Molecular Life Sciences – Microbiology, Biotechnology and Biochemistry

MSc/PhD Program

in Göttingen, Germany

- Biochemistry
- Structural Biology
- Molecular Genetics
- Cell Biology
- Microbiology
- Biotechnology
- Plant Molecular Biology
- Plant-Microbe Interactions

Deadline for your application is May 15th
Start of the program is October 1st
www.biologie.uni-goettingen.de/msc_mbb

GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN

basic structure

module	number	structure and options		C/ module	C total
core module	**3**	lecture + seminar/tutorial + methods course	choice of 6 different modules	**12**	**36**
profile module	**1**	additional core module MBB core module DNB, Msc Chemistry interdisciplinary courses*		**12**	**12**
key competence module		course offer ZESS course offer MBB, Chemistry, DNB, BEE interdisciplinary courses*		**2-12**	**12**
advanced module	**1**	7 weeks lab course I		**12**	**30**
	1	7 weeks lab course II		**12**	
	1	scientific project management		**6**	
Master thesis (26 weeks)					**30**
					120

*** Permission of examination board required**

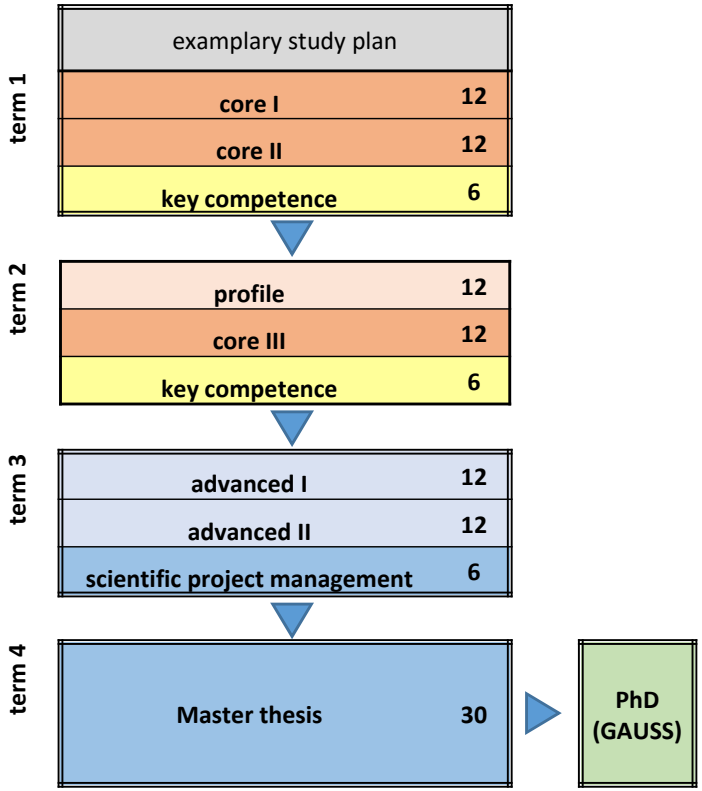
MBB = Master Molecular Life Sciences: Microbiology , Biotechnology and Biochemistry

DNB = Master Developmental, Neural and Behavioral Biology

BEE = Master Biodiversity, Ecology and Evolution

ZESS = Zentrale Einrichtung für Sprach- und Schlüsselkompetenzen

curriculum



Core discipline: "General and applied microbiology"

core module	advanced modules		master		key competence modules (components of the core module as single modules)		
M.Bio.101	**M.Bio.111**	**M.Bio.121**	**M.Bio.131 + master thesis**		**M.Bio.141**	**M.Bio.151**	**M.Bio.161**
lecture (3 SWS) + seminar (1 SWS) + methods course A or B **methods course A**: *Isolation and characterisation of biotechnologically relevant microorganisms* **methods course B**: *Signal transduction in bacteria*	**lab course (7 weeks)** *General and applied microbiology*	**lab course (7 weeks)** *General and applied microbiology*	**scientific project management (5 SWS)**	**Master thesis (26 weeks)**	**lecture (3 SWS)** *General and applied microbiology*	**methods course A (3 weeks)** *Isolation and characterisation of biotechnologically relevant microorganisms*	**methods course B (3 weeks)** *Signal transduction in bacteria*
12 C	**12 C**	**12 C**	**6 C**	**30 C**	**3 C**	**6 C**	**6 C**
winter term	**individual for each student: time frame has to be arranged with advisor**				**winter term**		

Core discipline: "Molecular genetics and microbial cell biology"

core module	advanced modules		master		key competence modules (components of the core module as single modules)		
M.Bio.102	**M.Bio.112**	**M.Bio.122**	**M.Bio.131 + masterthesis**		**M.Bio.142**	**M.Bio.152**	**M.Bio.162**
lecture (3 SWS) + seminar (1 SWS) + methods course A or B **methods course A**: *Genetics/ Cell biology A* **methods course B**: *Genetics/ Cell biology B*	**lab course (7 weeks)** *Eukaryotic microbiology and genetics*	**lab course (7 weeks)** *Eukaryotic microbiology and genetics*	**scientific project management (5 SWS)**	**Master thesis (26 weeks)**	**lecture (3 SWS)** *Molecular genetics and microbial cell biology*	**methods course A (3 weeks)** *Genetics/ Cell biology A*	**methods course B (3 weeks)** *Genetics/ Cell biology B*
12 C	**12 C**	**12 C**	**6 C**	**30 C**	**3 C**	**6 C**	**6 C**
winter term	**individual for each student: time frame has to be arranged with advisor**				**winter term**		

Core discipline: "Enzyme Catalysis and Chemical Biology"

core module	advanced modules		master		key competence module	
M.Bio.108	**M.Bio.118**	**M.Bio.128**	**M.Bio.131 + masterthesis**		**M.Bio.158**	**M.Bio.168**
lecture (3 SWS) + seminar (1 SWS) + methods course *Enzyme Catalysis and Chemical Biology*	**lab course (7 weeks)** *Enzyme Catalysis and Chemical Biology*	**lab course (7 weeks)** *Enzyme Catalysis and Chemical Biology*	**scientific project management (5 SWS)**	**Master thesis (26 weeks)**	**lecture (3 SWS)** *Enzyme Catalysis and Chemical Biology*	**methods course (3 weeks)** *Enzyme Catalysis and Chemical Biology*
12 C	**12 C**	**12 C**	**6 C**	**30 C**	**3 C**	**6 C**
winter term	**individual for each student: time frame has to be arranged with advisor**				**winter term**	

additional key competence modules

M.Bio.147	M.Bio.149	M.Bio.150
Applied bioinformatics in microbiology *lecture (2 SWS) + block course (3 weeks)*	**Planning and organization of industry excursions** (2 SWS)	**Industry excursions** 3 days lecture free time (5 SWS)
6 C	**3 C**	**3 C**
winter term	**winter term**	**winter term**

