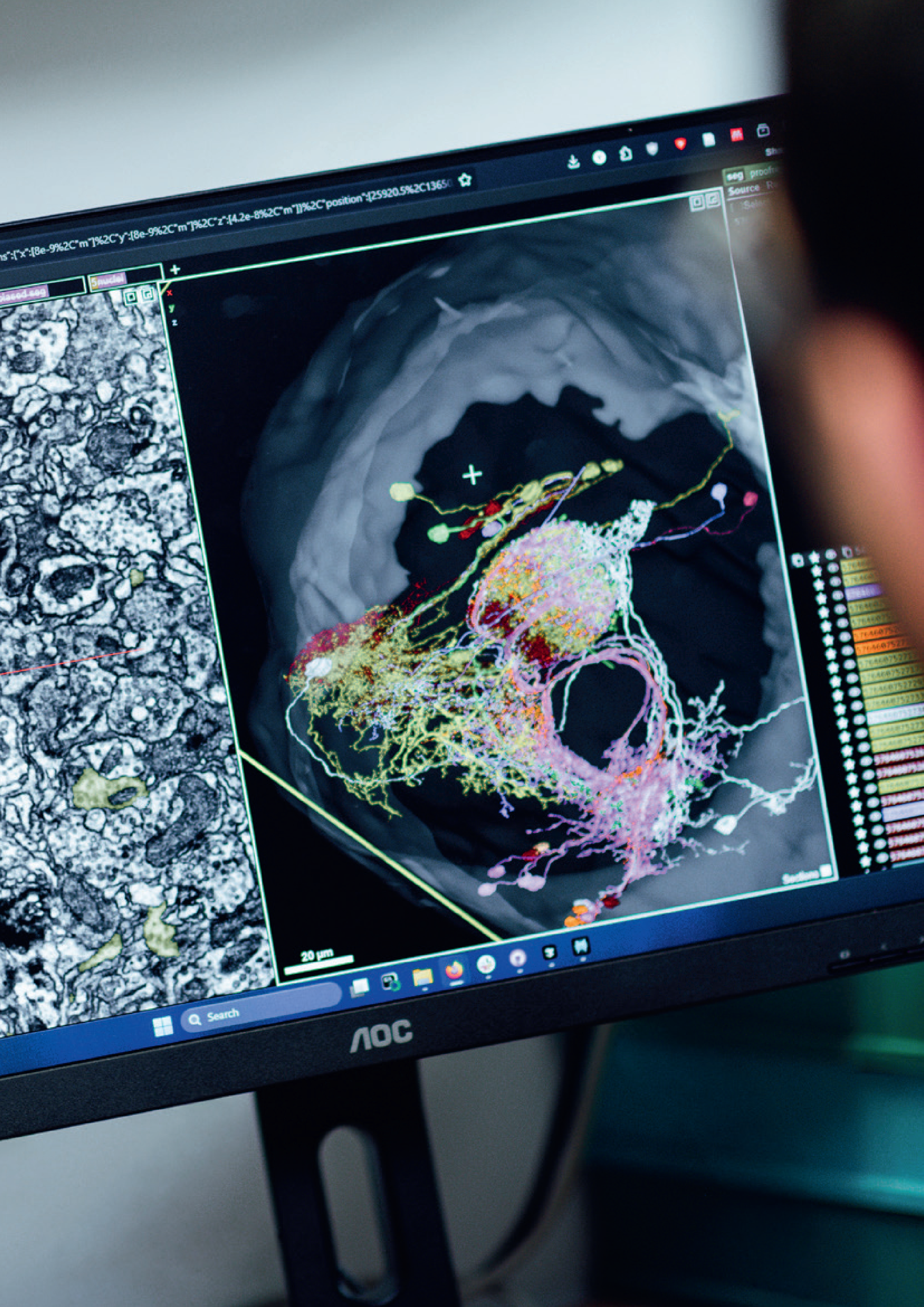
Research at the Würzburg Biocenter

2025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Research Areas

About the Würzburg Biocenter

Tackling today's complex scientific challenges in the life sciences requires interdisciplinary collaboration and innovative thinking. The Würzburg Biocenter serves as a catalyst for innovation and education by bringing together nearly fifty research groups from the Faculties of Biology, Chemistry & Pharmacy, and Medicine. Each group contributes its unique expertise and research focus, creating a vibrant, diverse, and synergistic scientific community.

At the heart of the Centre's mission is the promotion of cross-disciplinary cooperation and open scientific dialogue—both of which are essential for addressing fundamental scientific questions. Our research spans every level of biological organization, from individual molecules and cells to tissues, organisms, and entire ecosystems. This breadth not only drives innovation but also ensures that students and early-career scientists are immersed in a wide range of scientific approaches, preparing them for multifaceted careers in academia, industry, and policy.

Situated across two dynamic campuses—the Würzburg Hubland and Dallenberg sites—the Biocenter brings together the strengths of the Theodor Boveri Institute for Biosciences and the Julius von Sachs Institute for Plant Sciences. Our researchers benefit from access to a high-quality infrastructure, including state-of-the-art microscopy and metabolomics core facilities, the University's Botanical Gardens, greenhouses, laboratory animal facilities, a precision instrumentation workshop, and a high-end IT environment. In addition, technology platforms operated by individual groups, including proteomics, cryo-electron microscopy, next-generation sequencing and many more, provide our researchers with further access to modern key technologies.

In this brochure, I warmly invite you to explore the breadth and depth of scientific enquiry and innovative methodologies pursued by our research groups. Organised into six Research Areas, our groups are united by a shared commitment to advancing knowledge across a wide range of biological and biomedical disciplines. This unique blend of specialised expertise, interdisciplinary collaboration, and shared vision enables the Biocenter to serve as a vital hub for the life and natural sciences at the Julius-Maximilians-Universität Würzburg and beyond.

Christian Häring
Speaker of the Würzburg Biocenter 2024–2025

Building on a Strong Tradition

Since its inception in the 1970s, the core mission of the Würzburg Biocenter has been to unite scientists from across the natural sciences to address major contemporary challenges. The success of this vision is evident in the fact that the number of Biocenter research groups has more than doubled since its inauguration. This vision builds on Würzburg's rich scientific heritage and upholds the legacy of the two 19th-century scientists after whom our institutes are named—Theodor Boveri, a pioneer of chromosome and cell biology, and Julius von Sachs, one of the founding fathers of plant physiology. Their spirit of curiosity and collaboration continues to shape our research culture today.

Excellence in Research

Today, the Würzburg Biocenter is a focal point of world-class research that pushes the boundaries of scientific knowledge and drives groundbreaking innovations in many different areas of the life sciences, from biomedicine to environmental science. As of 2025, our researchers have secured eleven prestigious ERC grants, while a half dozen talented PIs have established independent research groups through career development awards from the DFG's Emmy Noether programme. Our graduate students and postdoctoral researchers consistently lead cutting-edge studies, frequently serving as first authors on publications in top-tier international scientific journals

Our Committment to Teaching

Outstanding multidisciplinary teaching is one of our central priorities. To equip the next generation of researchers, innovators, and decision-makers, we place strong emphasis on critical thinking, intellectual independence, and the confidence to question established ideas. Our faculty deliver lectures, seminars, and practical courses to students across the Biocenter's three affiliated faculties, all within an inclusive, multicultural learning environment where diverse perspectives are valued and collaboration is actively encouraged. Through our Service Centre Biocareers, we provide students with personalised guidance and support on a wide range of topics—from international internships to long-term career planning.

Postgraduate Training

Key to the Biocenter’s research efforts are highly dedicated pre- and postdoctoral researchers who drive ambitious projects under the mentorship of one or more faculty members in a supportive environment. Most doctoral candidates are enrolled in the Würzburg Graduate School of Life Sciences (GSLS), where they benefit from interdisciplinary training, extensive networking opportunities with academia and industry, and a wide range of transferable-skills courses. Postdoctoral researchers have access to additional resources, including a dedicated funding program designed to support their transition toward independent investigator roles.

