Dept. of Neurobiology Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1635 fax: +49-551-201 1639 e-mail: rjahn@gwdg.de

### **Further Information**

http://www.mpibpc.gwdg.de/abteilungen/190/

### **Reinhard Jahn**

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

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

#### **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 additional 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**

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

Jahn R, Fasshauer D (2012) Exocytosis of synaptic vesicles – molecular machines, calcium, and beyond (review). Nature 490(7419): 201-207

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



Dept. of NanoBiophotonics Mitochondrial Structure and Dynamics group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2531 fax: +49-551-201 2505 e-mail: sjakobs@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/groups/jakobs/

## **Stefan Jakobs**

## **Professor of High Resolution Microscopy in Neurodegenerative Diseases**

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

#### **Major Research Interests**

Our two major research interests are the investigation of the nanoscale architecture and dynamics of mitochondria and the analysis of reversibly switchable fluorescent proteins (RSFPs) as probes for super-resolution microscopy. Mitochondria are essential organelles in all eukaryotic cells and their dysfunction is involved in many devastating (neurodegenerative) diseases. We want to understand the organization of mitochondria on the nanoscale in healthy and challenged cells and investigate the molecular mechanisms that determine their intricate structure. We utilize a wide array of techniques, including molecular biology, biochemical methods as well as electron and super-resolution microscopy.

RSFPs are fluorescent proteins that may be switched by light between a non-fluorescent and a fluorescent state. Their unique properties open up numerous applications in microscopy and cell biology. We investigate the molecular switching mechanisms and aim to improve the properties of these fascinating proteins as probes for live-cell super-resolution microscopy.

#### **Selected Recent Publications**

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

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

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

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

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

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



Institute for Physical Chemistry Georg August University Göttingen Tammannstr. 6

37077 Göttingen Germany

phone: +49-551-201 10633 fax: +49-551-201 14411 e-mail: ajansho@gwdg.de

#### **Further Information**

http://www.uni-goettingen.de/en/208570.html

## **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**

Savic F, Kliesch TT, Verbeek S, Bao C, Thiart J, Kros A, Geil B, Janshoff A (2016) Epsin N-terminal Homology Domain (ENTH) activity as a function of membrane tension. Biophy J 110(10): 2216-2228

Rouven Brückner B, Pietuch A, Nehls S, Rother J, Janshoff A (2015) Ezrin is a Major Regulator of Membrane Tension in Epithelial Cells. Sci Rep 5: 14700

Brückner BR, Janshoff A (2015) Elastic properties of epithelial cells probed by atomic force microscopy. Biochim Biophys Acta 1853(11 Pt B):3075-82

Stephan M, Mey I, Steinem C, Janshoff A (2014) Combining reflectometry and fluorescence microscopy: An assay for the investigation of leakage processes across lipid membranes. Anal Chem 86: 1366-1371

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 Biol 4: 140046

Aggarwal S, Snaidero N, Pähler G, Frey S, Sánchez P, Zweckstetter M, Janshoff A, Schneider A, Weil M-T, Schaap IAT, Görlich D, Simons M (2013) Myelin membrane assembly is driven by a phase transition of myelin basic proteins into a cohesive protein meshwork. PLOS Biol 11: e1001577

Bao C, Pähler G, Geil B, Janshoff A (2013) An optical fusion assay based on membrane coated spheres in a 2D assembly. J Am Chem Soc 135: 12176-12179

Bakhti M, Snaidero N, Schneider D, Aggarwal S, Möbius W, Janshoff A, Eckhardt M, Nave K-A, Simons M (2013) Loss of electrostatic cell-surface repulsion mediates myelin membrane adhesion and compaction in the central nervous system. Proc Natl Acad Sci USA 110: 3143-3148

Krick R, Busse R A, 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. Proc Natl Acad Sci USA 109: E2042-E2049

Janke M, Rudzevich Y, Molokanova O, Metzroth T, Mey I, Diezemann G, Marszalek PE, Gauss J, Böhmer V, Janshoff A (2009) Mechanically locked nanocapsules under force allow reversible hydrogen bond breakage. Nat Nanotechnol 4: 225-229



Dept. of General, Visceral and Pediatric Surgery, University Medical Center Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 13711 fax: +49-551-39 13713 e-mail: steven.johnsen@ med.unigoettingen.de

#### **Further Information**

http://www.epigenesys. eu/index.php/fr/about-us/ associate-members/864steven-a-johnsen

## Steven Johnsen

#### **Full Professor for Translational Cancer Research**

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

#### **Major Research Interests**

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

## **Selected Recent Publications**

Kari V, Mansour WY, Raul SK, Baumgart SJ, Mund A, Grade M, Sirma H, Simon R, Will H, Dobbelstein M, Dikomey E, Johnsen SA (2016) Loss of CHD1 causes DNA repair defects and enhances prostate cancer therapeutic responsiveness. EMBO Reports 17(11): 1609-1623

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

Kosinsky RL, Wegwitz F, Hellbach N, Dobbelstein M, Mansouri A, Vogel T, Begus-Nahrmann Y, Johnsen SA. (2015) Usp22 deficiency impairs intestinal epithelial lineage specification *in vivo*. Oncotarget 6(35): 37906-18

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

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



Third Institute of Physics Dept. of Biophysics University of Göttingen Friedrich-Hund-Platz 1

37077 Göttingen Germany

phone: +49-551-39 13209 fax: +49-551-39 7720 e-mail: dklopfe@gwdg.de

#### **Further Information**

http://www.dpi.physik.unigoettingen.de/de/forschung/ dr-klopfenstein.html

## **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, 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



Dept of Molecular Genetics University of Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: +49-551-39 9653 fax: +49-551-39 3805 e-mail: wkramer@gwdg.de

#### **Further Information**

http://www.img.bio.unigoettingen.de/molgen.htm

## Wilfried Kramer

## **Privatdozent Molecular Biology and Genetics**

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

## **Major Research Interests**

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

#### **Selected Recent Publications**

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

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

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

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

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

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



Dept. of Molecular Genetics Institute for Microbiology and Genetics University of Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: +49-551-39 33801 fax: +49-551-39 33805 e-mail: heike.krebber@ biologie.unigoettingen.de

#### **Further Information**

http://www.img.bio.unigoettingen.de/molgen.htm

### 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 for Molecular Biology and Tumor Research, 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**

The compartmentalization of eukaryotic cells separates the place of transcription in the nucleus from the place of translation in the cytoplasm. Intron-containing premRNAs are retained in the nucleus until processing is completed. Only fully processed and spliced mRNAs are transported into the cytoplasm and translated at the ribosomes. The otherwise resulting gene products can be toxic to cells and harmful to organisms leading to diseases like cancer or neurodegenerative diseases. Our projects aim to identify and characterize the requirements for mRNA processing, transport and translation. In particular we focus mRNA quality control. In addition we work on the maturation, control and function of non-coding (nc) RNAs. Saccharomyces cerevisiae has been proven to be a useful model organism for eukaryotic cells and we use a combination of genetics, biochemistry and cell biology to uncover these processes.