Core discipline: "Cell- and molecular biology of plant-microbe-interactions"

core module	advanced modules		master		key competence module
M.Bio.104	M.Bio.114	M.Bio.124	M.Bio.131 + masterthesis		M.Bio.144
lecture (3 SWS) + seminar (1 SWS) + methods course *Plant-microbe-interactions*	lab course (7 weeks) *Plant-microbe-interactions*	lab course (7 weeks) *Plant-microbe-interactions*	scientific project management (5 SWS)	Master thesis (26 weeks)	lecture (3 SWS) *Plant-microbe-interactions*
12 C	12 C	12 C	6 C	30 C	3 C
summer term	individual for each student: time frame has to be arranged with advisor				summer term

Core discipline: "Biochemistry and Biophysics"

core module	advanced modules		master		key competence module	
M.Bio.107	M.Bio.117	M.Bio.127	M.Bio.131 + masterthesis		M.Bio.157	M.Bio.167
lecture (3 SWS) + seminar (1 SWS) + methods course *Biochemistry and Biophysics*	lab course (7 weeks) *Biochemistry and Biophysics*	lab course (7 weeks) *Biochemistry and Biophysics*	scientific project management (5 SWS)	Master thesis (26 weeks)	lecture (3 SWS) *Biochemistry and Biophysics*	methods course (3 weeks) *Biochemistry and Biophysics*
12 C	12 C	12 C	6 C	30 C	3 C	6 C
summer term	individual for each student: time frame has to be arranged with advisor				summer term	

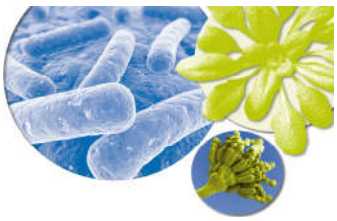
Core discipline: "Structural biology"

core module	advanced modules		master		key competence modules	
M.Bio.106	M.Bio.116	M.Bio.126	M.Bio.131 + masterthesis		M.Bio.156	M.Bio.166
lecture (3 SWS) + seminar (1 SWS) + methods course *Structural biology*	lab course (7 weeks) *Structural biology*	lab course (7 weeks) *Structural biology*	scientific project management (5 SWS)	Master thesis (26 weeks)	lecture (3 SWS) *Structural biology*	methods course (3 weeks) *Structural biology*
12 C	12 C	12 C	6 C	30 C	3 C	6 C
summer term	individual for each student: time frame has to be arranged with advisor				summer term	

additional modules

key competence modules		profile module
M.Bio.146	M.Bio.160	M.Bio.110
Applied methods of biosciences *practical course (5 SWS)*	Organization of a local iGEM-team (7 SWS)	International competition on Genetically modified Egineered Machines practical course (14 SWS)
3 C	6 C	12 C
changing offer	summer term	summer term

Authorized examiners



Core discipline "General and applied microbiology"

name	first name	title	e-mail	department	modules
Stülke	Jörg	Prof	jstuelk@gwdg.de	General Microbiology	FM: M.Bio.101 VM: M.Bio.111, M.Bio.121 SKM: M.Bio.141, M.Bio.151, M.Bio.161 M: M.Bio.131, Master
Commichau	Fabian	Prof	fcommic1@gwdg.de	General Microbiology	
Hoppert	Michael	PD	mhopper@gwdg.de	General Microbiology	
Daniel	Rolf	Prof	rdaniel@gwdg.de	Genomic and Applied microbiology	
Liesegang *	Heiko	Dr	hlieseg@gwdg.de	Genomic and Applied microbiology	

Core discipline "Molecular genetics and microbial cell biology"

name	first name	title	e-mail	department	modules
Braus	Gerhard	Prof	gbraus@gwdg.de	Molecular Microbiology and Genetics	FM: M.Bio.102 VM: M.Bio.112, M.Bio.122 SKM: M.Bio.142, M.Bio.152, M.Bio.162 M: M.Bio.131, Master
Heimel	Kai	Prof	kheimel@gwdg.de	Molecular Microbiology and Genetics	
Valerius *	Oliver	Dr	ovaleri@gwdg.de	Molecular Microbiology and Genetics	
Kramer	Wilfried	PD	wkramer@gwdg.de	Molecular Genetics	
Krebber	Heike	Prof	heike.krebber@biologie.uni-goettingen.de	Molecular Genetics	
Pöggeler	Stefanie	Prof	spoegge@gwdg.de	Genetics of Eukaryotic Microorganisms	

Core discipline: "Cell- and molecular biology of plant-microbe-interactions"

name	first name	title	e-mail	department	modules
Lipka	Volker	Prof	Volker.Lipka@biologie.uni-goettingen.de	Plant Cell Biology	FM: M.Bio.104 VM: M.Bio.114, M.Bio.124 SKM: M.Bio.144 M: M.Bio.131, Master
Teichmann	Thomas	PD	tteichm@gwdg.de	Plant Cell Biology	
Wiermer	Marcel	PD	wiermer@uni-goettingen.de	Plant Cell Biology	
Gatz	Christiane	Prof	cgatz@uni-goettingen.de	Plant Molecular Biology and Physiology	

Core discipline "Structural biochemistry"

name	first name	title	e-mail	department	modules
Adio *	Sarah	Dr.	sadio@gwdg.de	Molecular Structural Biology	FM: M.Bio.106 VM: M.Bio.116, M.Bio.126 SKM: M.Bio.156, M.Bio.166 M: M.Bio.131, Master
Ficner	Ralf	Prof	rficner@uni-goettingen.de	Molecular Structural Biology	
Dickmanns *	Achim	Dr.	adickma@uni-goettingen.de	Molecular Structural Biology	
Lührmann	Reinhard	Prof	reinhard.luehrmann@mpibpc.mpg.de	MPI-bpc: Cellular Biochemistry	
Stark	Holger	Prof	hstark1@gwdg.de	MPI-bpc: 3D Electron Cryomicroscopy	

Core discipline "Biochemistry and biophysics"

name	first name	title	e-mail	department	modules
Feußner	Ivo	Prof	ifeussn@uni-goettingen.de	Plant Biochemistry	FM: M.Bio.107 VM: M.Bio.117, M.Bio.127 SKM: M.Bio.157, M.Bio.167 M: M.Bio.131, Master
Hadacek	Franz	PD	fhadace@uni-goettingen.de	Plant Biochemistry	
Ischebeck	Till	PD	tischeb@gwdg.de	Plant Biochemistry	
Janshoff	Andreas	Prof	ajansho@gwdg.de	Institute for Physical Chemistry	
Steinem	Claudia	Prof	csteine@gwdg.de	Institute of Organic and Biomolecular Chemistry	

Core discipline "Enzyme catalysis and chemical biology"

name	first name	title	e-mail	department	modules
Tittmann	Kai	Prof	ktittma@uni-goettingen.de	Bioanalytics	FM: M.Bio.108 VM: M.Bio.118, M.Bio.128 SKM: M.Bio.158, M.Bio.166 M: M.Bio.131, Master
Diederichsen	Ulf	Prof	udieder@gwdg.de	Institute for Organic and Biomolecular Chemistry	
Thomas	Franziska	Dr.	fthomas@gwdg.de	Institute for Organic and Biomolecular Chemistry	
Rodnina	Marina	Prof	rodnina@mpibpc.mpg.de	MPI-bpc: Physical Biochemistry	