Family & Career

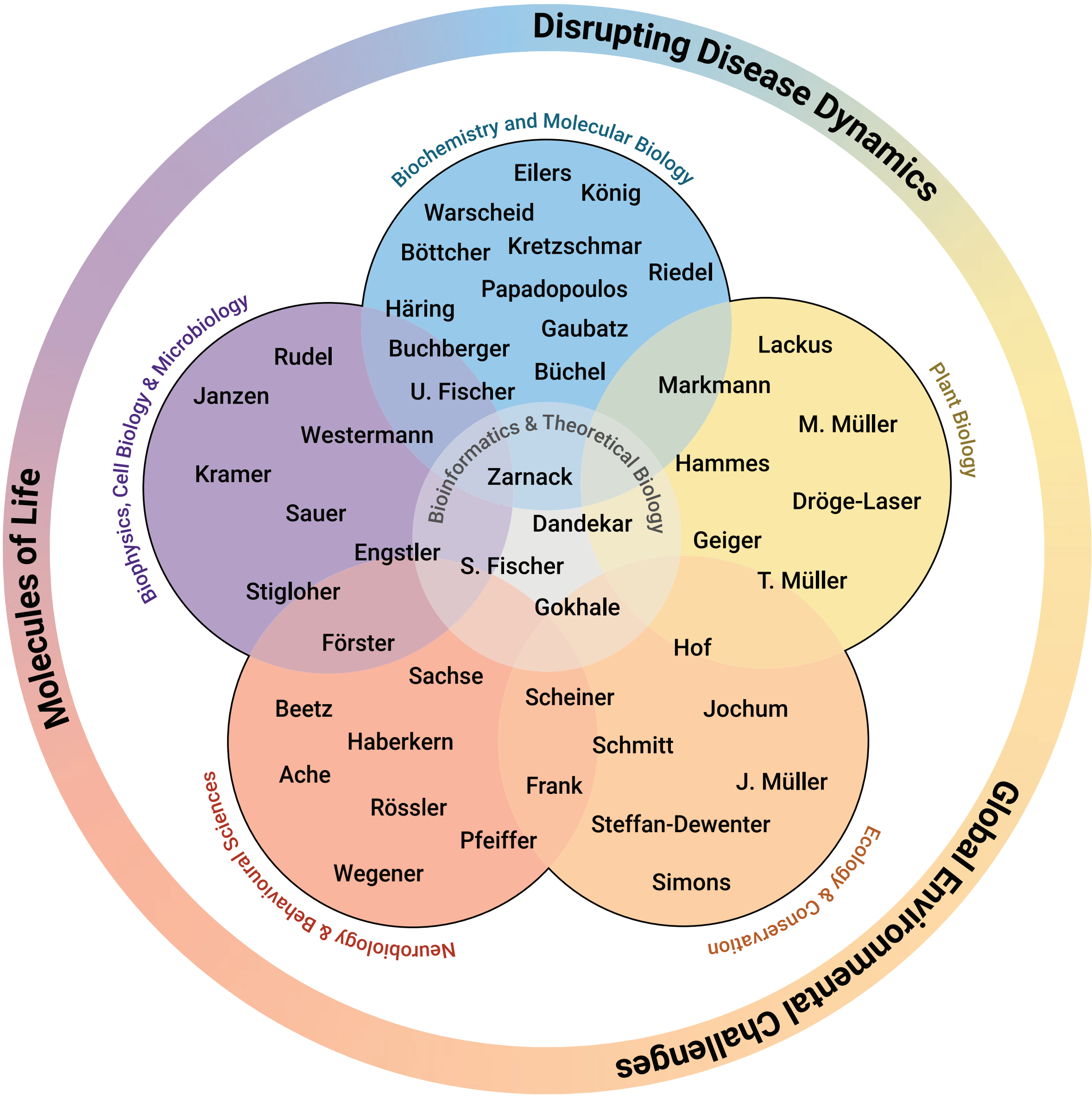
At the Würzburg Biocenter, we deeply value the balance between family and career. We are committed to fostering a family-friendly working environment and continuously seek ways to better support caregivers. In addition to the University’s comprehensive parental leave policies, our faculty strives to offer flexible working arrangements tailored to caregiving needs. We further support work–life balance through initiatives such as scheduling seminars within childcare facility hours and providing a ‘Kids Box’ to keep children engaged when parents need to focus on important tasks. Our sites on the Hubland Campus are just a short walk from the University’s nursery and kindergarten facilities.

Sustainable Research

Sustainable research is essential for driving long-term scientific and technological progress while minimizing environmental impact, enhancing resource efficiency, and supporting a healthier, more resilient future. Environmentally focused studies lie at the core of the Ecology & Conservation Research Area and play a significant role in the research programs of many other Biocenter groups. Beyond our research themes, we are committed to reducing energy consumption and waste in our daily operations. Our initiatives include the gradual installation of energy-efficient LED lighting, the adaptation of modern CFC-free climate-controlled cooling chambers, and efforts to reduce and reuse laboratory plasticware.

Research Areas

The research groups at the Würzburg Biocenter are organised into six Research Areas, each reflecting a distinct field within the life sciences. This structure fosters close collaboration and intellectual exchange—not only within each area, but also across their boundaries—creating an integrative research environment where scientists can address complex biological questions from multiple perspectives at the interfaces of different fields. Collectively, the Research Areas contribute to three overarching thematic priorities of the Julius-Maximilians-Universität Würzburg: Molecules of Life—Pioneering a Healthier Future, Disrupting Disease Dynamics—A Gateway to New Therapeutic Interventions, and Global Environmental Challenges—Ecosystems and Human Societies in Transition.

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Biochemistry & Molecular Biology

Prof. Dr. Bettina Böttcher

1991
PhD, University of Stuttgart

Postdoctoral research at LMB Cambridge

Group Leader at EMBL Heidelberg

Personal Chair at the University of Edinburgh

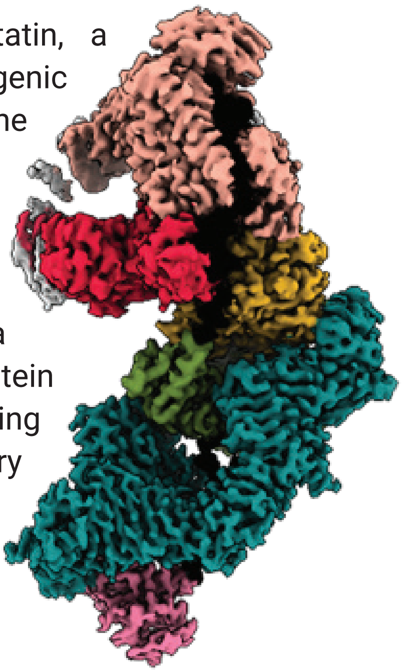
since 2016
Professor of Biochemistry (CryoEM) at JMU Würzburg

Electron Cryo Microscopy In, On and Across Membranes

The structural organization of molecular components determines the underlying mechanisms of biological processes. To understand these processes, we need to know the structures of the molecular players involved. We use electron cryo microscopy to determine the structures of these components in different functional and conformational states.

Our current research focuses on protein assemblies that participate in processes in, on, and across membranes. We investigate mechanosensitive channels of small conductance (MscS-like channels). These channels sense membrane tension and gate when the tension exceeds a certain threshold. We have found that different MscS-like channels follow different conformational routes in this process.

We also investigate Lymphostatin, a huge virulence factor of pathogenic E.coli. Lymphostatin helps the bacteria to colonize the gut by enhancing bacterial attachment and reducing mitogen-activated T-cell proliferation. Our structures reveal that Lymphostatin is a highly dynamic multi-domain protein with some domains resembling enzymes but lacking the necessary motifs to support activity.



Lymphostatin in conformation I

We will continue to work on both research topics. Our future research on MscS-like channels will aim to identify the minimal channel architecture and to reprogram the gating and sensing characteristics. For Lymphostatin, we will investigate how the different functionalities of the protein are released and how this compares to related virulence factors of other bacteria.

Selected Publications

VJ Flegler, A Rasmussen, R Hedrich *et al.* (2025). Mechanosensitive Channel Engineering: A Study on the Mixing and Matching of YnaI and MscS Sensor Paddles and Pores. **Nat Comm** in press

M Griessmann, T Rasmussen, VJ Flegler *et al.* (2025). Structure of lymphostatin, a large multi-functional virulence factor of pathogenic *Escherichia coli*. **Nat Comm** 16(1):5389

VJ Flegler, A Rasmussen A, K Borbil *et al.* (2021). Mechanosensitive channel gating by delipidation. **Proc Natl Acad Sci U S A** 118(33):e2107095118

✉ bettina.boettcher@uni-wuerzburg.de ☎ +49 931 31 84193 🦋 @boettchercryoem.bsky.social
🏛 Chair of Biochemistry II | Theodor Boveri Institute | Faculty of Chemistry and Pharmacy

Intracellular Protein Degradation

Prof. Dr. Alexander Buchberger

1996
PhD, University of Heidelberg

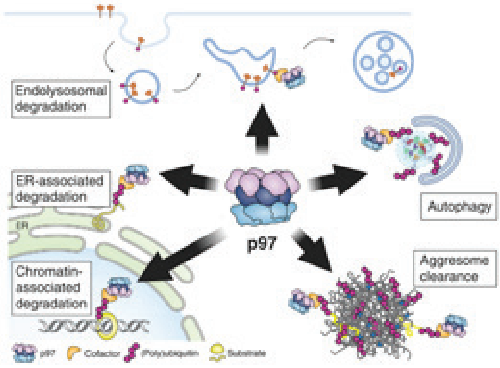
Postdoctoral research at University of Heidelberg and MRC CPE Cambridge

Group Leader at Max Planck Institute of Biochemistry Martinsried

since 2009
Professor of Biochemistry at JMU Würzburg

Our group studies the regulation of intracellular protein degradation in eukaryotic cells by the ubiquitin system. At the center of our research is the chaperone-like ATPase p97 (also known as VCP or Cdc48), which unfolds ubiquitin-tagged substrate proteins to facilitate their degradation via one of three major proteolytic pathways: the 26S proteasome, the endolysosomal system, and autophagy. Malfunction of p97 disrupts protein homeostasis and is causally linked to the fatal neuro-muscular degenerative disorder Multisystem Proteinopathy 1 (MSP1).

The diverse cellular functions of p97 are orchestrated by more than 30 regulatory cofactor proteins controlling its substrate specificity and subcellular localization. Our main research interest has been the identification of p97 cofactors and the elucidation of their cellular functions, in order to better understand how the p97–cofactor network contributes to normal physiology and, ultimately, to the pathogenesis of MSP1. Recent findings include the identification of Ubx2 in yeast and ZFAND1 and FAF1 in human cells, which recruit p97 to ubiquitin-tagged substrates under various stress conditions—at the Endoplasmic Reticulum, within biomolecular condensates termed stress granules, and at large protein aggregates known as aggresomes, respectively.



p97 is involved in various proteolytic pathways. Its diverse functions are controlled by specific cofactors. Created in https://BioRender.com

Moving forward, we aim to further dissect the p97–cofactor network using advanced cellular models for studying the pathogenic mechanisms of MSP1-associated p97 mutations.