#### **Selected Recent Publications**

Neumann B, Wu H, Hackmann A, Krebber H (2016) Nuclear export of pre-ribosomal subunits requires Dbp5, but not as a RNA-helicase as for mRNA export. PLOS ONE 11(2): e0149571

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

Tieg B, Krebber H (2013) Dbp5 – From nuclear export to translation. Biochem Biophys Acta 1829: 791-798

Hackmann A, Gross T, Baierlein C, Krebber H (2011) The mRNA export factor Npl3 mediates the nuclear export of large ribosomal subunits. EMBO Rep 12(10): 1024-1031

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

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

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



Dept. of Plant Cell Biology Department of Plant Cell Biology Schwann-Schleiden Research Center University of Göttingen Julia-Lermontowa-Weg 3

37077 Göttingen Germany

phone: +49-551-39 177801 e-mail: Volker.Lipka@ biologie.unigoettingen.de

#### **Further Information**

http://www.uni-goettingen.de/en/33181.html

## **Volker Lipka**

## **Professor of Plant Cell Biology**

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

### **Major Research Interests**

Our laboratory is interested in the molecular analysis of plant innate immunity. Our research is focused on 1) the molecular dissection of mechanisms that control activation of basal defence in the plant model *Arabidopsis thaliana* 2) the analysis of defence mechanisms that contribute to resistance against fungal pathogens 3) the identification of fungal effector molecules that interfere with the plant defence machinery and allow host plant colonization

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

#### **Selected Recent Publications**

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

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

Huang Y, Chen X, Liu Y, Roth C, Copeland C, McFarlane HE, Huang S, Lipka V, Wiermer M Li X (2013) Mitochondrial AtPAM16 is required for plant survival and the negative regulation of plant immunity. Nature Communications 4: 2558

Faulkner C, Petutschnig E, Benitez-Alfonso Y, Beck M, Robatzek S, Lipka V, Maule AJ (2013) LYM2-dependent chitin perception limits molecular flux via plasmodesmata. Proc Nat Acad Sci USA 110(22): 9166-9170

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



Dept. Cellular Biochemistry Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1407 fax: +49-551-201 1197 e-mail: reinhard.luehrmann @mpi-bpc.mpg.de

#### **Further Information**

http://www.mpibpc.gwdg.de/research/dep/luehrmann/

## Reinhard Lührmann

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

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

### **Major Research Interests**

Most metazoan pre-mRNAs contain multiple introns and exons. In order to generate mature mRNA, the introns must be excised from the pre-mRNA, a process termed pre-mRNA splicing. In many cases, alternative splicing generates different mRNAs from a single pre-mRNA by the regulated removal of different sections of the RNA, a process which greatly expands the complexity of the repertoire of proteins that can be expressed from relatively small genomes. Splicing is catalysed by a large macromolecular machine, termed the spliceosome which consists of the small nuclear RNAs (U1, U2, U4, U5 and U6) and more than 150 proteins, 50 of which are associated with the snRNAs to form snRNPs.

In our laboratory, intense efforts are focussed on understanding how the spliceosome recognizes and binds the intron ends and discriminates them from exons. This is an especially confounding problem in metazoans because, in contrast to lower eucaryotes such as yeast, pre-mRNA introns are often extremely long (104-105 nucleotides), while exons are generally small (less than 300 nucleotides). Another major goal of our research is the elucidation of the mechanisms by which the spliceosome assembles into a catalytically active machine and catalyses intron excision. None of the building blocks of the spliceosome contains an active site. Instead, the catalytically active domain must be assembled anew on to each intron, a highly dynamic process which entails dramatic structural rearrangements of the RNP structure of the spliceosome, and which is orchestrated by the successive action of more than 10 enzymes such as RNA helicases and GTPases, as well as by posttranslational phosphorylation of a multitude of spliceosomal proteins. Our studies involve a large number of experimental approaches, including biochemical purification of entire spliceosomes or large protein ensembles, and characterization of their proteins by mass spectrometry; RNA biology methods such as enzymatic engineering of RNA molecules, RNA structure probing and RNA interference methods; production of recombinant proteins and antibodies; procedures for the investigation of protein-protein and protein-RNA interactions in vitro and in vivo; and biophysical methods such as fluorescence spectroscopy.

Finally, we are investigating the 3D structure of purified spliceosomes or major building blocks thereof using electron microscopic approaches and X ray crystallography. Our studies on the regulatory mechanisms of constitutive and alternative pre-mRNA splicing involve mainly mammalian systems. As the basic mechanisms of splicing catalysis appear to be evolutionarily highly conserved, we are also taking advantage of molecular genetic approaches in baker yeast to elucidate the structure and function of the catalytic core domain of the spliceosome.

#### **Selected Recent Publications**

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

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

Wahl MC, Lührmann R (2015) Snapshot: Spliceosome Dynamics I-III. Cell 161: 1474, Cell 162: 456, Cell 162: 690

Warkocki Z, Schneider C, Mozaffari-Jovin S, Schmitzova J, Höbartner C, Fabrizio P, Lührmann R (2015) The G patch protein Spp2 couples the spliceosome-stimulated ATPase activity of the DEAH-box protein Prp2 to catalytic activation of the spliceosome. Genes Dev 29: 94-107

Mozaffari-Jovin S, Wandersleben T, Santos KF, Will CL, Lührmann R, Wahl MC (2013) Inhibition of RNA helicase Brr2 by the C-terminal tail of the spliceosomal protein Prp8. Science 341: 80-84

Wahl MC, Will CL, Lührmann R (2009) The spliceosome: design principles of a dynamic RNP machine. Cell 136: 701-718

Warkocki Z, Odenwälder P, Schmitzova J, Platzmann F, Stark H, Urlaub H, Ficner R, Fabrizio P, Lührmann R (2009) Reconstitution of both steps of *S. cerevisiae* splicing with purified spliceosomal components. Nature Struct Mol Biol 16: 1237-1243



Dept. of Molecular
Cell Biology
Molecular Cell
Differentiation
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1709 fax: +49-551-201 1504 e-mail: amansou@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/groups/gruss

## **Ahmed Mansouri**

#### **Molecular Developmental Genetics**

- Diploma (Chemistry), Technical University, Braunschweig (Germany) 1975
- Dr. rer. nat. Chemical Technology Institute, Technical University, Braunschweig (Germany), 1978
- Postdoc at the Institute of Human Genetics in Göttingen (1982 1986)
- · Postdoc at the Miescher Institute in Tübingen (MPI) and at the Max Planck
- Institute of Immunbiology in Freiburg (Germany) (1986 1989)
- Since 1989: Dept of Molecular Cell Biology at the MPI for Biophysical Chemistry in Göttingen
- Habilitation (Molecular Developmental Genetics), University of Göttingen, Germany, 1999
- Since 2005: Dr. Helmut Storz Stiftungsprofessur for "dopaminerge Stammzelltherapie", Dept. of Clinical Neurophysiology at the University of Göttingen

#### **Major Research Interests**

Studying the molecular mechanisms controlling cell fate destiny and diversity is of fundamental interest for understanding pathological processes and diseases. We are using mouse genetics to study the role of transcription factors during cell differentiation in the endocrine pancreas and in the ventral midbrain.