*** associated member**

FM: core module

VM: advanced module

SKM: key competence module

M: "scientific project management" + Master thesis

Department of General Microbiology
Institute for Microbiology and Genetics

Grisebachstraße 8, 37077 Göttingen
(Prof. Dr. Jörg Stülke, PD Dr. Michael Hoppert, PD Dr. Fabian Commichau)

Our group studies the regulation of metabolism in the pathogenic bacterium *Mycoplasma pneumoniae* and the model organism *Bacillus subtilis*. We are following global ("postgenomic") 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! So far, we have studied one of the few regulatory proteins of *M. pneumoniae* and determined its crystal structure. Interestingly, the mode of action of this protein is opposed to that of homologous proteins from other bacteria: a hint to the parasitic lifestyle of *M. pneumoniae*! We are now starting to study the metabolic responses of *M. pneumoniae* to the infection process. If we understand what happens upon infection, we may subsequently try to interrupt this chain of events.

Metabolism in *Bacillus subtilis* is studied by integrating transcriptomics, protein arrays, metabolome and fluxome analyses. Our specific interests are focused on central metabolic pathways: glycolysis, the citric acid cycle and glutamate biosynthesis, the decisive link between carbon and nitrogen metabolism. We discovered recently that genes for glutamate biosynthesis in *B. subtilis* are only expressed if rich carbon sources are available and we identified a regulatory protein-protein interaction that governs this sugar induction. 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. Interestingly glycolytic enzymes are also part of an RNA-degrading protein complex, the RNA degradosome. The structure and dynamics of this complex is under investigation in the Collaborative Research Center on structural biology. Recently, we found that the signaling nucleotide c-di-AMP is essential for the growth of B. subtilis. We characterize the activity and control of c-di-AMP-producing enzymes in *Listeria monocytogenes*, *B. subtilis*, and *M. pneumoniae*. Moreover, we investigate the targets of c-di-AMP to unravel its molecular mechanism of action. Bacteria can rapidly respond to changes in their environment. It is usually assumed that such responses take place at the level of gene expression. However, we discovered that such adaptation may also take place at the genome level with the rapid accumulation of mutations that allow better growth under changed conditions. The mechanisms behind this adaptive mutagenesis are under investigation in our department. Moreover, *B. subtilis* is an ideal platform to generate cells with a minimal genome. For this purpose we re-design the genome of this bacterium.

We are also interested in structure-functional relationships in bacterial cells and microbial communites. We try to understand how some bacteria may benefit from compartmentation of biotechnologically relevant metabolic processes, such as biopolymer degradation or incomplete oxidation of substrates. We are also interested in the question how biofilm structures (organisms, extracellular features such as polysaccharide capsules or enzyme complexes) are high competitive entities in nature, e.g. in terrestrial ecosystems, in deep sea marine habitats and in symbioses. In particular, we are interested in nanoscale initation of biomineral formation by deep sea microbial mats, and in symbioses between marine metazoa and chemolithotrophic bacteria.

Department of Genomic and Applied Microbiology and Göttingen Genomics Laboratory
Institute for Microbiology and Genetics

Grisebachstraße 8, 37077 Göttingen

(Prof. Dr. Rolf Daniel)

The major research interest is to explore and to exploit the enormous and largely untapped physiological, metabolic, and genetic diversity of environmental microorganisms by cultureindependent metagenomic and metatranscriptomic approaches. This comprises the direct isolation of high-quality DNA and mRNA from various habitats such as soils, marine sediments, freshwater sediments, glacier ice, and volcanic regions. The isolated mRNA is employed for generation of cDNA and functional profiling by pyrosequencing of cDNA. The environmental DNA is used to construct small-insert and large-insert metagenomic libraries. In this way, approximately 100 metagenomic libraries from different worldwide environments have been generated. Subsequently, function-driven or sequence-based screening of the constructed metagenomic libraries and recovery of novel genes and gene products are performed. This work has led, i.e., to the successful identification and characterization of novel oxidoreductases, B12-dependent dehydratases, lipases, proteases, DNA polymerases, antiporters, and genes conferring antibiotic resistance from metagenomes. The phylogenetic diversity represented in the studied metagenomes is analyzed by characterization of 16S rRNA gene diversity. To gain insights into the genomes and transcriptomes of uncultivated microorganisms present in the metagenomes, partial sequencing (snapshot sequencing) of the constructed libraries and isolated DNA and RNA is carried out. Currently, the research is focused on metagenomes from extreme environments such as glaciers, volcanic soils, and hot springs. In addition to metagenomic approaches, enrichment and isolation of novel single microorganisms from extreme environments is also performed.

The areas of work of the Göttingen Genomics Laboratory are whole-genome sequencing, transcriptomics, and functional genomics of archaea, bacteria, fungi and microbial communities. This includes gap closure, ORF-finding. annotation, pathway reconstruction, bioinformatic interpretation of sequence and transcriptome data, and genome comparison. In addition, the Göttingen Genomics Laboratory harbors the full bioinformatic pipeline to analyze large metagenomic and metatranscriptomic data sets. The majority of the sequenced organisms is of industrial importance or pathogenic. The analyzed organisms comprised, i.e., *Bacillus licheniformis, Clostridium kluyveri, Propionibacterium acnes*, *Clostridium tetani, Bacillus anthracis* and *Burkholderia glumae* as well as pathogenic *Escherichia coli*, *Listeria*, *Paenibacillus,* and *Staphylococcus* strains.

Dr. Heiko Liesegang

Based on the complete genome sequences of *B. licheniformis*, *B. amyloliquefaciens* and *B. cereus biovar anthracis* - all sequenced by the Göttingen Genomics Laboratory - we focus our work on central topics of *Bacillus* evolution. Based on functional and comparative genomics we address the questions:

- What are the molecular events (SNPs, INDELs, recombination, phage integration, ...) which shape a genome?
- What is the speed of evolution and how fast do strains adapt to new habitats?
- What is the impact of genome evolution on the biological activities of an organism?
- What distinguishes a pathogen from a commensal and a probiotic organism? In short: how do life styles evolve?

The topics are approached by genome sequencing, RNA-seq based transcriptomics, epigenome sequencing, molecular phylogeny and sequence based bioinformatics.

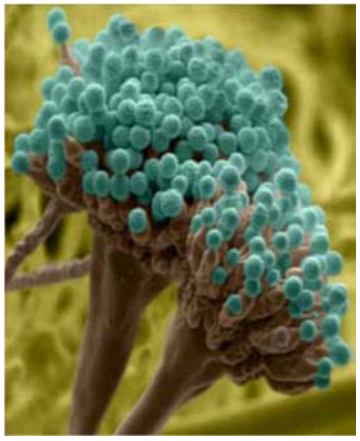
Department of Molecular Microbiology and Genetics
Institute for Microbiology and Genetics

Grisebachstraße 8, 37077 Göttingen
(Prof. Dr. Gerhard Braus, Dr. Oliver Valerius)

The major focus of the laboratory is on molecular genetics, biochemistry and cell biology using eukaryotic microorganisms (yeasts and filamentous fungi) as models. We analyse the control of developmental programs and host-microbe interactions (pathogenicity).