Selected Publications

M Körner, P Müller, H Das *et al.* (2025). p97/VCP is required for piecemeal autophagy of aggresomes. **Nat Commun** 16(1):4243

A Turakhiya, SR Meyer, G Marincola *et al.* (2018). ZFAND1 Recruits p97 and the 26S Proteasome to Promote the Clearance of Arsenite-Induced Stress Granules. **Mol Cell** 70(5):906-919

C Schuberth, A Buchberger (2005). Membrane-bound Ubx2 recruits Cdc48 to ubiquitin ligases and their substrates to ensure efficient ER-associated protein degradation. **Nat Cell Biol** 7(10):999-1006

✉ alexander.buchberger@uni-wuerzburg.de ☎ +49 931 31 88031
Chair of Biochemistry I | Theodor Boveri Institute | Faculty of Chemistry and Pharmacy

Prof. Dr. Gabriele Büchel

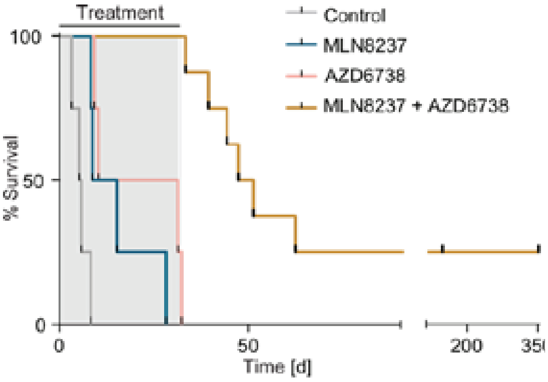
2015
PhD, University Duisburg- Essen (UDE)

Postdoctoral research at JMU Würzburg

since 2021
Junior Professor of Dynamics of Cellular Protein Complexes at JMU Würzburg

Protein Dynamics of MYCN/MYC And Translation into the Clinic

My group focuses on the protein dynamics of MYCN-dependent complexes and the resulting changes in the function of the MYCN oncogene (for example in transcriptional regulation). MYCN belongs to the MYC oncoprotein family, which is expressed at elevated levels in most human tumor diseases. Studies on the role of MYC/MYCN in tumor initiation and progression have shown that tumors depend on MYC or MYCN. Consequently, there is significant interest in comprehending the functions of MYC to explore the potential of inhibiting these oncogenic functions as novel therapeutic targets.



Survival of TH-MYCN mice treated for 32 days with MLN8237 (Aurora-A inhibitor) and AZD6738 (ATR inhibitor). From Roeschert *et al.*, 2021

Based on our findings we focus on different MYCN complexes:

1) Characterization the role of the MYCN/Aurora-A complex
    a) Identification and characterization of novel Aurora-A substrates
    b) Characterization of Aurora-A degradation using PROTACS
    c) Aurora-A inhibition and immunotherapy
2) Role of USP11 in transcription regulation
3) Identification of dependencies of MYCN complexe
    a) Identification and characterization the vulnerabilities of MYCN complexes
    b) *In vivo* analysis of the role of complexes of MYCN oncoprotein in the development and growth of neuroblastoma
    c) Targeting MYCN complexes or their function *in vivo*

Selected Publications

M Dehmer, K Trunk, P Gallant *et al.* (2025). The USP11/TCEAL1 complex promotes transcription elongation to sustain oncogenic gene expression in neuroblastoma. **Genes Dev** 39:751-769

I Roeschert, E Poon, AG Henssen *et al.* (2021). Combined inhibition of Aurora-A and ATR kinase results in regression of MYCN-amplified neuroblastoma. **Nat Cancer** 2(3):312-326

S Herold*, J Kalb*, G Büchel* *et al.* (2019). Recruitment of BRCA1 limits MYCN-driven accumulation of stalled RNA polymerase. **Nature** 567(7749): 545-549

✉ gabriele.buechel@uni-wuerzburg.de ☎ +49 931 31 84946
Chair of Biochemistry and Molecular Biology | Theodor Boveri Institute | Faculty of Medicine

MYC Oncoproteins

Prof. Dr. Martin Eilers

1998
PhD, University of Basel

Postdoctoral research at UC San Francisco

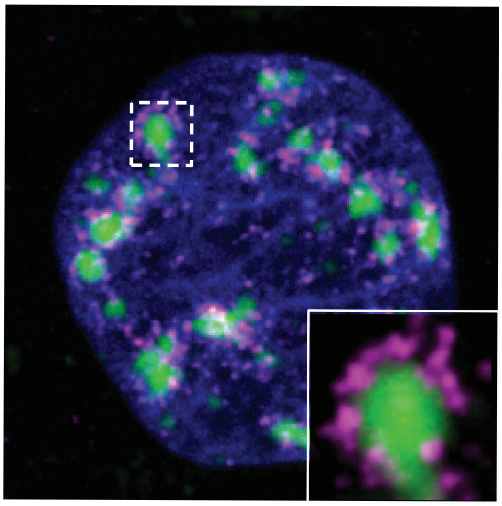
Group Leader at ZMBH Heidelberg

Professor at University of Marburg

since 2008
Professor and Chair of Biochemistry and Molecular Biology at JMU Würzburg

Our work focuses on the function of human MYC proteins. These proteins are oncoproteins that drive the development of most human tumors. Most tumors depend on MYC proteins throughout their development. Our goal is to understand the mechanistic basis of this dependence and exploit it for cancer therapy.

MYC proteins are traditionally viewed as transcription factors that establish a tumor-specific, oncogenic gene expression profile when active. However, our work has revealed that key functions of these proteins are unrelated to changes in gene expression. Instead, MYC proteins maintain genomic stability in rapidly growing cells. For instance, MYC proteins can prevent collisions between RNA polymerase and the replication fork during the S phase. MYC proteins exist in two states in tumor cells and undergo a phase transition when cells are stressed. While they bind to DNA and promoters in unstressed cells, they can multimerize and form sphere-like compartments that protect replication forks. Similar mechanisms enable MYC proteins to hide tumor cells from eradication by the immune system, and we are developing strategies to interfere with these immune-evasive mechanisms.



The figure shows the sphere-like structures that MYC forms in the nucleus of stressed cells. Magenta indicates MYC multimers, green is MYC, blue is DNA. Insert shows higher magnification (see Solvie *et al.* 2022).

Selected Publications

D Solvie, A Baluapuri, L Uhl L *et al.* (2022). MYC multimers shield stalled replication forks from RNA polymerase. **Nature** 612(7938):148-155

S Herold, J Kalb, G Büchel *et al.* (2019). Recruitment of BRCA1 limits MYCN-driven accumulation of stalled RNA polymerase. **Nature** 567(7749):545-549

S Walz, F Lorenzin, J Morton *et al.* (2014). Activation and repression by oncogenic MYC shape tumour-specific gene expression profiles. **Nature** 511(7510):483-487

✉ martin.eilers@uni-wuerzburg.de ☎ +49 931 31 84111 🦋 @mycgyvers.bsky.social
🏛 Chair of Biochemistry and Molecular Biology | Theodor Boveri Institute | Faculty of Medicine

Prof. Dr. Utz Fischer

1992
PhD, FU Berlin

Postdoctoral research at
University of Marburg and
University of Pennsylvania

Max Planck Young Investigator,
MPI for Biochemistry

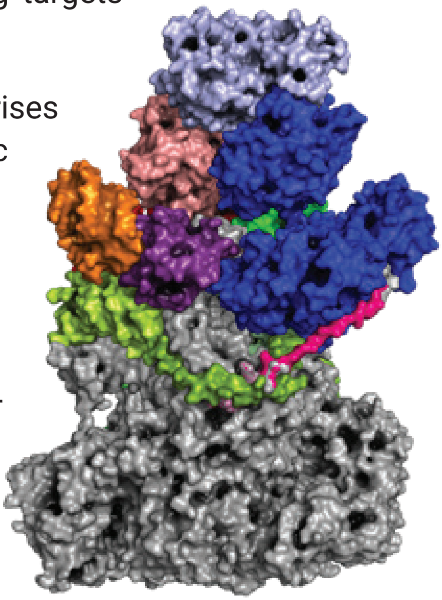
since 2003
Professor and Chair of
Biochemistry I at JMU Würzburg

Macromolecular Machines
RNA Biology of Human Diseases

The generation of messenger RNAs (mRNAs) and their translation into proteins depends on the elaborate interplay of numerous trans-acting factors. These factors are often organized in macromolecular machines, which enable all steps in mRNA metabolism and coordinate their progression in time. Our group studies the functional dynamics of key macromolecular machines acting on RNA using a combination of biochemical, structural and systems biology approaches.

RNA-related pathways have been linked to a broad spectrum of human hereditable diseases and viral infections. By combining basic RNA research with biomedical approaches, we investigate how these pathways and networks are changed in different disease settings. Our research hence contributes to detailed insights into disease etiologies and the identification of novel drug targets for therapeutic approaches.

The Poxviridae family comprises a group of large cytosolic DNA viruses, including the highly pathogenic Variola and MPXV. Because these viruses replicate in the cytoplasm of their respective host, they have no access to the nuclear gene expression machinery. Instead, they use their own RNA-polymerases, transcription and mRNA processing factors. We investigate the gene expression machinery by structural and functional means and use high-throughput approaches to identify novel antiviral compounds.



Structure of the poxviral RNA polymerase. This machine consists of 15 proteins and one RNA and produces viral mRNA (Grimm *et al.* 2019)

Selected Publications

AB Prusty, A Hirmer, JA Sierra-Delgado *et al.* (2024). RNA helicase IGHMBP2 regulates THO complex to ensure cellular mRNA homeostasis. **Cell Rep** 43(2):113802

C Grimm, J Bartuli, B Boettcher *et al.* (2021). Structural basis of the complete poxvirus transcription initiation process. **Nat Struct Mol Biol** 28(10):779-788

C Grimm, HS Hillen, K Bedenk *et al.* (2019). Structural Basis of Poxvirus Transcription: Vaccinia RNA Polymerase Complexes. **Cell** 179(7):1537-1550

✉ utz.fischer@uni-wuerzburg.de ☎ +49 931 31 84029 𝕏 @BiochemistryWr1

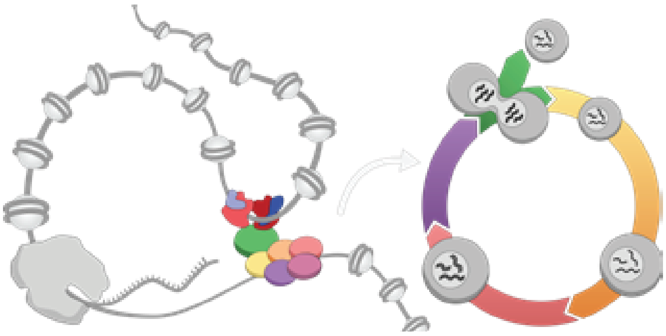
🏛 Chair of Biochemistry I | Theodor Boveri Institute | Faculty of Chemistry and Pharmacy

Transcription Regulation Of the Cell Cycle

Progression through the cell cycle depends on tightly regulated changes in transcriptional activity, ensuring that proteins needed in each phase are produced at the correct time. When cell cycle progression is disrupted, this can lead to a number of diseases such as cancer.