In the pancreas, we are interested in molecules that control the endocrine cell subtype specification. In addition, we are studying animal models to uncover molecular pathways promoting beta-cell regeneration in the adult pancreas.

In the midbrain the specification of dopaminergic neurons is under the control of several transcription and secreted factors. Specifically, we want to identify factors that interact with Lmx1 a/b in order to promote the generation of functionally distinct dopaminergic neuron populations.

### **Selected Recent Publications**

Ahmad Z, Rafeeq M, Collombat P, Mansouri A (2015) Pax6 Inactivation in the Adult Pancreas Reveals Ghrelin as Endocrine Cell Maturation Marker. PLoS One 2015 Dec 11;10(12): e0144597

Liao MC, Diaconu M, Monecke S, Collombat P, Timaeus C, Kuhlmann T, Paulus W, Trenkwalder C, Dressel R, Mansouri A (2014) Embryonic stem cell-derived neural progenitors as non-tumorigenic source for dopaminergic neurons. World Journal of Stem Cells 6(2): 248-255

Shamsi F, Parlato R, Collombat P, Mansouri A (2014) A genetic mouse model for progressive ablation and regeneration of insulin producing beta-cells. Cell Cycle 13(24): 3948-3957

Al-Hasani K, Pfeifer, A, Courtney M, Ben-Othman N, Gjernes E, Vieira A, Druelle N, Avolio F, Ravassard P, Leuckx G et al. (2013) Adult duct-lining cells can reprogram into  $\beta$ -like cells able to counter repeated cycles of toxin-induced diabetes. Developmental Cell 26 (1): 86-100

Courtney M, Gjernes E, Druelle N, Ravaud C, Vieira A, Ben-Othman N, Pfeifer A, Avolio F, Leuckx G, Lacas-Gervais S et al. (2013) The inactivation of Arx in pancreatic alpha-cells triggers their neogenesis and conversion into functional beta-like cells. PLoS Genetics 9(10): e1003934



Dept. of Bioinformatics University of Göttingen Goldschmidtstrasse 1

37077 Göttingen Germany

phone: +49-551-39 14628 fax: +49-551-39 14966 e-mail: bmorgen@gwdg.de

#### **Further Information**

http://www.gobics.de/ burkhard/

## **Burkhard Morgenstern**

#### **Professor of Bioinformatics**

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

#### **Major Research Interests**

The focus of our research work is algorithm and software development for nucleic acid and protein sequence analysis; the multiple-alignment program "DIALIGN" and the gene-finding program "AUGUSTUS" are widely used tools that have been developed in our department. More recently, we started to work on alignment-free approaches to comparative sequence analysis, here we developed the tools "kmacs" and "spaced words".

Other areas of research in our department include: metabolomics and mass, spectroscopy data analysis, phylogeny reconstruction, metagenomics, motif discovery and remote homology detection using machine learning methods, genome annotation for prokaryotes, recombinations in viral genomes and HIV classification using coalescent theory.

#### **Selected Recent Publications**

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

Kaever A, Landesfeind M, Feussner K, Mosblech A, Heilmann I, Morgenstern B, Feussner I, Meinicke P (2015) MarVis-Pathway: integrative and exploratory pathway analysis of non-targeted metabolomics data. Metabolomics 11: 764-777

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

Leimeister C-A, Boden M, Horwege S, Lindner S, Morgenstern B (2014) Fast alignment-free sequence comparison using spaced-word frequencies. Bioinformatics 30: 1991-1999

Al Ait L, Yamak Z, Morgenstern B (2013) DIALIGN at GOBICS - multiple sequence alignment using various sources of external information. Nucleic Acids Res 41: W3-W7

Schultz A-K, Bulla I, Abdou-Chekaraou M, Gordien E, Morgenstern B, Zoulim F, Dény P, Stanke M (2012) jpHMM: Recombination analysis in viruses with circular genomes such as the hepatitis B virus. Nuc Acids Res 40: W193-W198



Institute for Auditory Neuroscience University Medical Center Göttingen Robert-Koch-Str. 40

37075 Göttingen Germany

phone: +49-551-39 22803 fax: +49-551-39 22299 e-mail: tmoser@gwdg.de

#### **Further Information**

http://www.auditory-neuro-science.uni-goettingen.de/

http://www.innerearlab.unigoettingen.de/

https://www.mpibpc.mpg.de/14722384/moser

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

## **Tobias Moser**

#### **Professor of Auditory Neuroscience**

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

### **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**

Jung S, Maritzen T, Wichmann C, Jing Z, Neef A, Revelo NH, Al-Moyed H, Meese S, Wojcik SM, Panou I, Bulut H, Schu P, Ficner R, Reisinger E, Rizzoli SO, Neef J, Strenzke N, Haucke V, Moser T (2015) Disruption of adaptor protein  $2\mu$  (AP- $2\mu$ ) in cochlear hair cells impairs vesicle reloading of synaptic release sites and hearing. EMBO J 34(21): 2686-702

Jung S, Oshima-Takago T, Chakrabarti R, Wong AB, Jing Z, Yamanbaeva G, Picher MM, Wojcik SM, Göttfert F, Predoehl F, Michel K, Hell SW, Schoch S, Strenzke N, Wichmann C, Moser T (2015) Rab3-interacting molecules  $2\alpha$  and  $2\beta$  promote the abundance of voltage-gated CaV1.3 Ca<sup>2+</sup> channels at hair cell active zones. Proc Natl Acad Sci USA 112(24): E3141-9

Pangršič T, Gabrielaitis M, Michanski S, Schwaller B, Wolf F, Strenzke N, Moser T (2015) EF-hand protein Ca<sup>2+</sup> buffers regulate Ca<sup>2+</sup> influx and exocytosis in sensory hair cells. Proc Natl Acad Sci USA 112(9): E1028-37

Chapochnikov NM, Takago H, Huang CH, Pangršič T, Khimich D, Neef J, Auge E, Göttfert F, Hell SW, Wichmann C, Wolf F, Moser T (2014) Uniquantal release through a dynamic fusion pore is a candidate mechanism of hair cell exocytosis. Neuron 83(6): 1389-403

Mendoza Schulz A, Jing Z, Sánchez Caro JM, Wetzel F, Dresbach T, Strenzke N, Wichmann C, Moser T (2014) Bassoon-disruption slows vesicle replenishment and induces homeostatic plasticity at a CNS synapse. EMBO J 33(5): 512-27

Wong AB, Rutherford MA, Gabrielaitis M, Pangrsic T, Göttfert F, Frank T, Michanski S, Hell S, Wolf F, Wichmann C, Moser T (2014) Developmental refinement of hair cell synapses tightens the coupling of Ca<sup>2+</sup> influx to exocytosis. EMBO J 33(3): 247-64



Dept. of Neurogenetics Max Planck Institute for Experimental Medicine Hermann-Rein-Strasse 3

37075 Göttingen Germany

phone: +49-551-38 99757 fax: +49-551-38 99758 e-mail: nave@em.mpg.de

#### **Further Information**

http://www.em.mpg.de/index.php?id=34&no\_cache=1

## **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
- 2000 Director, Department of Neurogenetics, Max Planck Institute for Experimental Medicine Göttingen and Professor of Biology, University of Heidelberg