Topics:

1. We are interested in exploring the potential of studying fungal models to learn more about neuronal diseases including Parkinson and are therefore part of the DFG research center of molecular physiology of the brain (CMPB).



2. Adhesion represents an initial step in the infection process as well as in biofilm formation. We are interested in the molecular control of adehsion and primarily analyse the control of *FLO* genes which are encoding the adhesins of the model yeast *S. cerevisiae*.

3. In yeast and filamentous fungi, starvation activates a complex genetic network including a signal transduction pathway and the transcriptional activator Gcn4p/CpcAp. The *Aspergillus fumigatus* transcriptional activator CpcA contributes significantly to virulence ofthis fungal pathogen. We analyse how the amount ofGcn4p/CpcA is controlled in the fungal cell and what are the target genes of this transcription factor.

4. We analyse the control points and the molecular switches which connect secondary metabolism (including toxin formation) and development. As key regulator of development in filamentous fungi we have recently identified the COP9 signalosome which is involved in protein turnover.

5. Fungal development and secondary metabolism are coordinated by light. We have recently discovered the trimeric VelB-VeA-LaeA complex which is required for sexual development and secondary metabolism in darkness. VeA is a light-sensitive bridging factor which results in disruption of the trimeric complex in light. Furthermore we have found a single gene which as well functions as photolyase to repair DNA in response to UV light as a cryptochrome which controls developmental programmes in a light-dependent manner.

6. We are interested in the interaction of fungi with human blood (*Aspergillus fumitatus* in blood results in high mortality rates) and with the plant xylem sap (*Verticillium longisporum* is a growing problem as a plant pathogen infecting the rapese ed *Brassica napus*). What are common and what are distinct molecular mechanisms of survival for the pathogen?

7. We are interested in polarity and in understanding regulatory components of the cytoskeleton that are important to generate and maintain this high degree of polar cell shape. Equally important is the analysis of molecular motor proteins that allow the distribution of vesicular organelles within the hypha and transport secretory vesicles towards the growing tip. The motor proteins are also necessary for localizing specific landmark proteins that determine the site of polar growth. The analysis of this transport machinery in a fungal system that is accessible for experimental tools will help us to distinguish the special needs in these highly elongated cells from transport processes in spherical cells.

Heimel (Junior Professor of Microbial Cell Biology):

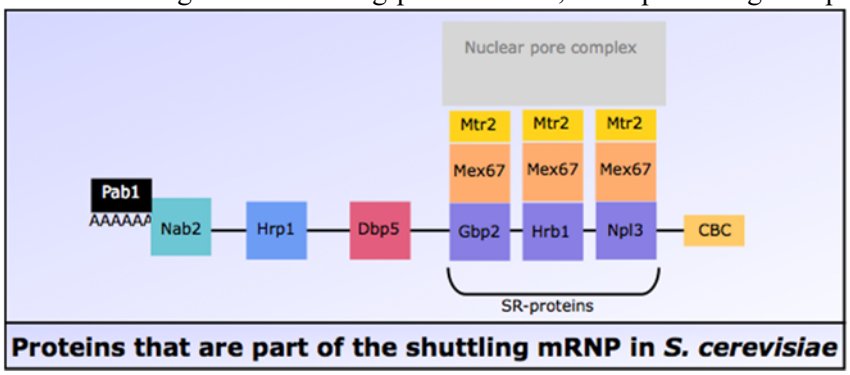
We use the model fungus *Ustilago maydis* to study the role of the UPR in controlling development and adaptation to different environmental conditions. Cells need to re-adjust and modify their cellular programs in response to a wide range of biotic and abiotic stimuli. The UPR is a highly conserved cellular 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.

Department of Molecular Genetics
Institute for Microbiology and Genetics
Grisebachstraße 8, 37077 Göttingen

(Prof. Dr. Heike Krebber, PD Dr. Wilfried Kramer)

The co mpartimentation of eukary otic cells requires a machinery that is able to transport a great number of molecules into and out of the nucleus in a rapid, accurate and regulated manner. The natural cargos for this machinery are proteins and RNA-pr otein co mplexes. One of our main topics is: How does mRNA get out of t he nucleus? For the mRNA export it has to be assured that intron containing pre mes senger RNAs ar e retained in the nucleus until processing is co mpleted. Only fully processed and spliced mRNAs should be transpo rted into the cytoplasm and translated at the ribosomes. In case the quality control m achinery is defective, not fully processed pre-mRNA s reach the cy toplasm, resulting in the translation of toxic gene products and in multicellular organism s in diseases like cancer or neu rodegenerative diseases. T herefore, a se cond important topic in t he lab is: How does the quality control of mRNAs work?

Yeast shuttling mRNA bi nding proteins Pab1, the cap binding com plex (CBC), Dbp5, Hrp1, Nab2, Npl3, Gbp2 and Hrb1 bind to the mRNA during exp ort. The export receptor Mex67-Mtr2 is recruited to t he RNA by several export adapter proteins, e.g. Npl3 allowing the transport of t he ribonucleoparticle throug h the nuclear pore com plex (NPC).



Proteins that are part of the shuttling mRNP in *S. cerevisiae*

In ongoing studies we anal yze the function and regula tion of these proteins further and investigate the following questions in detail:

- How can a cell distinguish between a pre-mRNA and an export competent mRNA molecule?
- Which RNA binding proteins accompany the mRNAs to the cytoplasm?
- What are the functions of each individual mRNA binding protein in this process?
- How is the mRNA export from the nucleus regulated?

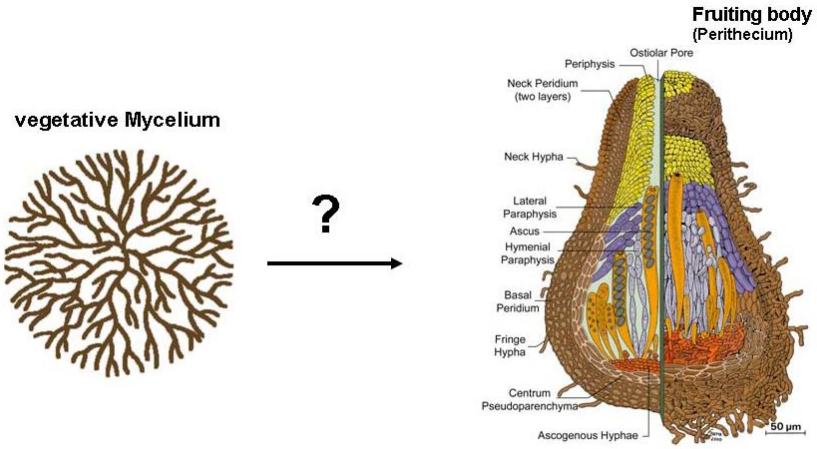
With our recent studies we gained insights into the transformation of an exporting to a translating mRNA/protein com plexes. We found t hat the th ree SR-proteins, Npl3, Gbp2 and Hrb1 and the DEAD-box RNA-helicase Dbp5 remain boun d to t he mRNA d uring translation. Consequ ently, we identified Db p5 is as a novel pla yer in translation termination. Dbp5 interacts genetically with both release factors eRF1 and eRF3 and Pab1. A phy sical interaction was specifically detected with eRF1. We have shown that during tran slation term ination the helicase activity of Dbp5 is required for efficient stop -codon recognition, and i ntact Dbp5 is essential for the recruitm ent of eRF3 into termination complexes. Moreover, Gle1 and Rli1 were identified as additional new factors involved in translation termination.
Further studies aim to answer the following questions in detail:

- What are the functions of the SR-proteins during translation?
- Is there a crosstalk between translation and trans cription/mRNA-export m ediated b y the shuttling mRNA binding proteins?
- How can we unite all termination factors in a new model for the translation term ination process?