Our research focuses on the MuvB multiprotein complexes, which are key regulators of cell cycle gene transcription in mammalian cells. MuvB complexes are modular and undergo dynamic changes as cells transition through different phases of the cycle. In quiescent cells and early G1 phase, the MuvB core forms the DREAM complex by associating with the retinoblastoma family protein p130 and with E2F4. DREAM represses a broad set of E2F target genes to maintain cell cycle arrest. Upon entry into the cell cycle, p130 and E2F4 dissociate and are replaced by the B-MYB (MYBL2), forming the Myb-MuvB complex (MMB). MMB drives the activation of genes needed for mitosis and cytokinesis. Through biochemical, genetic, and genomic approaches, we have shown that MuvB complexes play a central role in expression of cell cycle genes to ensure proper cell division and genomic stability.

In our ongoing work we investigate how MuvB activates mitotic genes and how it interfaces with major signaling pathways — including Hippo-YAP, which regulates growth and proliferation, and ATR-CHK1, a key DNA damage response pathway — to fine-tune gene expression in normal and cancer cells



Schematic depiction of transcriptional control by DREAM and MMB complexes at different time points in the cell cycle

Prof. Dr. Stefan Gaubatz

1996

PhD, Heidelberg University

Postdoctoral research at Dana Farber Cancer Institute, Boston

Junior Group Leader at Philipps-Universität Marburg

since 2006

Professor of Physiological Chemistry at JMU Würzburg

Selected Publications

D Gertzmann, C Presek, AL Mattes *et al.* (2025). Oncogenic YAP sensitizes cells to CHK1 inhibition via CDK4/6 driven G1 acceleration. **EMBO Rep** in press

G Pattschull, S Walz, M Gründl *et al.* (2019). The Myb-MuvB Complex Is Required for YAP-Dependent Transcription of Mitotic Genes. **Cell Rep** 27(12):3533-3546

S Stopp, M Gründl, M Fackler, *et al.* (2017). Deletion of Gas2l3 in mice leads to specific defects in cardiomyocyte cytokinesis during development. **Proc Natl Acad Sci U S A** 114(30):8029-8034

✉ stefan.gaubatz@uni-wuerzburg.de ☎ +49 931 31 84138

🏛 Chair of Biochemistry and Cell Biology | Theodor Boveri Institute | Faculty of Medicine

Prof. Dr. Christian Häring

2003
PhD, University of Vienna

Postdoctoral research at IMP Vienna and University of Oxford

Group Leader at EMBL Heidelberg

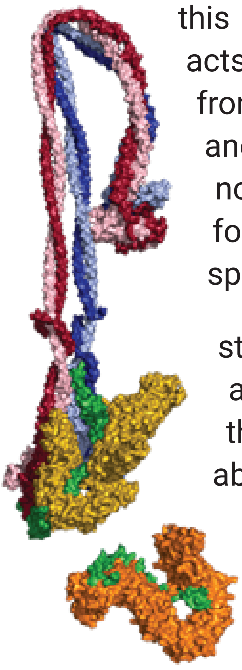
since 2020
Professor and Chair of Biochemistry and Cell Biology at JMU Würzburg

Chromosome Structure And Dynamics

The three-dimensional architecture of the genome is fundamental to its function, influencing processes such as gene regulation and the accurate segregation of chromosomes during cell division. Our research aims to uncover the molecular mechanisms by which eukaryotic chromosomes are spatially organized.

We focus on condensin, a central member of the Structural Maintenance of Chromosomes (SMC) protein complex family. To investigate its function, we adopt a highly interdisciplinary approach, integrating cutting-edge techniques from biochemistry, molecular cell biology, biophysics, and structural biology. Through this approach, we have shown that condensin acts as a molecular motor, using the energy from ATP hydrolysis to translocate along DNA and fold it into large loops. This activity is now recognized as a universal mechanism for chromosome organization across diverse species.

We have determined the structure of the entire condensin complex and mapped the trajectory of DNA through the complex. The insights gained have enabled us to construct a detailed mechanistic model explaining how condensin moves in large, unidirectional steps with remarkable energy efficiency



Cryo-EM structure of the yeast condensin complex

We are currently validating this model in reconstituted biochemical systems, cultured human cells, and model organisms. By uncovering the fundamental principles of SMC complex function, our work seeks to illuminate how genome architecture is regulated and how its dysregulation contributes to human disease.

Selected Publications

Shaltiel IA, Datta S, Lecomte L *et al.* (2022). A hold-and-feed mechanism drives directional DNA loop extrusion by condensin. **Science** 376(6597):1087-1094

Lee B-G, Merkel F, Allegretti M *et al.* (2020). Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. **Nat Struct Mol Biol** 27(8): 743-751

Ganji M, Shaltiel IA, Bisht S *et al.* (2018). Real-time imaging of DNA loop extrusion by condensin. **Science** 360(6384):102-105

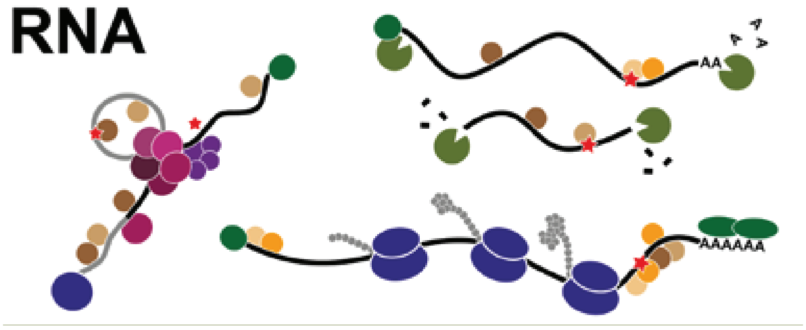
✉ christian.haering@uni-wuerzburg.de ☎ +49 931 31 84148 @haeringlab.bsky.social
Chair of Biochemistry and Cell Biology | Theodor Boveri Institute | Faculty of Medicine

RNA Processing and Modificatio

Our research investigates the molecular mechanisms of RNA regulation and modification, with a focus on their roles in cellular function and diseases such as cancer. Using a functional genomics approach, we have developed high-throughput methods including iCLIP (to map protein–RNA interactions), in vitro iCLIP (for recombinant protein binding), miCLIP2 (for detecting m6A RNA modifications), and massively parallel reporter assays (to decode RNA regulatory elements).

Our key findings include the discovery that m6A RNA modifications mediate X-to-autosome dosage compensation (Rücklé *et al.*, 2023) and a novel m6A-triggered RNA decay pathway (Zhou *et al.*, 2024). In the context of RNA splicing, we identified FUBP1 as a core factor required for the splicing of long introns (Ebersberger *et al.*, 2023), mapped RNA elements regulating specific splicing decisions, and identified regulators linked to CART-19 therapy resistance in B-ALL (Braun *et al.*, 2018; Cortes-Lopez *et al.*, 2021). We also revealed how RNA-binding proteins interact to shape regulation (Sutandy *et al.*, 2018; Kang *et al.*, 2020) and discovered Makorin as a sensor for faulty RNAs (Hildebrandt *et al.*, 2019).

Current efforts focus on three areas: (1) splicing regulation in disease, (2) the role of m6A in gene expression and dosage compensation, and (3) mechanisms of RNA quality control. Our aim is to uncover fundamental RNA regulatory principles to inform future therapies for age-related diseases.



The complex life of RNA: RNA binding proteins and RNA modifications control splicing, translation and RNA decay.

Prof. Dr. Julian König

2008
PhD, University of Marburg

Postdoctoral research at LMB Cambridge and UC London

Group Leader at IMB Mainz

since 2024
Professor and Chair of Biochemistry and RNA Biology at JMU Würzburg

Selected Publications

Y Zhou, M Corovic, P Hoch-Kraft *et al.* (2024). m6A sites in the coding region trigger translation-dependent mRNA decay. **Mol Cell** 84(23): 4576-4593

S Ebersberger, C Hipp, MM Mulorz *et al.* (2023). FUBP1 is a general splicing factor facilitating 3’ splice site recognition and splicing of long introns. **Mol Cell** 83(15):2653-2672

C Rücklé, N Körtel, MF Basilicata *et al.* (2023). RNA stability controlled by m6A methylation contributes to X-to-autosome dosage compensation in mammals. **Nat Struct Mol Biol** 30(8):1207-1215

✉ julian.koenig@uni-wuerzburg.de ☎ +49 931 31 84730 🦋 @koenig-lab.bsky.social
🏛 Chair of Biochemistry and RNA Biology | Theodor Boveri Institute | Faculty of Medicine

Adult Stem Cell Niches In Cancer

Dr. Kai Kretzschmar

2014
PhD, University of Cambridge

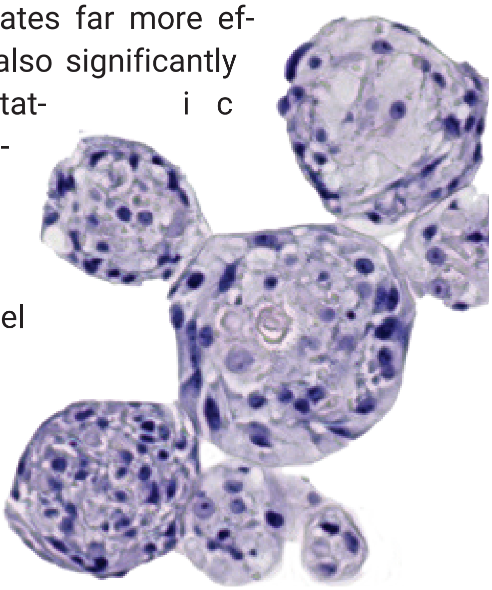
Postdoctoral research at
Hubrecht Institute Utrecht

since 2020
Group Leader at JMU Würzburg

Adult stem cells, which maintain and regenerate tissues in our body, reside in a specialised microenvironment known as the stem cell niche. Although stem cell niches are tissue-specific, two cellular components – fibroblasts and immune cells – have emerged as prominent members of niches throughout the body. Stem cells receive signals from their microenvironment that control the smooth transition between several plastic states, which are critical for maintaining tissue homeostasis and regenerating in response to injury. Conversely, aberrant (stem) cells can acquire the ability to remodel their microenvironment in diseases such as cancer, allowing the disease to progress.