#### **Major Research Interests**

We are interested in the mechanisms of neuron-glia interactions in the higher nervous system, and in the genes that are required for normal glial cell function. Here, transgenic and mutant mice have become important to study developmental processes as well as genetic diseases. For example, oligodendrocytes are glial cells highly specialized for enwrapping CNS axons with multiple layers of membranes, known to provide electrical insulation for rapid impulse propagation. We found that oligodendrocytes are also essential for maintaining the long-term integrity of myelinated axons, independent of the myelin function itself. The mechanisms by which oligodendrocytes support long-term axonal survival are still under investigation. The importance of glial cells as the "first line of neuroprotection", however, is illustrated by several myelin-associated diseases in which axonal neurodegeneration contribute to progressive disability. These range in humans from peripheral neuropathies (CMT1) to spastic paraplegia (SPG2), and presumably multiple sclerosis (MS) and certain forms of psychiatric disorders. We are developing transgenic animal models for some of these diseases, in order to dissect the underlying disease mechanisms and, in the case of CMT1A, have used these models to design novel therapeutic strategies.

The glial "decision" to myelinate an axonal segment is partly controlled by the axon itself, but the signaling mechanism is not understood. We have found that axonal neuregulin-1 (NRG1) is the major determinant of myelination in the peripheral nervous system. We are now investigating NRG1 dysregulation also in CNS myelination, using quantifiable behavioural functions in mice. By combining genetics with environmental risk factors for schizophrenia (in collaboration with H. Ehrenreich) we will explore the hypothesis that NRG1, a known human schizophrenia susceptibility gene, points to an important role of myelinating glia in some psychiatric disorders.

#### **Selected Recent Publications**

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 doi: 10.1038/nn.4425 [Epub ahead of print]

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

Tzvetanova ID, Nave KA (2014) Axons hooked to Schwann cell metabolism. Nat Neurosci 17(10): 1293-5

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



Macromolecular Crystallography Research Group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1046 fax: +49-551-201 1197 e-mail: vpena@gwdg.de

#### **Further Information**

http://www.mpibpc.mpg.de/home/pena/

### **Vladimir Pena**

## Research Group Leader at the MPI for Biophysical Chemistry

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

### **Major Research Interests**

The majority of genes in higher eukaryotes contain protein-coding exons that can be joined in a combinatorial fashion. The process, termed pre mRNA splicing, is an essential step in gene expression, and it expands tremendously the proteome and the complexity of an organism. Our goal is to understand the structural basis of pre-mRNA splicing. Here we place particular emphasis on the spliceosome's regulation, as well as on the misregulation that causes various diseases.

DNA catalysts are an increasingly important topic in the work pursued in our laboratory. The surprisingly complex fold that these molecules adopt raises questions about the structural importance of DNA in the cell, and it enables us to manipulate the molecules' properties for technological applications.

For our investigations we make use of biochemistry, X ray crystallography and – increasingly – electron microscopy.

#### **Selected Recent Publications**

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

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

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

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

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

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

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



Dept. of Developmental Biochemistry University Medical Center Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 5683 +49-551-39 14613 fax: +49-551-39 14614 e-mail: tpieler@gwdg.de

#### **Further Information**

http://www.uni-bc.gwdg.de/entwickl/index.html

### **Tomas Pieler**

## Professor of Biochemistry

- Dr. rer. nat. Biochemistry, Freie Universität Berlin, 1984
- · Guest Investigator, Rockefeller University, New York (1985/86)
- Heisenberg fellow, Freie Universität Berlin and Rockefeller University, New York (1986/87)
- Junior group leader, Max-Planck-Institut für Molekulare Genetik, Berlin (1988 – 1992)
- Professor of Biochemistry, Georg-August-Universität Göttingen (since 1992)
- Head of the Department of Developmental Biochemistry, Georg-August-Universität Göttingen

### **Major Research Interests**

The differentiation of complex organisms has its origin in the asymmetric distribution of regulatory proteins or of the corresponding mRNAs in the egg, as well as in a complex system of cell/cell communication events via extracellular signalling molecules during early stages of embryogenesis. The genes that encode for these different activities form functional networks which provide the basis for the genetic programming of embryonic development. Our primary research interest is in the identification of such regulatory genes and networks in vertebrates, as well as in the definition of their regulation and function on the molecular level. For this purpose, we use Xenopus laevis, a frog from South Africa, as a model system. As a traditional object in experimental embryology and in comparison with other experimental systems such as the mouse, use of Xenopus offers a number of practical advantages. Oocytes and embryos are easy to collect in large numbers, they are easy to manipulate by relatively simple techniques, also because embryonic development proceeds in the petridish, and, more recently, it has even become possible to generate hundreds of transgenic frogs within a single experimental day. The research topics that we are focussing on are:

- Transport and function of vegetally localized maternal mRNAs
- Organogenesis: formation of pancreas and liver in vertebrate embryos
- · Early neural development: primary neurogenesis
- · Germ cell specification and migration

#### **Selected Recent Publications**

Claußen M, Lingner T, Pommerenke C, Opitz L, Salinas G, Pieler T (2015) Global analysis of asymmetric RNA enrichment in oocytes reveals low conservation between closely related *Xenopus* species. Mol Biol Cell 26(21): 3777-87

Bauermeister D, Claußen M, Pieler T (2015) A novel role for Celf1 in vegetal RNA localization during *Xenopus* oogenesis. Dev Biol 405(2): 214-24

Claußen M, Tarbashevich K, Pieler T (2011) Functional dissection of the RNA signal sequence responsible for vegetal localization of XGrip2.1 mRNA in *Xenopus* oocytes. RNA Biol 8(5): 873-82

Tarbashevich K, Dzementsei A, Pieler T (2011) A novel function for KiF13B in germ cell migration. Dev Biol 349: 169-178

Koebernick K, Löber J, Arthur P, Tarbashevich K, Pieler T (2010) Elr-type proteins protect *Xenopus* Dead end mRNA from miR-18-mediated clearance in the soma. Proc Nat Acad Sci 107: 16148-16153

Arthur PK, Claussen M, Koch S, Tarbashevich K, Jahn O, Pieler T (2009) Participation of *Xenopus* Elr-type proteins in vegetal mRNA localization during oogenesis. J Biol Chem 284(30): 19982-92



Dept. of Genetics of Eukaryotic Microorganisms Institute of Microbiology and Genetics University of Göttingen Grisebachstr.8

37077 Göttingen Germany

phone: +49-551-39 13930 fax: +49-551-39 10123 e-mail: spoegge@gwdg.de

## Stefanie Pöggeler

#### **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**

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

Voigt O, Pöggeler S (2013) Autophagy genes Smatg8 and Smatg4 are required for fruiting-body development, vegetative growth and ascospore germination in the filamentous ascomycete *Sordaria macrospora*. Autophagy 9: 33-49

Bloemendal S, Bernhards Y, Bartho K, Dettmann A, Voigt O, Seiler S, Wolters DA, Pöggeler S, Kück U (2012) A homolog of the human STRIPAK complex controls sexual development in fungi. Mol Microbiol 84: 310-323