Department Genetics of Eukaryotic Microorganisms
Institute for Microbiology and Genetics
Grisebachstraße 8, 37077 Göttingen

(Prof. Dr. Stefanie Pöggeler)

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 (see figure below). Since *S.macrospora* is able to complete the sexual cycle without a mating partner, recessive mutations affecting fruiting body development are directly visible. 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. These include genes encoding transcription factors, a conserved WD40 repeat protein, a putative membrane protein and an ATP citrate lyase. 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.



Sordaria macrospora

The fruiting body of *Sordaria macrospora* is composed of many different cell types. The question mark represents our research interest in the genes involved in fruiting body development.

We are also interested in the impact of autophagy on fungal developmental processes. 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, the exact role of autophagy in multicellular fruiting-body development is largely unknown.
Two types of macroautophagy have been described: non-selective and selective autophagy. Non-selective autophagy is the random engulfment of cytoplasm and organelles into double-membrane vesicles, the autophagosomes, and the delivery of the cargo to the vacuole for degradation. In selective autophagy, specific cargos such as organelles, protein aggregates or enzymes are recognized by cargo receptors and enwrapped into autophagosomes.
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 *S. macrospora*. Our aim is to understand how selective autophagy contributes to vegetative growth and fruiting- body development in filamentous ascomycetes.

For further informations, please contact Stefanie Pöggeler (spoegge@gwdg.de) phone: 0551-3913930.

Department Molecular Biology and Physiology of Plants
Albrecht-von-Haller-Institute for Plant Sciences

Schwann-Schleiden Centre, Julia-Lermontowa-Weg 3, 37077 Göttingen

(Prof. Dr. Christiane Gatz)

General information about the department

The Department of Plant Molecular Biology and Physiology is integrated in the Albrecht-von-Haller-Institute for Plant Sciences at the Georg-August-University of Goettingen and member of the Goettingen Centrum for Molecular Biosciences (GZMB). The Department is headed by Prof. Dr. Christiane Gatz, who is a member of the Faculty of Biology and the Goettingen Graduate School for Neurosciences and Molecular Biosciences (GGNB). For further information, please contact Prof. Dr. Christiane Gatz (cgatz@biologie.uni-goettingen.de; phone ++49 (0)551-39 7843).

Main Research Field: Plant signal transduction processes after attack by microbial pathogens

We analyze plant signal transduction processes using genetics, molecular biology and biochemistry. Plants have developed a highly sophisticated defense system that is activated upon recognition of pathogens. Massive transcriptional reprogramming is coordinated by the phytohormones salicylic acid (SA), jasmonic acid (JA) and ethylene (ET). While infection with biotrophic pathogens (pathogens that exploit living cells) evokes SA-mediated defense responses, infection with necrotrophic pathogens (pathogens that kill their host cells) elicits JA/ET-dependent responses. Both signaling pathways crosscommunicate in an antagonistic manner, so that defense pathways can be prioritized upon demand. The graded transcriptional responses associated with immunity clearly indicate the existence of a complex regulatory circuitry comprised of transcriptional activators and repressors fine-tuning the expression of defense genes. Very little is known how specific transcription factors are activated by the signal transduction events initiated by the defense hormones and how the cross-talk between different signal transduction pathways is realized at the molecular level.

Our research focuses on a family of transcription factors that are involved in different signaling pathways, including the SA-activated and the JA/ET-activated pathway. In addition, they are necessary for the activation of a subset of genes that are activated in a hormone-independent manner upon pathogen stress. This central position enables them to coordinate the different defense pathways appropriately. As TGA transcription factors are expressed even in the absence of pathogens, they must be activated after interaction with different regulatory proteins that are themselves activated by different signaling pathways. Using different molecular strategies we have already isolated three TGA-interacting proteins that influence different TGA-mediated responses (1,2). Our aim is to elucidate how these proteins are regulated and how they contribute to transcriptional activation. The use of plant mutants, the comprehensive comparison of their transcriptomes and their responses to different biotrophic and necrotrophic pathogens belong to the molecular tool box that we use to dissect TGA-mediated defense responses.

Department of Plant Cell Biology
Albrecht-von-Haller-Institute for Plant Sciences

Schwann-Schleiden Centre, Julia-Lermontowa-Weg 3, 37077 Göttingen

General information about the department

The Department of Plant Cell Biology is integrated in the Albrecht-von-Haller-Institute for Plant Sciences at the Georg-August-University of Goettingen and member of the Goettingen Centrum for Molecular Biosciences (GZMB). The Department is headed by Prof. Dr. Volker Lipka, who is faculty member of the Faculty of Biology and the Goettingen Graduate School for Neurosciences and Molecular Biosciences (GGNB). Currently, 21 people work at the Department of Plant Cell Biology. Subgroups within the department are headed by Prof. Dr. Volker Lipka, PD Dr. Thomas Teichmann and PD Dr. Marcel Wiermer. For further information, please contact
Prof. Dr. Volker Lipka (vlipka@gwdg.de; phone ++49 (0)551-39 13581).

Main Research Field: Plant Innate Immunity to microbial pathogens

Our research is focused on the
1) Molecular dissection of mechanisms that control activation of basal defense in the plant model Arabidopsis thaliana
2) Analysis of defense mechanisms that contribute to resistance against microbial pathogens
3) Identification of fungal effector molecules that interfere with the plant defense machinery and allow host plant colonization

We combine genetics, cell & molecular biology with biochemical experimental strategies to gain novel insights into these complex mechanisms. For further information, please visit our website (http://www.uni-goettingen.de/de/33181.html).

Individual work groups

Lipka: Molecular dissection of Arabidopsis basal resistance and compatibility to fungal pathogens

This group is working on the basal defense mechanisms plants mount against non-adapted fungi. These include perception of pathogen attack by plasma membrane resident receptor molecules and subsequent activation of transport and secretion processes that limit fungal invasion success at the cell periphery. Further, effector molecules that allow co-evolved and adapted fungi to suppress these plant defenses are subjects of interest in our group.