Among the stem cell systems in the human body, the oral epithelium has unique and poorly understood properties. Despite its similarities to the skin epidermis, the oral epithelium regenerates far more efficiently; however, it is also significantly more prone to metastatic squamous cell carcinoma. These contrasts suggest fundamental differences in stem cell behaviour, niche remodelling and immune surveillance, making the oral mucosa an ideal model for studying cancer, ageing and tissue regeneration.

To unravel the fundamental mechanisms regulating the stem cells and their niches, we employ lineage tracing, organoid technology, organoid-based immune and stromal cell co-cultures, 3D whole-mount imaging, single-cell and spatial transcriptomics, utilising both mouse models and patient samples.



Histological image of patient-derived oral cancer organoids

Selected Publications

AC Seubert, M Krafft, S Bopp *et al.* (2024). Spatial transcriptomics reveals molecular cues underlying the site specificity of the adult mouse oral mucosa and its stem cell niches. **Stem Cell Reports** 19(12):1706-1719

L Szabó, AC Seubert, K Kretzschmar (2023). Modelling adult stem cells and their niche in health and disease with epithelial organoids. **Semin Cell Dev Biol** 144:20-30

E Driehuis, K Kretzschmar, H Clevers (2020). Establishment of patient-derived cancer organoids for drug-screening applications. **Nat Protoc** 15(10):3380-3409

✉ kai.kretzschmar@uni-wuerzburg.de ☎ +49 931 31 88085 🦋 @kaikretzschmar.bsky.social
🏛 Chair of Biochemistry and Cell Biology | Theodor Boveri Institute | Faculty of Medicine

MYC(N)-Driven Cancers
Regulation of RNA Fate

Our research focuses on basic molecular mechanisms maintaining human cancers. We are particularly interested in MYC oncoproteins and their newly discovered RNA-binding properties.

We want to understand the MYC-driven mechanisms that determine RNA export and degradation in a malignant cell. In addition, we want to elucidate how perturbing these mechanisms impacts the ability of cancers to repair DNA damage and evade the host immune system.

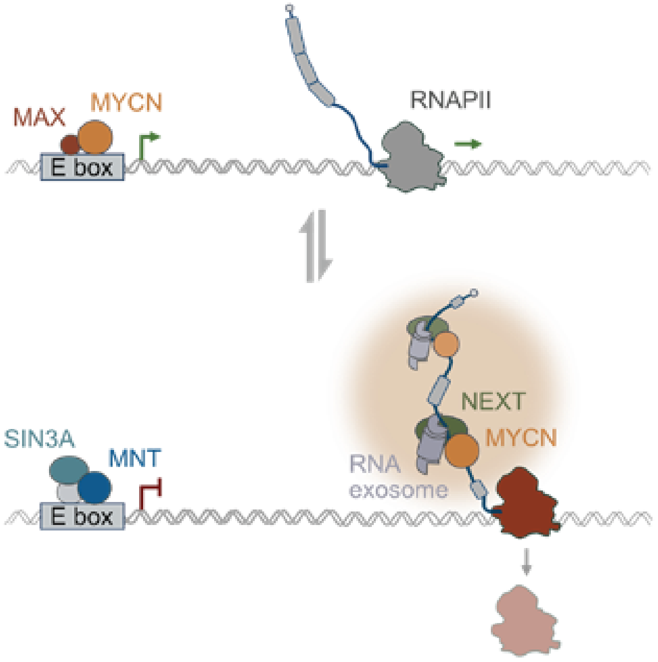
In the future, we will specifically target these mechanisms with state-of-the-art tools including proteolysis targeting chimeras (PROTACs) and specialized ribozymes.

Prof. Dr. Dimitrios Papadopoulos

2017
PhD, University of Giessen

Postdoctoral research at JMU Würzburg

since 2025
Professor of Tumor Systems Biology at JMU Würzburg



Depiction of the MYCN oncogenic transcription in its distinct DNA- and RNA-bound states

Selected Publications

D Papadopoulos, SA Ha, D Fleischhauer *et al.* (2024). The MYCN oncoprotein is an RNA-binding accessory factor of the nuclear exosome targeting complex. **Mol Cell** 84(11):2070-2086

D Papadopoulos, L Uhl, SA Ha, M Eilers (2023). Beyond gene expression: how MYC relieves transcription stress. **Trends Cancer** 9(10):805-816

D Papadopoulos, D Solvie, A Baluapuri *et al.* (2022). MYCN recruits the nuclear exosome complex to RNA polymerase II to prevent transcription-replication conflicts. **Mol Cell** 82(1):159-176

✉ dimitrios.papadopoulos@uni-wuerzburg.de ☎ +49 931 31 89352
Chair of Biochemistry and Molecular Biology | Theodor Boveri Institute | Faculty of Medicine

Dr. Angela Riedel

2012
PhD at University of Southern Denmark

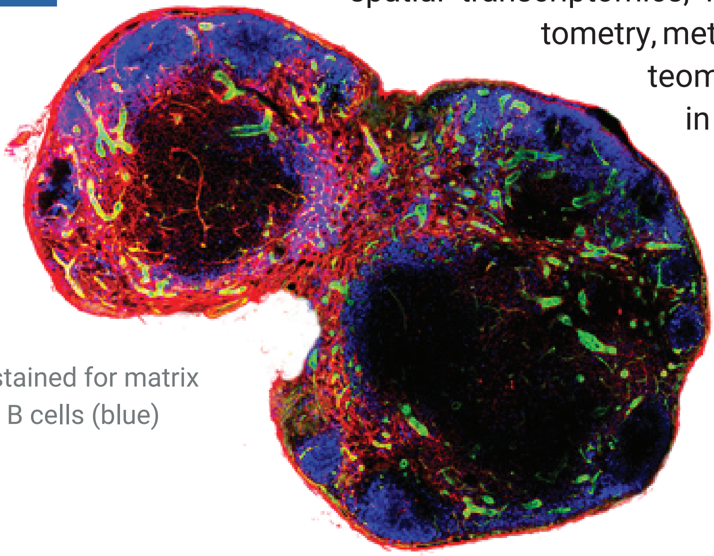
Postdoctoral research at University of Cambridge and DKFZ Heidelberg

since 2020
Group Leader at JMU Würzburg

Metastatic Niches and Tumor Immunology

Metastatic disease and tumor immune evasion are two major hurdles in cancer therapy. Around 70% of solid cancer related deaths are caused by metastatic systemic disease. Tumor-draining lymph nodes (TDLNs) are immunological hubs and often the first site where metastatic tumor cells are detected and thus sit at the crossroad of both processes. We are interested in the cells of the metastatic TDLN niche and how these influence metastatic spread and anti-tumor immune responses. A main goal is to characterize the cellular cross-talk between tumor cells, cells of the immune system and the lymph node stroma.

Our central hypothesis is that tumor progression, particularly in metastatic disease, is associated with an altered immune response. This altered immune response can either be caused by tumor cell intrinsic or extrinsic, host derived, factors. To find the underlying mechanisms, we decipher how the tumor cell interacts within its local and distant, e.g. draining lymph node, niche, and how to target these interactions to ultimately modulate immune evasion and metastasis. In all our projects, we combine state-of-the-art technologies, such as single-cell and spatial transcriptomics, multi-color flow cytometry, metabolomics, and proteomics with advanced in vitro models, such as organoids, in vivo mouse models and patient samples.



A tumor-draining lymph node stained for matrix (red), endothelium (green) and B cells (blue)

Selected Publications

M John, M Helal, J Duell J *et al.* (2024). Spatial transcriptomics reveals profound subclonal heterogeneity and T-cell dysfunction in extramedullary myeloma. **Blood** 144(20):2121-2135

T Hongu, M Pein, J Insua-Rodríguez *et al.* (2022). Perivascular tenascin C triggers sequential activation of macrophages and endothelial cells... **Nat Cancer** 3(4):486-504

A Riedel, M Helal, L Pedro L *et al.* (2022). Tumor-Derived Lactic Acid Modulates Activation and Metabolic Status of Draining Lymph Node Stroma. **Cancer Immunol Res** 10(4):482-497

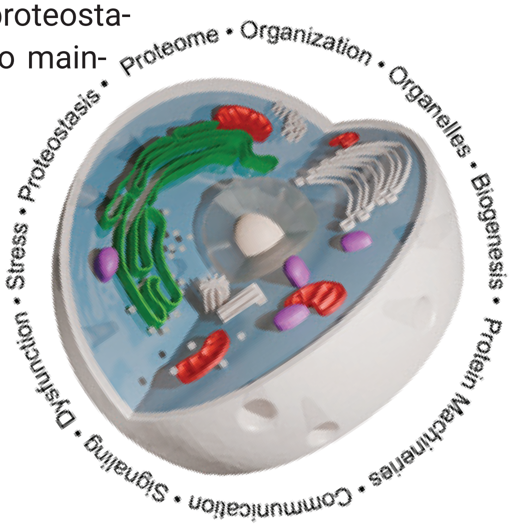
✉ angela.riedel@uni-wuerzburg.de ☎ +49 931 31 86933
Chair of Biochemistry and Cell Biology | Theodor Boveri Institute | Faculty of Medicine

Proteome Biology & Proteomics From Organelles to Proteostasis

The human proteome comprises over 15,000 proteins expressed in cells or tissues. Proteins are the functional units of cellular activity, making it crucial to understand how cells organize, maintain and remodel their proteome to perform an array of functions. A healthy proteome is essential for life, while even a single malfunctioning protein can lead to severe disorders. Our research centers on understanding the spatial organization and dynamics of the proteome using cutting-edge proteomics and mass spectrometry techniques.

We focus on systematically studying the biogenesis and functions of two vital organelles: mitochondria and peroxisomes. Their dysfunction is linked to both rare and prevalent human diseases, prompting our studies into how these organelles integrate into the cell's complex protein network. Key research questions include: How do mitochondria and peroxisomes communicate within this network? What roles do they play in metabolic and cellular processes? How do nascent proteins find their specific locations in a cell, which import mechanisms do they use, and what happens when these pathways fail? A major aim is to understand the different cellular responses to stress on these organelles and which specific branches of the cell's proteostasis network are activated to maintain proteome health.