Klix V, Nowrousian M, Ringelberg C, Lorros JJ, Dunlap JC, Pöggeler S (2010) Functional characterization of MAT1-1-specific mating type genes in the homothallic ascomycete Sordaria macrospora provides new insights into essential and non-essential sexual regulators. Eukaryotic Cell 9: 894-905

Elleuche S, Pöggeler S (2009)  $\beta$ -Carbonic anhydrases play a role in fruiting body development and ascospore germination in the filamentous fungus *Sordaria macrospora*. PloS One 4:e5177

Storlazzi A, Tesse S, Ruprich-Robert G, Gargano S, Pöggeler S, Kleckner N, Zickler D (2008) Coupling meiotic chromosome axis integrity to recombination. Genes Dev 15: 796-809



Infection Biology Unit German Primate Center Kellnerweg 4 37077 Göttingen Germany

phone: +49-551-38 51150 fax: +49-551-39 51184 e-mail: spoehlmann@ dpz.eu

#### **Further Information**

http://www.dpz.eu/en/ career/leibnizgraduate-schools/ emerging-infectiousdeseases.html

## Stefan Pöhlmann

## Professor, Head of the Infection Biology Unit, German Primate Center

- 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 and Head of the Infection Biology Unit of the German Primate Center

#### **Major Research Interests**

The Infection Biology Unit investigates virus host cell interactions with a focus on the first step of the infection process, viral entry into target cells.

Emerging viruses, like the Middle East Respiratory Syndrome (MERS) coronavirus, can pose a serious threat to public health. Activation by host cell proteases is essential for infectivity of many emerging viruses. We are elucidating which proteolytic systems are hijacked by emerging corona-, filo-, bunya- and influenza viruses for activation. On the basis of this information we will identify inhibitors and evaluate their antiviral activity in cell culture and animal models. Moreover, we are interested in defining which host cell receptors are used by emerging viruses for cellular entry. Finally, we are investigating how interferon-induced antiviral effector molecules inhibit infection by emerging viruses.

Human immunodeficiency virus (HIV) is the causative agent of the acquired immunodeficiency syndrome (AIDS), a major global health crisis. We seek to understand how the composition of the glycan coat of the HIV envelope protein modulates viral spread in and between individuals. This question will be addressed by employing simian immunodeficiency virus (SIV) infection of macaques as model system for HIV infection of humans.

#### **Selected Recent Publications**

Zmora P, Moldenhauer AS, Hofmann-Winkler H, Pöhlmann S (2015) TMPRSS2 Isoform 1 Activates Respiratory Viruses and Is Expressed in Viral Target Cells. PLoS One 10(9): e0138380

Karsten CB, Buettner FF, Cajic S, Nehlmeier I, Neumann B, Klippert A, Sauermann U, Reichl U, Gerardy-Schahn R, Rapp E, Stahl-Hennig C, Pöhlmann S (2015) Exclusive Decoration of Simian Immunodeficiency Virus Env with High-Mannose Type N-Glycans Is Not Compatible with Mucosal Transmission in Rhesus Macaques. J Virol 89(22): 11727-33

Gnirß K, Zmora P, Blazejewska P, Winkler M, Lins A, Nehlmeier I, Gärtner S, Moldenhauer AS, Hofmann-Winkler H, Wolff T, Schindler M, Pöhlmann S. Tetherin (2015) Sensitivity of Influenza A Viruses Is Strain Specific: Role of Hemagglutinin and Neuraminidase. J Virol 89(18): 9178-88

Wrensch F, Winkler M, Pöhlmann S (2014) IFITM proteins inhibit entry driven by the MERS-coronavirus spike protein: evidence for cholesterol-independent mechanisms. Viruses 6(9): 3683-98

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

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



Dept. of Cellular Biochemistry University Medical Center Göttingen Humboldtallee 23

37073 Göttingen Germany

phone: +49-551-39 5947 fax: +49-551-39 5979 e-mail: peter.rehling@ medizin.unigoettingen.de

#### **Further Information**

http://www.uni-bc.gwdg.de/index.php

## **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 2009 Speaker of the Study Section "Molecular Cell Biology" of the German Society for Biochemistry and Molecular Biology (GBM)
- 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 addresses the question how newly imported proteins assemble into multi-protein complexes in the inner membrane. In case of the respiratory chain complexes the assembly process is especially demanding since central subunits of the complexes are made within mitochondria. Dedicated chaperone- like factors are required to assist and regulate assembly and translation in mitochondria. The analysis of the principles of the biogenesis process and the activities of the assembly factors is of central importance for our understanding of the molecular basis of human mitochondrial disorders.

#### **Selected Recent Publications**

Melin J, Kilisch M, Neumann P, Lytovchenko O, Gomkale R, Schendzielorz A, Schmidt B, Liepold T, Ficner R, Jahn O, Rehling P, Schulz C (2015) A presequence-binding groove in Tom70 supports import of Mdl1 into mitochondria. Biochim Biophys Acta 1853(8): 1850-9

Schulz C, Rehling P (2014) Cell biology. Powering the cell cycle. Science 346(6213): 1059-60

Melin J, Schulz C, Wrobel L, Bernhard O, Chacinska A, Jahn O, Schmidt B, Rehling P (2014) Presequence recognition by the tom40 channel contributes to precursor translocation into the mitochondrial matrix. Mol Cell Biol 34(18): 3473-85

Lytovchenko O, Melin J, Schulz C, Kilisch M, Hutu DP, Rehling P (2013) Signal recognition initiates reorganization of the presequence translocase during protein import. EMBO J 32: 886-898

Mick DU, 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

Vukotic M, Oeljeklaus S, Wiese S, Vögtle FN, Meisinger C, Meyer HE, Zieseniss A, Katschinski DM, Jans DC, Jakobs S, Warscheid B, Rehling P\*, Deckers M (2012) Rcf1 mediates cytochrome oxidase assembly and respirasome formation, revealing heterogeneity of the enzyme complex. Cell Metab 7: 336-347 (\*corresponding author)



Dept. of Neuro- and Sensory Physiology University Medical Center Göttingen Grisebachstr. 5

37077 Göttingen Germany

phone: +49-551-39 3630 fax: +49-551-39 12346 e-mail: srizzol@gwdg.de

### **Further Information**

http://rizzoli-lab.de/

### 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) Multiprotein 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



Dept. of Physical Biochemistry Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2901 fax: +49-551-201 2905 e-mail: rodnina@mpibpc. mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/research/dep/rodnina/

### 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**

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

Caliskan N, Katunin VI, Belardinelli R, Peske F, Rodnina MV (2014) Programmed –1frameshifting by kinetic partitioning during impeded translocation. Cell 157: 1619-1631

Samatova E, Konevega AL, Wills NM, Atkins JF, Rodnina MV (2014) High-efficiency translational bypassing of non-coding nucleotides specified by mRNA structure and nascent peptide. Nature Communications 5: 4459

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

Mittelstaet J, Konevega AL, Rodnina MV (2013) A kinetic safety gate controlling the delivery of unnatural amino acids to the ribosome. J Am Chem Soc 135: 17031-17038