Lipka/Teichmann:
Analysis of plant pathogen effects on plant differentiation and hormone homeostasis

Investigation of the fungal pathogen *Verticillium longisporum* causing vascular disease in members of the family *Brassicaceae* is the central topic in this research group. Mechanisms that allow *Verticillium* to trigger trans-differentiation of mesophyll cells into xylem vessels are studied with emphasis on fungal effector molecules identified by comparative genomics. In addition, this group analyses the role of changes in plant hormone homeostasis and signaling during establishment of *Verticillium* infection.

Wiermer: Nucleocytoplasmic signaling in plant cellular immunity

Research efforts in this group are directed towards understanding the molecular mechanisms regulating spatial communication between the cytoplasm and the nucleus in*Arabidopsis* defense responses against microbial pathogens. Several components of the nuclear pore and nucleocytoplasmic trafficking machinery that are essential for distinct immune responses have been identified and are characterized with regard to their regulatory function in plant immunity, using biochemical, cell biological, genetic and molecular approaches. Work in this group further aims to identify novel biochemical and genetic interactors involved in defense-related nucleocytoplasmic transport of proteins and RNAs and to reveal additional signal transduction pathways that make use of this regulatory potential.

Department of Molecular Structural Biology
Institute for Microbiology and Genetics;

Ernst-Caspari-House (ECH; Main Building of the Göttingen Center for Molecular Biosciences)
Justus-von-Liebig-Weg 11, 37077 Göttingen

General information about the department

The MSB headed by Prof. Dr. R. Ficner, was established in 2001 and there are currently 25 employees working at the MSB. Progress reports and literature seminars are held in English. Due to the location in an active scientific environment quite a few seminars may be attended at the ECH each week. The MSB is in close collaboration with the Department of Cellular Biochemistry (Prof. Dr. R. Lührmann) and the Department of Theoretical and Computational Biophysics (Prof. Dr. H. Grubmüller) both at the Max-Planck-Institute of Biophysical Chemistry and the 3D Cryo Electron Microscopy group of Prof. Dr. H. Stark. For further information, please contact Achim Dickmanns (adickma@uni-goettingen.de).

Main Research Field: Structural Biology

The underlying and unifying elements of research techniques are two fold: On the one hand the cloning, expression and purification of protein, first to test their expression levels and solubility subsequently followed by large scale preparation. On the other hand the crystallization of the purified proteins or protein-protein or protein-RNA/DNA complexes and their structure determination by means of X-ray crystallography.
For further information, please visit our website (http://www.uni-goettingen.de/msb).

Specific Research Fields

Nucleo-cytoplasmic trafficking: Structure and Function relationship of transport receptors and their cargo.

The transport of proteins and RNAs in and out of the nucleus requires the transit through aqueous channel within the nuclear pore complexes, the gatekeepers of the nucleus. This transfer requires specific transport receptors that interact with the cargo, the proteins to be transferred. The individual steps in the recognition of the cargo, their integration in the respective transport complex (import or export) and the disassembly of these complexes due to the GTPase Ran is in the focus of our investigation.

Spliceosome: Protein-RNA and Protein-Protein Complexes of the Spliceosome.

Spliceosomes are huge macromolecular ribonucleoprotein particles catalyzing the removal of non-coding sequences so called introns from pre-mRNAs. The removal of the introns requires the ordered assembly of five large protein/RNA complexes and major structural rearrangements during the splicing reaction involving the addition or removal of many proteins. The ultimate goal is to understand the underlying steps and processes on a structural level.

Using these tools we develop **new strategies to introduce spectroscopic probes** into proteins to study the **dynamic properties of chromatin**. We are also interested in the effect of the post-translational **acetylation of lysine** residues on protein structure and function.

Department of Structural Dynamics

Max-Planck-Institute for biophysical Chemistry, Am Fassberg 11, 37077 Göttingen

General information about the department

The aim of our group is to determine three-dimensional structures of macromolecules with the single particle electron cryomicroscopy technique. Our work is mainly focused on spliceosomal components called snRNPs to obtain structural information about the eucaryotic pre-mRNA splicing. Apart from that we are working on ribosomal, viral and oxygen carrier projects.. For further information, please contact **Prof. Holger Stark** (hstark1@gwdg.de).

Main Research Field:

Structure determination of large macromolecular complexes.

We use electron cryomicroscopy (cryo-EM) to record images of large macromolecules with the aim to reconstruct their three-dimensional structure to the highest possible resolution. For structure determination by electron cryomicroscopy only very little material is required and no crystals need to be grown. This makes cryo-EM the method of choice for structure determination of large macromolecular complexes with low abundance in the cell that are difficult to purify in the amounts and quality needed for structure determination by X-ray crystallography. The main projects are focused on structure determination of the spliceosome in collaboration with Prof. Reinhard Lührmann and the ribosome with Prof. Marina Rodninas group at the Max-Planck-Institute for biophysical Chemistry.

Another major focus of the group is the development of biochemical tools for improved sample preparation and optimization of complex stability. Structure determination by cryo-EM also requires extensive computational image processing to extract the information from 2D projection images to finally obtain a 3D representation of the macromolecular complex. Therefore, a large part of the group is focused on methods development for image processing with the aim to develop novel algorithms for improved image processing and to obtain a higher degree of automation. The ultimate goal of the group is to determine high-resolution 3D structures of dynamic macromolecular complexes and at the same time to visualize the conformational dynamics and variability of these macromolecules.

Department of Cellular Biochemistry

Max-Planck-Institute for biophysical Chemistry, Am Fassberg 11, 37077 Göttingen

The Department of Cellular Biochemistry at the Max Planck Institute for Biophysical Chemistry is headed by **Prof. Reinhard Lührmann**, who is also a member of the Göttingen Graduate School for Neurosciences and Molecular Biosciences (GGNB) and the IMPRS for Molecular Biology.

Main Research Field:

Structure and function of the splicing machinery.

The primary goal of our research is to understand the structure and the function of the splicing machinery. One main question that we wish to address is how the structural rearrangements of the spliceosome during its work cycle are directed and regulated. Another is what is the nature of the catalytic center of the spliceosome – for example, does it consist only of RNA components (like a ribozyme), or do RNA and protein both contribute to catalysis (as in an RNP enzyme)? To answer these questions we are using an integrated experimental approach that involves a broad palette of methods. We are using biochemical and molecular-genetic methods to study the functions of the proteins and snRNA molecules in splicing, mainly by focussing on the spliceosomes of human cells and those of baker's yeast. At the same time we are using electron cryomicroscopy, X-ray crystallography, mass spectrometry, and fluorescence spectroscopy to investigate the spatial organization and the structural dynamics of isolated spliceosomes.