Looking ahead, our work will delve into processes at organellar interfaces and mechanisms for translation regulation and protein degradation in response to cellular stress.



Prof. Dr. Bettina Warscheid

2002
PhD, TU Dortmund and ISAS

Postdoctoral research at University of Maryland and Johns Hopkins University

Professor at Universities of Bochum and Duisburg-Essen

Professor and Chair at University of Freiburg

since 2022
Professor and Chair of Biochemistry II at JMU Würzburg

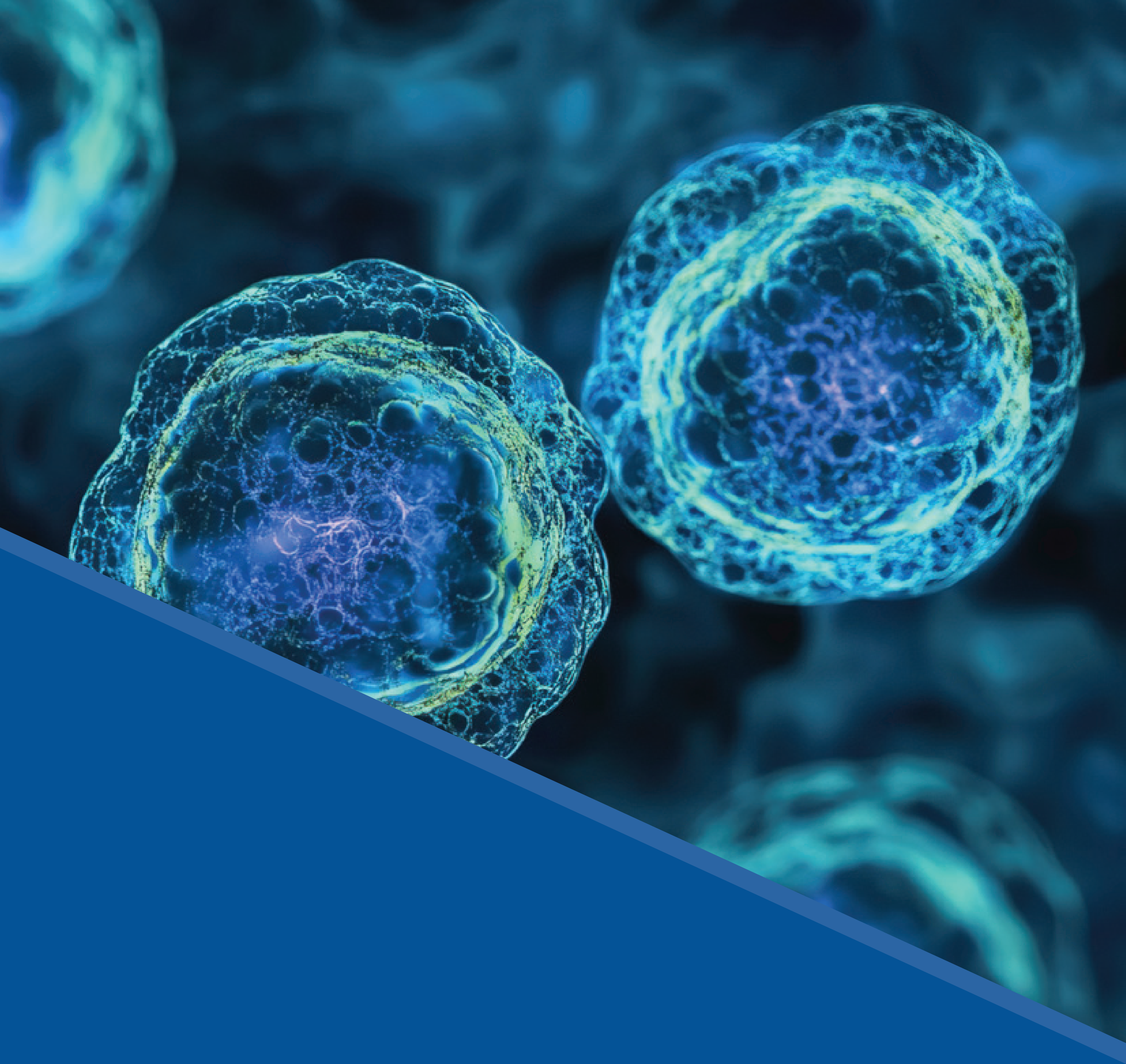
Selected Publications

WW Chen, TA Rodrigues, D Wendscheck *et al.* (2025). PEX39 facilitates the peroxisomal import of PTS2-containing proteins **Nat Cell Biol** 27(8):1256-1271

M Morgenstern, CD Peikert, P Lübbert *et al.* (2021). Quantitative high-confidence human mitochondrial proteome and its dynamics in cellular context. **Cell Metab** 33(12):2464-2483

L Wrobel, U Topf, P Bragoszewski *et al.* (2015). Mistargeted mitochondrial proteins activate a proteostatic response in the cytosol. **Nature** 524(7566):485-488

✉ bettina.warscheid@uni-wuerzburg.de ☎ +49 931 31 86772
Chair of Biochemistry II | Theodor Boveri Institute | Faculty of Chemistry and Pharmacy



Biophysics, Cell Biology & Microbiology

Prof. Dr. Markus Engstler

1994
PhD, CAU Kiel

Postdoctoral research at Rockefeller University and MPI of Biochemistry

Senior Staff Scientist at FU Berlin

Project Leader at LMU Munich

Professor of Genetics at TU Darmstadt

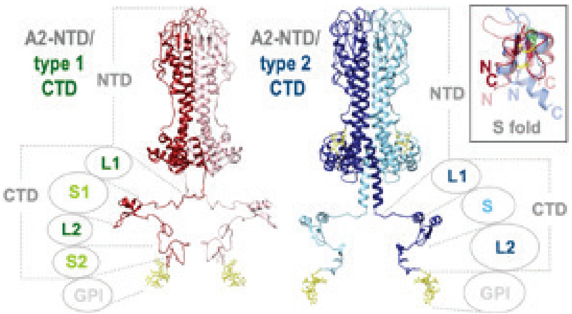
since 2009
Professor and Chair of Cell Biology at JMU Würzburg

Biology of the Cell Surface
Physics of Parasitism

We work with an exciting model system in cell biology – the unicellular parasite Trypanosoma brucei. This organism is not only of major scientific interest but also of medical relevance, as it causes severe diseases in humans and cattle in the global South. Our research is therefore both curisity-driven and socially responsible.

Trypanosomes possess a unique surface coat composed essentially of a single dominant protein family known as VSGs. We are interested in how this surface is assembled at the molecular level, how its integrity is maintained, and how it remains dynamic despite being packed with proteins at the highest physically possible density. Remarkably, VSGs are highly mobile and undergo continuous and extremely rapid exchange with the endomembrane system. We investigate the molecular mechanisms that enable this extraordinary rate of surface dynamics.

We have uncovered a close functional link between cellular motility, surface organisation, and membrane recycling. Trypanosomes actively harness hydrodynamic flow, generated by their own swimming motion, to transport surface-bound antibodies to the cell's posterior, where they are efficiently removed. We are now beginning to understand how this complex system is orchestrated. These insights into general membrane cell biology and biophysics are made possible by advanced technologies – ranging from single-molecule microscopy and tissue engineering to state-of-the-art single-cell analyses and computational biology.



Variant surface glycoproteins cover the trypanosome cell surface. There are hundreds of different VSGs, which form the basis for antigenic variation

Selected Publications

T Müller, T Krüger, M Engstler (2025). Subcellular dynamics in unicellular parasites. **Trends Parasitol** 41(3):222-234

F Link, A Borges, O Karo *et al.* (2024). Continuous endosomes form functional subdomains and orchestrate rapid membrane trafficking in trypanosomes. **Elife** 12:RP91194

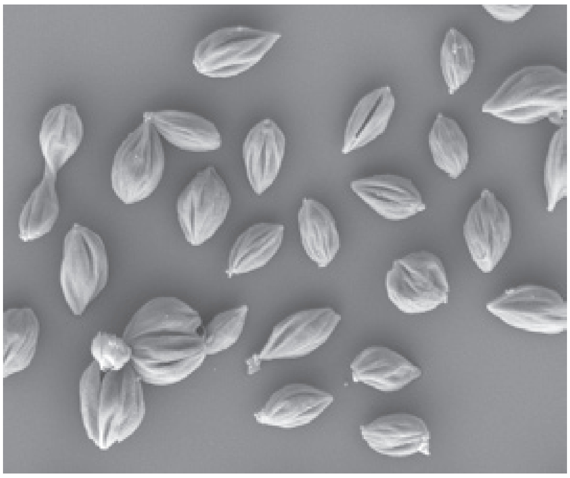
C Reuter, L Hauf, F Imdahl *et al.* (2023). Vector-borne Trypanosoma brucei parasites develop in artificial human skin and persist as skin tissue forms. **Nat Commun** 14(1):7660

✉ markus.engstler@uni-wuerzburg.de ☎ +49 931 31 80060
🏛 Chair of Cell and Developmental Biology | Theodor Boveri Institute | Faculty of Biology

Parasite Adaptation Strategies For Different Host Environments

After establishing the foundation for current projects in our group through pioneering work on post-translational histone modifications and their influence on chromatin structure in African trypanosomes, we are now focusing on the strategies that parasites have developed to adapt to extremely different environments as they transition between host organisms. Trypanosomes must adjust their morphology, metabolism, and energy sources throughout a complex life cycle involving multiple hosts, and changes in chromatin structure and nuclear architecture have been observed during these processes. We use high-throughput proteomic techniques to investigate how chromatin remodeling and other essential cellular processes are regulated during developmental differentiation.

Additionally, we are interested in how replication initiation is regulated in trypanosomes. We discovered that post-translational histone modifications, mediated by DOT1 methyltransferases, are essential for replication initiation. However, the underlying regulatory mechanisms remain unclear. To address this, we employ biochemical and cell biology approaches to further investigate replication regulation in African trypanosomes.