Department of Meiosis Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

e-mail: melina.schuh@ mpibpc.mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/mschuh

### **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 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**

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 doi: 10.1038/nature14568, \*equal contribution

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

Clift D, Schuh M (2015) A three-step MTOC fragmentation mechanism facilitates bipolar spindle assembly in mouse oocytes. Nat Commun doi: 10.1038/ncomms8217

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

Holubcová Z, Howard G, Schuh M (2013) Vesicles modulate an actin network for asymmetric spindle positioning. Nat Cell Biol 15, 937-947

Schuh M (2011) An actin-dependent mechanism for long-range vesicle transport. Nat Cell Biol 13: 1431-1436



Molecular Organogenesis Research Group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1758 fax: +49-551-201 1755 e-mail: rschuh@gwdg.de

### **Further Information**

http://www.mpibpc.gwdg.de/abteilungen/170/schuh/

### **Reinhard Schuh**

### Research Group Leader at the MPI for Biophysical Chemistry

- · Dr. rer. nat., University of Tübingen, Germany, 1986
- Postdoctoral Fellow at the Max Planck Institute for Developmental Biology, Tübingen, Germany, 1986 – 1988
- Postdoctoral Fellow at the University of Munich, Germany, 1989 1991
- Group leader in the Department of Molecular Developmental Biology at the Max Planck Institute for Biophysical Chemistry, Göttingen, Germany, 1992 – 2004
- Habilitation in Cellular and Molecular Biology, Technical University of Braunschweig, Germany, 2001
- Leader of the Research Group Molecular Organogenesis at the Max Planck Institute for Biophysical Chemistry, since 2005
- since 2008: Teaching as an adjunct professor on the Faculty of Biology at the University of Göttingen

### **Major Research Interests**

Branched tubular networks are a fundamental structural design of many organs including lung, vascular system and kidney. Critical for organ function, i.e. the transport of fluids or gases, is the proper size and diameter of the tubular branches as well as an elaborated network formation. How do these networks develop? How do the branches grow out, detect their fusion partners and interconnect? How are tube size and dia-meter controlled? How can the system respond to different physiological needs? How do epidermal sheets control the paracellular passage of solutes?

We investigate the development of the *Drosophila* tracheal (respiratory) system since it provides an ideal model to address such questions, because of its simple stereotypic architecture, accessible genetics and molecular tools.

### **Selected Recent Publications**

Hildebrandt A, Pflanz R, Behr M, Tarp T, Riedel D, Schuh R (2015) Bark beetle controls epithelial morphogenesis by septate junction maturation in *Drosophila*. Dev Biol 400(2): 237-47

Jaspers MH, Pflanz R, Riedel D, Kawelke S, Feussner I, Schuh R (2014) The fatty acyl-CoA reductase Waterproof mediates airway clearance in *Drosophila*. Dev Biol 385(1): 23-31

Jaspers MH, Nolde K, Behr M, Joo SH, Plessmann U, Nikolov M, Urlaub H, Schuh R (2012) The claudin Megatrachea protein complex. J Biol Chem 287(44): 36756-65

Weiss A, Charbonnier E, Ellertsdottir E, Tsirigos A, Wolf C, Schuh R, Pyrowolakis G, Affolter M (2010) A conserved activation element in BMP signaling during *Drosophila* development. Nature Struct Mol Biol 17: 69-76

Harder B, Schomburg A, Pflanz R, Küstner KM, Gerlach N, Schuh R (2008) TEV protease-mediated cleavage in *Drosophila* as a tool to analyze protein functions in living organisms. BioTechniques 44: 765-772

Krause C, Wolf C, Hemphälä J, Samakovlis C, Schuh R (2006) Distinct functions of the leucine-rich repeat transmembrane proteins Capricious and Tartan in the *Drosophila* tracheal morphogenesis. Dev Biol 296: 253-264

Adryan B, Schuh R (2004) Gene Ontology-based clustering of gene expression data. Bioinformatics 20: 2851-2852

Behr M, Riedel D, Schuh R (2003) The claudin-like Megatrachea is essential in septate junctions for the epithelial barrier function in *Drosophila*. Dev Cell 5: 611-620



Medical School Department of Molecular Biology University of Göttingen Humboldtallee 23

37073 Göttingen Germany

phone: +49-551-39 5962 fax: +49-551-39 5960 e-mail: blanche.schwappach@med.unigoettingen.de

### **Further Information**

http://www.uni-bc.gwdg.de/index.php?id=681

### **Blanche Schwappach**

### **Professor, Director of Molecular Biology**

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

### **Major Research Interests**

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

### **Selected Recent Publications**

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

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

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

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

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

Wilhelm Voth, Markus Schick, Stephanie Gates, Sheng Li, Fabio Vilardi, Irina Gostimskaya, Daniel R. Southworth, Blanche Schwappach and Ursula Jakob (2014) The protein targeting factor GET3 functions as an ATP-independent chaperone under oxidative stress conditions. Molecular Cell 56: 116-127

Powis K, Schrul B, Tienson H, Gostimskaya I, Breker M, High S, Schuldiner S, Jakob U, Schwappach B (2013) Get3 is a holdase chaperone and moves to deposition sites for aggregated proteins when membrane targeting is blocked. J Cell Sci 126: 473-483



Gene Expression and Signaling Group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1656 fax: +49-551-201 1755 e-mail: halyna.shcherbata @mpibpc.mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/research/ags/shcherbata/

### Halyna Shcherbata

### Max Planck Research Group Leader

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

### **Major Research Interests**

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

### **Selected Recent Publications**

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

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

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

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

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



Computational Biology Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 2890 fax: +49-551-201 2803 e-mail: soeding@ mpibpc.mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/de/soeding

### Johannes Söding

# Research Group Leader at the Max Planck Institute for Biophysical Chemistry

- 1988 –1994 Studies of physics and maths at Universities of Munich (LMU), Sussex (UK), and Heidelberg
- 1992 Diploma in physics at the University of Heidelberg
- 1994 1997 PhD thesis work with Rudi Grimm at the Max-Planck-Institute for Nuclear Physics in Heidelberg
- · 1996 PhD in physics at the University of Heidelberg
- 1996 1998 Post-doc with C. Cohen-Tannoudji and J. Dalibard at the École Normale Supérieure in Paris
- 1999 2002 Strategy management consultant for the Boston Consulting Group in Frankfurt
- 2002 2007 Staff scientist with Andrei Lupas at the Max-Planck-Institute for Developmental Biology in Tübingen
- 2007 2013 Group leader at the Gene Center and Department of Biochemistry, University of Munich (LMU)
- Since 2014 Group Leader of the Computational Biology Group at the Max Planck Institute of Biophysical Chemistry

### **Major Research Interests**

We are interested in two broad areas of research. First, we develop computational methods for predicting the structure, function, and evolution of proteins from sequence. We develop statistical methods that enable us to make use of the vast amount of sequence information that is becoming available at an ever-increasing pace. The goal is to provide life scientists with more and more powerful tools for predicting the functions and structures of proteins in order to guide their experimental work.