Department of Plant Biochemistry
Albrecht-von-Haller-Institute for Plant Sciences

Ernst-Caspari-Building (Main Building of the Göttingen Center for Molecular Biosciences)
Justus-von-Liebig-Weg 11, 37077 Göttingen

General information about the department

Currently, there are 35 people employed by the Department of Plant Biochemistry. Besides the encompassing group of Prof. Feussner, the department hosts the research groups of Dr. Ischebeck and Dr. Hadacek which work on interrelated topics. Weekly group seminars are held in English. The regular visit of scientific seminars, some given by internationally renowned invited speakers, is also a great opportunity. The proportion of supervising scientists holding a PhD vs. those still working towards their degrees (MSc-students and PhD-students) calculates to 2/3, which is extraordinary and enables efficient mentoring. For further information, please contact Dr. Ellen Hornung (ehornun@uni-goettingen.de; phone +49-(0)551-39-5748).

Main Research Field

Metabolism and Function of Plant Lipids

The unifying element of research conducted in the Department of Plant Biochemistry is our work on the structure, function and metabolism of plant lipids. Besides proteins, carbohydrates and nucleic acids, lipids are the fourth class of biological macromolecules. Lipids are characterized by their hydrophobic or amphiphilic nature and have important functions in living organisms. For instance, lipids are the building blocks of all biological membranes. Also, lipids serve as storage substances, making them an important target of research, because many crop plants represent important resources based on the oil content of their seeds. Another important field of research relates to the role of lipids as hydrophobic messenger molecules in signaling events during plant development and during adaptational processes to exogenous stresses. Research in the Department of Plant Biochemistry is mainly concerned with basic science, but a number of applied aspects of some of the topics mentioned above are also pursued. The Department of Plant Biochemistry is well known beyond Germany's borders and is well connected through numerous international cooperations. Frequent visits by foreign scientists facilitate personal communication and are the basis for mutual scientific exchange efforts. Financial support is coming from various industrial partners. For further information, please visit our website: http://www.plant-biochem.uni-goettingen.de.

Individual work groups

Feussner: Function and Biochemistry of Structural Lipids and Oxylipins in Plants and Fungi

This group is working on the **lipid metabolism** in plants, algae, mosses and fungi by chemical, analytical, biochemical and molecular approaches. We are analyzing the formation and physiological function of oxidized lipid signaling molecules (oxylipins) during development and plant fungal interactions. Another research focus is the analysis of **enzymes** that introduce new functional groups in fatty acids for industrial purposes. Furthermore the group is running the metabolomics lab of the Goettingen Center of Molecular Biology (GZMB) and is developing analytical tools for the analysis of specific groups of metabolites (i.e. lipidomics) or the entire metabolom.

Ischebeck:

Research focuses on four partly interconnected topics: plant lipid droplets (also referred to as oil bodies or oleosomes), pollen development and pollen tube growth, analytics of small metabolites, and plant-pathogen interactions. Main subject of our research are the model organisms *Arabidopsis thaliana* and *Nicotiana tabacum*, but also less well-studied plants like tiger nuts (*Cyperus esculentus*, also called earth almond) are examined.

Hadacek: Ecological Biochemistry

Research interests cover redox and coordination chemistry of plant metabolites in abiotic and biotic interactions. Currently the phenomenon of rose replant disease represents the main focus.

Faculty of Chemistry
Institute of Physical Chemistry / Section Biophysical Chemistry

Tammannstr. 6, 37077 Göttingen
(**Prof. Dr. Andreas Janshoff**, apl. Prof. Dr. Burkhard Geil)

The main research interest of our group is the dynamics and mechanics of small biological systems ranging from cells and liposomes to single molecules such as DNA or proteins. The behavior of small systems has attracted great interest in biology, chemistry and physics since their display striking properties as a direct result of their small size. The physics of small systems is strongly governed by fluctuations that produce significant deviations from the behavior of large ensembles. The ultimate small device is a single molecule, where fluctuations can be considered to be large and stochasticity dominates its thermal behavior. We combine physical principles and also a variety of methods such as acoustic resonators, impedance analysis, high-resolution imaging using scanning probe microscopy paired with optical microscopy and single molecule as well as single cell force spectroscopy with questions posed by biological systems and discoveries.

Our group addresses the following topics:

- Single molecule mechanics (protein unfolding) using atomic force microscopy and optical tweezers.
- Mimicking biological adhesion and membrane fusion using membrane-based model systems.
- Motility and chemotaxis of cells and their response to physical and chemical stimuli.
- Simulations of bond cluster formation in cellular adhesion.
- Cortex mechanics of epithelial cells
- Rheological properties of cells as a function of substrate properties
- Dynamics and mechanics of wound healing triggered by cytokines

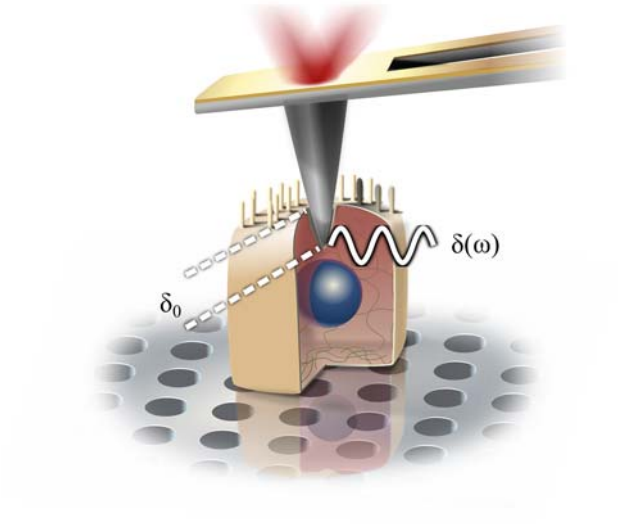


Figure: AFM-based microrheology of cells cultured on porous substrates.

Faculty of Chemistry
Institute of Organic and Biomolecular Chemistry

Tammannstr. 2, 37077 Göttingen

(Prof. Dr. Claudia Steinem)

The main research interests of my group are centered on membrane-confined processes such as fusion and fission, ion transport mediated by ion channels and protein pumps as well as protein-lipid and protein-protein interactions occurring at the membrane interface. To understand these processes on a molecular level, we pursue a bottom-up approach and develop and apply model membrane systems. In particular, we have established functional lipid bilayers on highly ordered pore arrays. These so-called pore-spanning membranes suspend nanometer- to micrometer-sized pores in an aluminum or silicon substrate. They separate two aqueous compartments and can hence be envisioned as an intermediate between solid supported and freestanding membranes. With these model system in hand, we are able to investigate transport processes mediated by ion channels such as connexons and protein pumps such as bacteriorhodopsin. Recently, we managed to reconstitute parts of the neuronal fusion machinery enabling us to study the fusion process between a planar pore-spanning membrane and a single vesicle on a molecular level. As pore-spanning membranes are similar to freestanding ones such as giant unilamellar vesicles, domain formation as well as membrane reorganization can be readily observed. We exploit this by studying the impact of protein binding on membrane domain reorganization, a process that is discussed in the context of Shiga toxin uptake into a cell. Similarly, we study the coupling of the plasma membrane to the underlying cytoskeleton mediated by the protein ezrin, making use of our pore-spanning membrane systems.