Our current challenge is to transfer our knowledge, methodologies, and expertise to address similar questions in Leishmania parasites, which are responsible for devastating diseases worldwide.

Scanning electron microscopy of human-infective amastigote stages of *Leishmania mexicana* parasites

Prof. Dr. Christian Janzen

2000
PhD, University of Freiburg

Postdoctoral research at Rockefeller University New York

Group leader at LMU Munich

since 2011
Professor of Developmental Biology at JMU Würzburg

Selected Publications

N Eisenhuth, T Vellmer, ET Rauh *et al.* (2021). A DOT1B/Ribonuclease H2 Protein Complex Is Involved in R-Loop Processing, Genomic Integrity, and Antigenic Variation in *Trypanosoma brucei*. **mBio** 12(6):e0135221

H Reis, M Schwebs, S Dietz *et al.* (2018). TelAP1 links telomere complexes with developmental expression site silencing in African trypanosomes. **Nucleic Acids Res** 46(6):2820-2833

M Dejung, I Subota, F Bucerius *et al.* (2016). Quantitative Proteomics Uncovers Novel Factors Involved in Developmental Differentiation of Trypanosoma brucei. **PLoS Pathog** 12(2):e1005439

✉ christian.janzen@uni-wuerzburg.de ☎ +49 931 31 86685 🦋 @agjanzen.bsky.social
🏛 Chair of Cell and Developmental Biology | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Susanne Kramer

2005
PhD, LMU München

Postdoctoral research at the University of Cambridge

Group Leader at JMU Würzburg

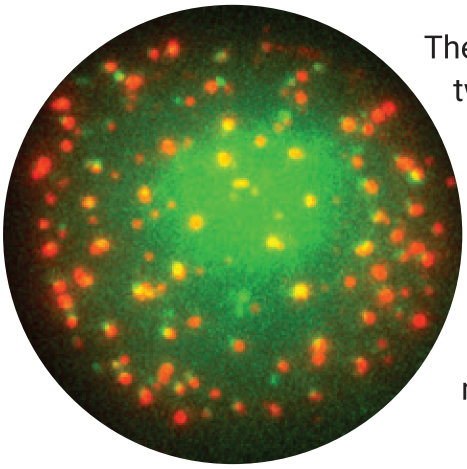
since 2022
Heisenberg-Professor of RNA Biology of Kinetoplastida at JMU Würzburg

Euglenozoa
Cell Biology of mRNA Metabolism

We are interested in answering cell biological questions of *Euglenozoa* that are related to mRNA metabolism. *Euglenozoa* are close to the root of the last common eukaryotic ancestor and our research aims to explore how eukaryote-specific features of mRNA metabolism have evolved. In addition, differences between trypanosomes and mammals can be exploited for drug development against Kinetoplastida-caused diseases, including African Trypanosomiasis (sleeping sickness), Chagas disease and Leishmaniasis. We are currently working with *Trypanosoma brucei* and *Euglena gracilis*. We have a strong background in all molecular and cell biology methods, including single molecule RNA FISH, BioID and expansion microscopy.

Major achievements of the lab were the purification and analysis of starvation stress granules, the discovery of the unique trypanosome mRNA decapping enzyme and a detailed description of the trypanosome nuclear pore with many novel components.

The current lab interest is divided twofold: (i) We study the novel mRNA decapping enzyme ALPH1, with a focus to employ the enzyme as a drug target and (ii) We study the nuclear pore complex and the mechanism of mRNA export.



Expansion microscopy of the *trypanosome* nucleus

Selected Publications

BP Gabiatti, J Krenzer, S Braune *et al.* (2025). Detailed characterisation of the trypanosome nuclear pore architecture reveals conserved asymmetrical functional hubs... **PLoS Biol** 23(2):e3003024.

S Kramer, NK Karolak, J Odenwald *et al.* (2023). A unique mRNA decapping complex in trypanosomes. **Nucleic Acids Res** 51(14):7520-7540

C Goos, M Dejung, AM Wehman *et al.* (2019). Trypanosomes can initiate nuclear export co-transcriptionally. **Nucleic Acids Res** 47(1):266-282

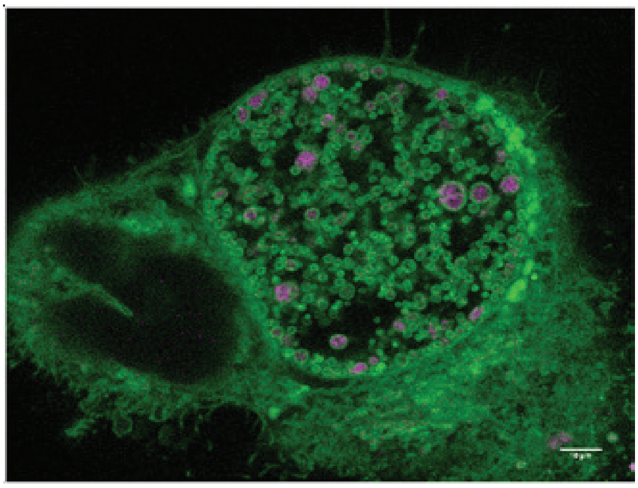
✉ susanne.kramer@uni-wuerzburg.de ☎ +49 931 31 86785
🏛 Chair of Cell and Developmental Biology | Theodor Boveri Institute | Faculty of Biology

Infection Biology of Bacteria

The group investigates the pathogenic mechanisms of major human pathogens, including *Chlamydia trachomatis* and *Neisseria gonorrhoeae*, with a particular focus on bacterial and viral co-infections and their contribution to human diseases, such as cancer.

Our research on *Chlamydia trachomatis*, a leading cause of sexually transmitted infections and an obligate intracellular pathogen, centers on two main areas: (i) how it reprograms host cell metabolism to support intracellular replication, and (ii) how it evades the host immune response. We have shown that *Chlamydia* depends on c-Myc-driven metabolic reprogramming, while the host counters this through IFN-γ-mediated metabolic restriction targeting c-Myc. In addition, *Chlamydia* secretes effector proteins such as the deubiquitinase Cdu1, which shields its intracellular replication niche from ubiquitination. It also impairs immune clearance by secreting the protease CPAF, which inactivates polymorphonuclear leukocytes through cleavage of their surface activation receptors, allowing the pathogen to persist within host cells.

Moving forward, we aim to further explore bacterial pathogenicity mechanisms, particularly how obligate intracellular bacteria adapt metabolically to the host environment. We are also investigating the broader impact of infections on cancer initiation, progression, and immune modulation.



HeLa229 cells infected with *Chlamydia trachomatis* (anti-cHSP60 and Alexa488, magenta) after 4× expansion microscopy. Scale bar: 10 µm.

Prof. Dr. Thomas Rudel

1994

PhD, MPI for Infection Biology

Postdoctoral research at Scripps Research Institute San Diego

Group leader and Associate Professor at MPI for Infection Biology Berlin

since 2008

Professor and Chair of Microbiology at JMU Würzburg

Selected Publications

N Vollmuth, L Schlicker, Y Guo *et al.* (2022). c-Myc plays a key role in IFN-γ-induced persistence of *Chlamydia trachomatis*. **Elife** 11:e76721

K Rajeeve, N Vollmuth, S Janaki-Raman *et al.* (2020). Reprogramming of host glutamine metabolism during *Chlamydia trachomatis* infection and its key role in peptidoglycan synthesis. **Nat Microbiol** 5(11):1390-1402

K Rajeeve, S Das, BK Prusty, T Rudel (2018). *Chlamydia trachomatis* paralyses neutrophils to evade the host innate immune response. **Nat Microbiol** 3(7):824-835

✉ thomas.rudel@uni-wuerzburg.de ☎ +49 931 31 84401

🏛 Chair of Microbiology | Theodor Boveri Institute | Faculty of Biology

Super-Resolution Microscopy Single-Molecule Detection

Prof. Dr. Markus Sauer

1995
PhD, University of Heidelberg

Postdoctoral research at University of Heidelberg

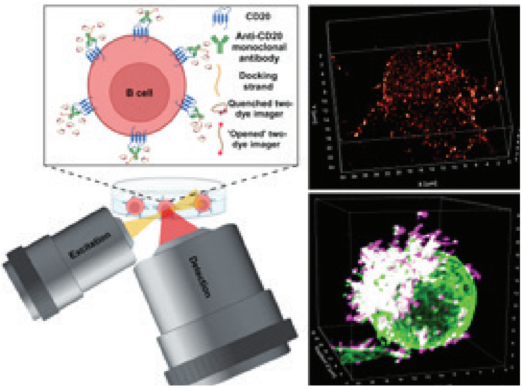
Group Leader at University of Heidelberg

Professor at University of Bielefeld

since 2009
Professor and Chair of Biophysics at JMU Würzburg

The work of my group focusses on the development of new refined fluorescence imaging methods with a particular focus on single-molecule sensitive super-resolution microscopy. The ultimate goal of the work is to understand the functional three-dimensional organization of cells and their building blocks with molecular resolution.

We developed the basis for reliable photoswitching of fluorophores in thiol-buffers, which laid the foundation for the development of single-molecule localization microscopy by direct stochastic optical reconstruction microscopy (dSTORM). We collaborate with several labs around the world to bring new technologies and analysis tools to the study of complex tissues, in health and disease. For example, we develop tools to decode the interplay of therapeutic antibodies with tumor cells to induce killing by the complement system and immune cells.



Decoding the molecular interaction of therapeutic antibodies with tumor cells by 3D-Lattice Light-Sheet TDI-DNA-PAINT and live cell imaging

We currently focus our research on improving the spatial resolution of super-resolution microscopy methods to enable true molecular resolution fluorescence imaging in cells. This work includes the investigation of fluorophore interactions in the sub-10 nm range as well as methods to bypass these limitations by using TDI-DNA-PAINT and Photoswitching Fingerprint Analysis. Finally, we are currently developing methods that combine Expansion Microscopy and super-resolution microscopy to achieve a structural resolution of 1-5 nm in cells and tissue.