Second, we want to understand how transcriptional regulation, which represents the most important level of cellular regulation, is encoded in each gene's regulatory regions. We develop computational methods to analyse regulatory sequences and to detect regulatory motifs. We also want to predict transcription rates, using probabilistic modeling, statistical physics, and machine learning techniques. We collaborate extensively with experimental groups to elucidate the molecular processes regulating transcription initiation, elongation, mRNA processing, and chromatin states.

### **Selected Recent Publications**

Siebert M, Söding J (2016) Markov models consistently outperform PWMs at predicting regulatory motifs in nucleotide sequences. Nucleic Acids Res 44(13): 6055-69

Hauser M, Steinegger M, Söding J (2015) MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. Bioinformatics 32(9):1323-30

Meier A, Söding J (2015) Automatic Prediction of Protein 3D Structure by Probabilistic Multi-template Homology Modeling. PLoS Computational Biology 11: e1004343

Baejen C, Torkler P, Gressel S, Essig K, Söding J\*, Cramer P\* (2014) Transcriptome maps of mRNP biogenesis factors dene pre-mRNA recognition. Mol Cell 55(5):745-57. Equal contributions; \*Corresponding authors

Schulz D, Schwalb B, Kiesel A, Baejen C, Torkler P, Gagneur J, Söding J\*, Cramer P\* (2013) Transcriptome surveillance by selective termination of non-coding RNA synthesis. Cell 155: 1075-1087



Dept. of Structural Dynamics Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1305 fax: +49-551-201 1197 e-mail: holger.stark@ mpibpc.mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/groups/stark/

### **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 premRNA 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**

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, 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

Hauer F, Gerle C, Fischer N, Oshima A, Shinzawa-Itoh K, Shimada S, Yokoyama K, Fujiyoshi Y, Stark H (2015) GraDeR: Membrane Protein Complex Preparation for Single-Particle Cryo-EM. Structure 23(9):1769-75

Fischer N, Konevega AL, Wintermeyer W, Rodnina MV, Stark H (2010) Ribosome dynamics and tRNA movement as visualized by time-resolved electron cryomicroscopy. Nature 466: 329-333

Herzog F, Primorac I, Dube P, Lenart P, Sander B, Mechtler K, Stark H, Peters JM (2009) Structure of the anaphase-promoting complex/cyclosome interacting with a mitotic checkpoint complex. Science 323: 1477-1481



Membrane Protein Biochemistry Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1621 fax: +49-551-201 1499 e-mail: astein@ mpibpc.mpg.de

### **Further Information**

http://www.mpibpc.mpg.de/stein

### **Alexander Stein**

### **Group Leader at the Max Planck Institute for Biophysical Chemistry**

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

### **Major Research Interests**

The removal of misfolded proteins is an essential process in all cells. Failure to discard such proteins often results in disease. A particularly intriguing process serves to discard misfolded proteins from the endoplasmic reticulum (ER). The ER does not itself degrade proteins, so a machinery has evolved that moves misfolded proteins into the cytosol where they can be degraded by the proteasome. This retro-translocation process is called ERAD (for ER-associated protein degradation) and is conserved in all eukaryotes. Besides its function in the removal of misfolded proteins, it plays an important role in the controlled degradation of metabolic enzymes, like the ones involved in sterol biosynthesis. The ERAD pathway is also co-opted by certain viruses (e.g. Human cytomegalovirus) and bacterial toxins (e.g. cholera toxin).

Compared to other membrane translocation processes, the mechanism of ERAD is still poorly understood. How are misfolded proteins distinguished from folding intermediates? How are proteins moved across the membrane? How are they extracted from the membrane? How is the energy for membrane translocation provided? The aim of our research is to provide answers to these fundamental questions. To study the mechanism of ERAD we use the budding yeast *Saccharomyces cerevisiae* as a model organism. We take a bottom-up approach and try to understand the mechanism of ERAD by reconstituting the entire process with purified individual components. These experiments will be complemented by studies in intact yeast cells.

In a second project, we investigate an ERAD-like process that moves proteins into the apicoplast, a plastid-like organell in unicellular parasites, like the malaria parasite *Plasmodium falciparum*. The apicoplast performs metabolic reactions essential for the parasite's survival, which include the synthesis of lipid precursors, heme and iron-sulfur clusters. The apicoplast is the target of many antimalarial drugs. We hope that a better understanding of its cell biology will facilitate the development of new drugs against malaria.

### **Selected Recent Publications**

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

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

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



Institute for Organic and Biomolecular Chemistry University of Göttingen Tammannstr. 2

37077 Göttingen Germany

phone: +49-551-39 33294 fax: +49-551-39 33228 e-mail: csteine@gwdg.de

### **Further Information**

http://www.unigoettingen.de /de/ 213067.html

### Claudia Steinem

### **Professor of Biophysical 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**

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

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

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

Braunger J A, 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

Gleisner M, Mey I, Barbot M, Dreker C, Meinecke M, Steinem C (2014) Driving a planar model system into the 3rd dimension: Generation and control of curved pore-spanning membrane arrays. Soft Matter 10: 6228-6236

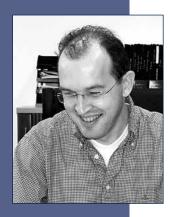
Neubacher H, Carnarius C, Mey I, Lazzara TD, Steinem C (2014) Permeabilization assay for antimicrobial peptides based on pore-spanning lipid membranes on nanoporous alumina. Langmuir 30: 4767-4774

Kozuch J, Weichbrodt C, Millo D, Becker S, Giller K, Hildebrandt P, Steinem C (2014) Voltage-dependent structural changes of the membrane-bound anion channel hVDAC1 probed by SEIRA and electrochemical impedance spectroscopy. Phys Chem Chem Phys 16: 9546-9555

Song C, Weichbrodt C, Salnikovc ES, Dynowskid M, Forsberg BO, Bechinger B, Steinem C, de Groot BL, Zachariae U, Zeth K (2013) Crystal structure and functional mechanism of a human antimicrobial membrane channel. Proc Natl Acad Sci USA 110: 4586-4591

Lazzara T D, Carnarius C, Kokun M, Janshoff A, Steinem C (2011) Separating attoliter-sized compartments using fluid pore-spanning lipid bilayers. ACS Nano 5: 6935–6944

Bosk S, Braunger J, Gerke V, Steinem C (2011) Activation of F-actin binding capacity of ezrin: synergism of PIP2 interaction and phosphorylation. Biophys J 100: 1708-1717



Department of General Microbiology University of Göttingen Grisebachstr. 8

37077 Göttingen Germany

phone: +49-551-39 33781 fax: +49-551-39 33808 e-mail: jstuelk@gwdg.de

### **Further Information**

http://genmibio.unigoettingen.de/

### 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**

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

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

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

Mehne FM, Schröder-Tittmann K, Eijlander RT, Herzberg C, Hewitt L, Kaever V, Lewis RJ, Kuipers OP, Tittmann K, Stülke J (2014) Control of the diadenylate cyclase CdaS in *Bacillus subtilis*: an autoinhibitory domain limits cyclic di-AMP production. J Biol Chem 289: 21098-107