Our topics include:

- Membrane systems:
- Transport processes across artificial membranes
- Protein-membrane and protein-protein interactions
- Membrane fusion and fission
- Silica Nano- to Micro-Patterning

(Prof. Dr. Ulf Diederichsen)

Research areas: Modification, specific detection and conformational switching of oligonucleotides, peptides and proteins. Examination of suitable model systems; influencing function and properties by synthesising analogues of biomolecules.

- Synthesis of linear DNA base-stack models, application in DNA diagnostics, electron transfer and intercalation studies; enzyme mimetics.
- Molecular architecture: reversible helix and beta strand organisation, higher aggregates.
- Conformational switch in peptides and proteins.
- Stabilisation of Z-DNA; induction of bent DNA.
- Unnatural amino acids in peptides and proteins.
- DNA double helix detection

For further information please see our homepage: http://www.diederichsen.chemie.uni-goettingen.de/

Department of Physical Biochemistry

Max Planck Institute for Biophysical Chemistry;
Am Fassberg 11, 37077 Göttingen

General information about the department

The Department of Physical Biochemistry at the MPI bpc (head Prof. M. Rodnina) was established in 2008 and has currently 40 employees. Additionally the department hosts the MPI Fellow group of Ribosome Dynamics headed by Prof. Dr. W. Wintermeyer. The working language of the group is English. The scientific environment at the MPI provides numerous opportunities to attend seminars and to exchange ideas and technical know-how with other groups. The department has established collaborations with the 3D-Cryo-Electron Microscopy group (Prof. Dr. H. Stark), the Department of Theoretical and Computational Biophysics (Prof. Dr. H. Grubmüller), the Bioanalytical Mass Spectrometry Group (Prof. Dr. H. Urlaub), and the Department of Molecular Structural Biology at the University (Prof. Dr. R. Ficner). For further information, please contact Dimitra Papastavrou (office.rodnina@mpibpc.mpg.de).

Main research field

Dynamics of macromolecular machines.

The main interest of our group is to understand the function of the ribosome, a macromolecular machine which synthesizes proteins in all cells. We reconstitute translation in vitro from purified components. Using a broad spectrum of biophysical techniques, we follow the assembly of translation complexes and the reactions on the ribosome in real time (milliseconds-seconds). This allows us to determine the timing and the order of events and to study the dynamics of ribosome complexes. Kinetic mechanisms are dissected by rapid kinetics, including stopped-flow, monitoring fluorescence, or quench-flow coupled with the analysis of products of chemical reactions. Further aims are to identify translation intermediates and solve their structures, and to decipher the nature of the transition states of the translation reactions.

Specific research fields

Ribosome function and dynamics.

The ribosome is a fascinating molecular machine that recognizes its substrates with high precision, moves its own parts and the elements of the translational machinery relative to each other, and catalyzes diverse chemical reactions, such as GTP hydrolysis by translation factors, peptide bond formation, and hydrolysis of peptidyl-tRNA. Our goal is to acquire a quantitative understanding of translation, including the control of initiation, mechanisms of substrate selection and catalysis, and to study the conformational dynamics of the ribosome during protein synthesis.

Regulation and fidelity of translation.

Speed and accuracy of protein synthesis are fundamental parameters for understanding the fitness of living cells, the quality control of translation, and the evolution of ribosomes. The accuracy-determining steps of tRNA selection have been identified by previous work in the department. Our goal is to systematically evaluate the error frequency of proteins synthesis in vivo in bacteria using mass spectrometry and to identify regulators of decoding that control initial selection and proofreading, using a combination of genetic and kinetic approaches.

Protein targeting to membranes.

Proteins of the plasma membrane are inserted into the membrane cotranslationally. Ribosomes synthesizing membrane proteins are targeted to the membrane by the signal recognition particle (SRP) cycle. The cycle involves the recognition by SRP of a signal anchor sequence near the N terminus of the nascent protein and the transfer, via the SRP receptor, of the translating ribosome to the protein-conducting channel in the membrane (translocon). The Ribosome Dynamics group is studying the interactions within the SRP cycle, using fluorescence and rapid kinetic methods.

Department of Bioanalytics
Albrecht-von-Haller-Institute for Plant Sciences

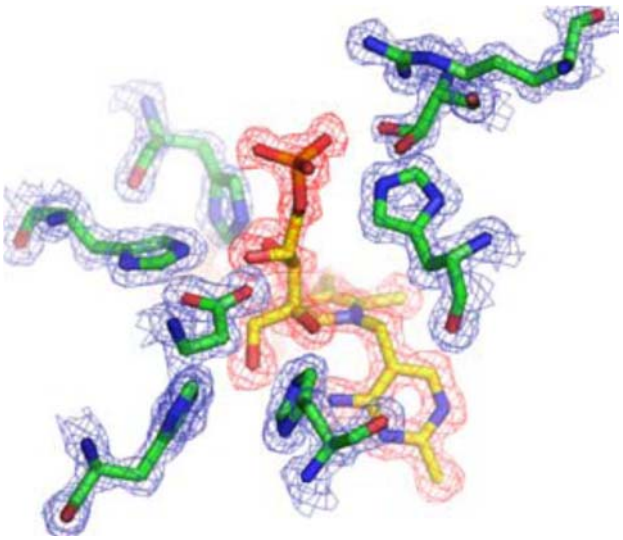
Ernst-Caspari-Haus and Schwann-Schleiden-Centre
Julia-Lermontowa-Weg 3, 37077 Göttingen

General information about the department

Currently, there are approximately 10 people working in our department comprising two PostDocs and several PhD and Master students. Weekly group seminars are held in English.
For further information, please contact Prof. Dr. Kai Tittmann
(Kai.Tittmann@biologie.uni-goettingen.de; phone +49-(0)551-39-177811).

Main Research Field:
Structure and function of enzymes

Research in our laboratories focuses on the mechanistic and structural analysis of different enzymes (biocatalysts) in cellular carbon metabolism and hormone maturation. A particular emphasis is laid on the time-resolved detection and structural characterization of enzymatic reaction intermediates by means of rapid reaction kinetics (stopped-flow, quench-flow), NMR and optical spectroscopy, protein X-ray crystallography, isothermal titration calorimetry and theoretical studies. Current projects address the elucidation of the reaction mechanism of transketolase and transaldolase, which act in tandem in the pentose phosphate pathway, and analysis of electron transfer reactions in proteins. Although our research is mostly concerned with basic aspects, we also pursue applied facets such as the utilization of enzymes for chemoenzymatic synthesis of chiral compounds or the development of inhibitors targeting enzymes involved in the pathogenesis of different disorders (Alzheimer's disease).
Our group is committed in vivid cooperations with different groups of Göttingen University and numerous national and international research groups. Moreover, we have established collaborations with industrial partners. Research is funded by the Deutsche Forschungsgemeinschaft, Bundesministerium für Wirtschaft and other funding agencies.



X-ray structure of a reaction intermediate in transketolase solved in our group.

Contact and services

Academic advisory of the program

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Enrolment

German students

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international students

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37075 Göttingen
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Submission of Bachelor Certificate and proof of English/German proficiencies until November 15th (deadline) via our upload portal