Rothe FM, Bahr T, Stülke J, Rak B, Görke B (2012) Activation of *Escherichia coli* antiterminator BglG requires its phosphorylation. Proc Natl Acad Sci USA 109: 15906-15911

Nicolas P, Mäder U, Dervyn E, ..., Stülke J ..., Völker U, Bessières P, Noirot P (2012) The condition-dependent whole-transcriptome reveals high-level regulatory architecture in bacteria. Science 335: 1103-1106

Görke B, Stülke J (2008) Carbon catabolite repression in bacteria: many ways to make most out of nutrients. Nature Rev Microbiol 6: 613-624



Dept. of Cellular Biochemistry University Medical Center Göttingen Humboldtallee 23

37073 Göttingen Germany

phone: +49-551-39 5958 fax: +49-551-39 5979 e-mail: mthumm@unigoettingen.de

### **Michael Thumm**

### **Professor of Biochemistry and Molecular Cell Biology**

- · 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  $\beta$ -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



Dept. of Molecular Enzymology Albrecht von Haller Institute University of Göttingen Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 14430 fax: +49-551-39 5749 e-mail: ktittma@gwdg.de

### **Further Information**

http://www.bioanalytik.unigoettingen.de/

### 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

### **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**

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

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

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

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

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

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

Meyer D, Neumann P, Koers E, Sjuts H, Lüdtke S, Sheldrick, GM, Ficner R, Tittmann K (2012) Unexpected tautomeric equilibria of the carbanion-enamine intermediate in pyruvate oxidase highlight unrecognized chemical versatility of the thiamin cofactor. Proc Natl Acad Sci USA 109(27): 10867-72

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. Nature Chem Biol 7: 678-684



Bioanalytical Mass Spectrometry Group Max Planck Institute for Biophysical Chemistry Am Fassberg 11

37077 Göttingen Germany

phone: +49-551-201 1060 fax: +49-551-201 1197 e-mail: henning.urlaub@ mpibpc.mpg.de

University Medical Center Goettingen Bioanalytics Institute for Clinical Chemistry Robert Koch Strasse 40

37075 Göttingen Germany

phone: +49-551-39 8506 +49-551-39 12501 fax: +49-551-39 9506 e-mail: henning.urlaub@ med.unigoettingen.de

### **Further Information**

http://www.mpibpc.gwdg.de/english/research/ags/urlaub/index.html

## **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 methods to monitor interactions and dynamic changes of protein and protein-ligand complexes through use of crosslinking and chemical probing.

### **Selected Recent Publications**

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

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

Kırlı K, Karaca S, Dehne HJ, Samwer M, Pan KT, Lenz C, Urlaub H\*, Görlich D\* (2015) A deep proteomics perspective on CRM1-mediated nuclear export and nucleocytoplasmic partitioning. Elife, 4. pii: e11466

Wilhelm BG, Mandad S, Truckenbrodt S, Krohnert K, Schafer C, Rammner B, Koo SJ, Classen G A, Krauss M, Haucke V, Urlaub H, Rizzoli SO (2014) Composition of isolated synaptic boutons reveals the amounts of vesicle trafficking proteins. Science 344: 1023-1028

Kramer K, Sachsenberg T, Beckmann BM, Qamar S, Boon KL, Hentze MW, Kohlbacher O, Urlaub H (2014) Photo-cross-linking and high-resolution mass spectrometry for assignment of RNA-binding sites in RNA-binding proteins. Nat Methods 11(10): 1064-70



Dept. of Primate Genetics German Primate Center Kellnerweg 4

37077 Göttingen Germany

phone: +49-551-3851 161 fax: +49-551-3851 228 e-mail: lwalter@gwdg.de

### **Further Information**

http://dpz.eu/index.php?id=86

### **Lutz Walter**

## Head of Department of Primate Genetics at the German Primate Center

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

### **Major Research Interests**

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

A further focus of our research is genomics of nonhuman primates with phylogenetic, demographic, evolutionary, and bioinformatic analyses.

Methods: single-cell RNA sequencing, single-cell qRT-PCR, flow cytometry, next-generation sequencing, bioinformatic analysis tools.

### **Selected Recent Publications**

Byrareddy et al. 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, Mc-Nicholl JM, Hanson D, Reimann KA, Brameier M, Walter L, Rogers K, Mayne AE, Dunbar P, Villinger T, Little D, Parslow TG, Santangelo PJ, Villinger F, Fauci AS, Ansari AA (2014) Blockade of alpha4beta7 integrin, a T-cell gut-homing receptor, reduces mucosal transmission and dissemination of simian immunodeficiency virus infection. Nat Med 20: 1397-1400

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



Dept. of Cellular and Molecular Immunology University Medical Center Göttingen Humboldtallee 34

37073 Göttingen Germany

phone: +49-551-39 5812 fax: +49-551-39 5843 e-mail: jwienan@unigoettingen.de

### **Further Information**

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

### Jürgen Wienands

### **Professor of Cellular and Molecular Immunology**

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

### **Major Research Interests**

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

### **Selected Recent Publications**

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

Engelke M, Pirkuliyeva S, Kühn J, Wong L, Boyken J, Herrmann N, Becker S, Griesinger C, Wienands J (2014) Macromolecular assembly of the adaptor SLP-65 at intracellular vesicles in resting B cells. Sci Signal 7(339): ra79

for review see:

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



Dept. of Developmental Biology Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology Georg-August-University Göttingen GZMB, Ernst-Caspari-Haus Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49-551-39 22889 fax: +49-551-39 5416 e-mail: ewimmer@gwdg.de

### **Further Information**

http://www.uni-goettingen.de/en/sh/49202.html

### **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 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. Our focus lays on the biological function of odorant binding proteins (OBPs) and sensory neuron membrane proteins (SNMPs) which is still largely unknown, despite their necessity for olfaction.

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 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**

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

Dippel S, Oberhofer G, Kahnt J, Gerischer L, Opitz L, Schachtner J, Stanke M, Schütz S, Wimmer EA\* Angeli S (2014) Tissue-specific transcriptomics, chromosomal localization, and phylogeny of chemosensory and odorant binding proteins from the red flour beetle Tribolium castaneum reveal subgroup specificities for olfaction or more general functions. BMC Genomics 15: 1141, \* corresponding author

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

Ogaugwu CE, Schetelig MF, Wimmer EA (2013) Transgenic sexing system for *Ceratitis capitata* (Diptera: Tephritidae) based on female-specific embryonic lethality. Insect Biochem Mol Biol 43, 1-8

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### **Students**

Lars Henning Hansen

Julia Börke

### **Program Coordination**

### **Molecular Biology Program**

Dr. Steffen Burkhardt (Program Coordinator)



Kerstin Grüniger (Program Assistant)



Georg-August-Universität Göttingen Coordination Office Molecular Biology Justus-von-Liebig-Weg 11

37077 Göttingen Germany

phone: +49 - 551 - 39 12110 / 12111

+49 - 551 - 39 33811

e-mail: gpmolbio@gwdg.de **Further Information** 

http://www.gpmolbio.unigoettingen.de

### **Neuroscience Program**

Prof. Dr. Michael Hörner (Program Coordinator)

Sandra Drube (Program Assistant)

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