Selected Publications

A Ghosh, M Meub, DA Helmerich *et al.* (2025). Decoding the molecular interplay of CD20 and therapeutic antibodies with fast volumetric nanoscopy. **Science** 387(6730):eadq4510

DA Helmerich, M Budiarta, D Taban *et al.* (2024). PCNA as Protein-Based Nanoruler for Sub-10 nm Fluorescence Imaging. **Adv Mater** 36(7):e2310104

DA Helmerich, G Beliu, D Taban *et al.* (2022). Photoswitching fingerprint analysis bypasses the 10-nm resolution barrier. **Nat Methods** 19(8):986-994

✉ markus.sauer@uni-wuerzburg.de ☎ +49 931 31 88687 🦋 @sauer-lab.bsky.social
🏛 Chair of Biotechnology and Biophysics | Theodor Boveri Institute | Faculty of Biology

Multimodal Correlative Imaging

Prof. Dr. Christian Stigloher

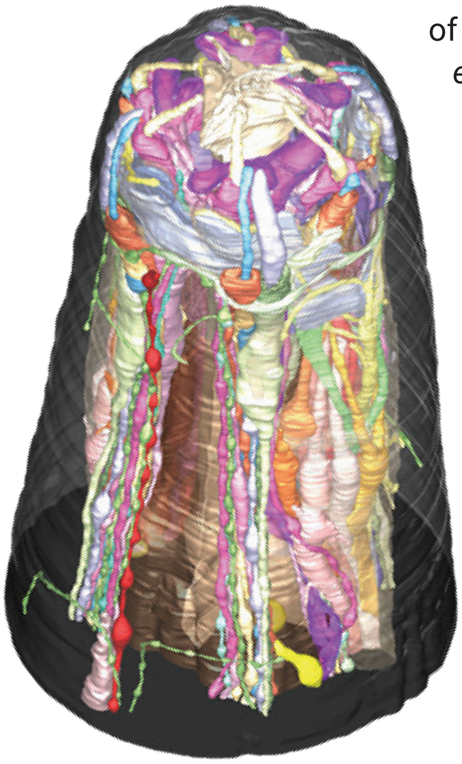
2008
PhD, TU München

Postdoctoral research at ENS Paris

Junior Professor of Microscopy at JMU Würzburg

since 2017
Professor of Microscopy at JMU Würzburg

Our group develops and applies a broad scale of imaging techniques. We combine light and electron microscopy to gain the advantages of both modalities: identification of multiple molecular identities in their full ultrastructural context. We apply correlative light and electron microscopy (CLEM) approaches to a broad range of biological questions for services and collaborations of the imaging core facility. To broaden the versatility of the CLEM techniques, we established precise identification of molecular identities with antibodies, RNA-probes and lipids or small molecules labelled by click-chemistry together with our collaboration partners. To bring these approaches to a new level we develop novel techniques in the light of biological questions. Driving force is the establishment of technical advances in *C. elegans* and zebrafis as versatile model systems to better understand neuronal signalling - from novel nanoscale insights into chemical and electrical synapses as well as non-synaptic release sites for volume transmission to a larger view onto neural network architecture and resulting behaviour.



3D-reconstructions of the sensory dendrites in the head tip of a *C. elegans* dauer larva based on FIB-SEM data published in Britz et al. 2021.

Selected Publications

S Britz, SM Markert, Witvliet D *et al.* (2021). Structural Analysis of the *Caenorhabditis elegans* Dauer Larval Anterior Sensilla by Focused Ion Beam-Scanning Electron Microscopy. **Front Neuroanat** 15:732520

KV Kaltdorf, K Schulze, F Helmprobst *et al.* (2017). FIJI Macro 3D ART VeSElecT: 3D Automated Reconstruction Tool for Vesicle Structures of Electron Tomograms. **PLoS Comput Biol** 13(1):e1005317

C Stigloher, H Zhan, M Zhen *et al.* (2011). The presynaptic dense projection of the *Caenorhabditis elegans* cholinergic neuromuscular junction ... **J Neurosci** 31(12):4388-4396

✉ christian.stigloher@uni-wuerzburg.de ☎ +49 931 31 89850
Imaging Core Facility | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Alexander Westermann

2015
PhD, JMU Würzburg

Postdoctoral research at UC Davis and Imperial College London

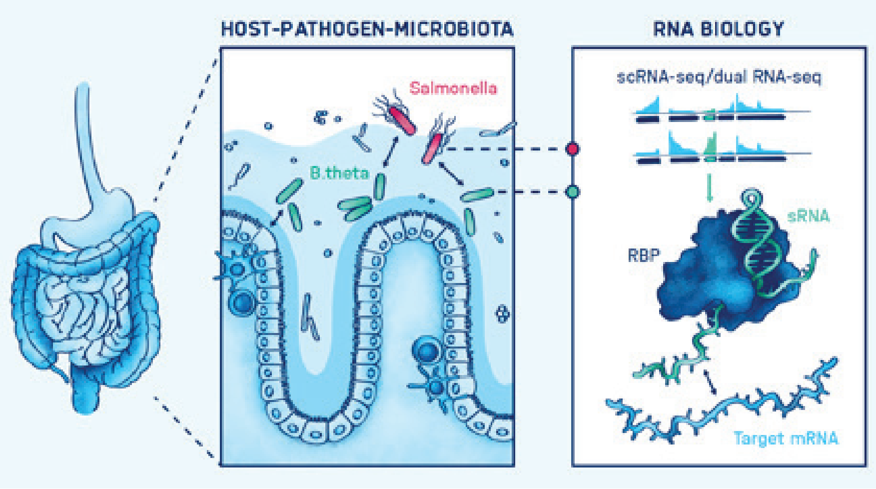
Group Leader at HIRI Würzburg

since 2023
Professor of Microbiology at JMU Würzburg

RNA Biology of Gut Bacteria Host-Microbe Interaction

Our intestinal tract offers an attractive environment for both beneficial and pathogenic bacteria. The beneficial bacteria of our microbiota feast on undigested foods and provide numerous health benefits. Enteric pathogens see this environment as an entry point for infection. Both groups influence each other, creating a tripartite interaction with us, the host.

Understanding the regulatory processes that decide on the outcome of these encounters represents an emerging research area to combat infectious diseases. While the field has focused on protein-mediated processes, our group investigates the role of RNA-centric mechanisms in controlling microbial interactions in the gut. Our current work focuses on obligate anaerobic human gut commensals of the Bacteroidota phylum as well as the model enteropathogen Salmonella Typhimurium. We leverage sophisticated in vitro models of the human intestinal tract and advanced RNA sequencing technologies, such as Triple RNA-seq and single-bacterium RNA-seq.



Research foci of the Westermann lab

Our group's long-term goal is to identify and functionally characterize noncoding RNA molecules and RNA-binding proteins in pathogens, the host and its microbiota to advance the development of targeted RNA-based diagnostics and therapeutics.

Selected Publications

A-S Rüttiger, D Ryan, L Spiga *et al*.(2025). The global RNA-binding protein RbpB is a regulator of polysaccharide utilization in *Bacteroides thetaiotaomicron*. **Nature Comm** 16(1):208

D Ryan, E Bornet, G Prezza *et al.* (2024). An expanded transcriptome atlas for *Bacteroides thetaiotaomicron* reveals a small RNA that modulates tetracycline sensitivity. **Nature Microbiol** 9(4):1130-1144

G Prezza, C Liao, S Reichardt *et al.* (2024). CRISPR-based screening of small RNA modulators of bile susceptibility in *Bacteroides thetaiotaomicron*. **PNAS** 121(6): e2311323121

✉ alexander.westermann@uni-wuerzburg.de ☎ +49 931 31 83781 🦋 @westermannlab.bsky.social
🏛 Chair of Microbiology | Theodor Boveri Institute | Faculty of Biology

Bioinformatics & Theoretical Biology

Prof. Dr. Thomas Dandekar

1986
MD, LMU Munich

Postdoctoral research at Institute Pasteur

Group leader at University of Freiburg

Visiting Fellow at EMBL Heidelberg (ongoing)

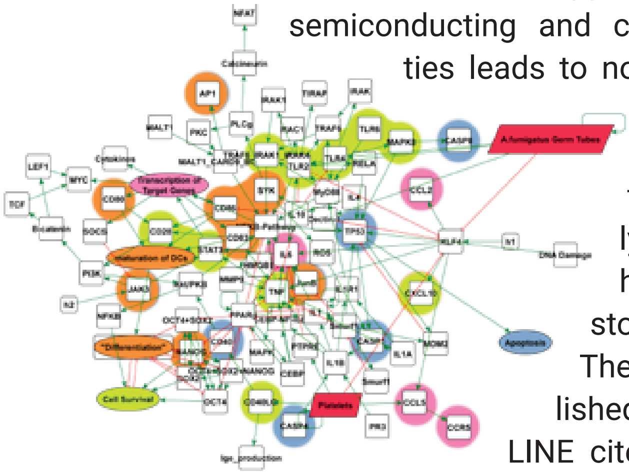
since 2001
Professor and Chair of Bioinformatics at JMU Würzburg

Bioinformatics of Biomolecules And Networks

We investigate regulatory and metabolic networks in human cells, animals, plants, bacteria and viruses.

Individual RNA and protein molecules are analysed for structure and function. Next, in regulatory networks the Boolean logical connectivity is modelled and on this the dynamic signalling simulated and iteratively refined using experimental data. Metabolic pathways are calculated for metabolic networks and their flux strength under different conditions using expression data.

Medical applications include modelling networks for platelets and cardiovascular disease, cancer, aging and infectious disease. Biology and Biotechnology investigates bacterial and plant growth on different substrates and conditions. Climate plants are strongly carbon harvesting plants, for this synthetic pathways and natural variants ("Protzen" in beech trees) are investigated. DNA storage by light-gated enzymes and using nanocellulose as support and studying its semiconducting and compound properties leads to novel nanocellulose chip devices as environmental-friendly, highly resilient and high-density data storage technology. The chair has published over 300 MEDLINE cited papers, mainly on description of biomedical networks under different conditions with targeted validation experiments, usually in collaborations. Three topical papers below show some progress in some areas, but missing others such as our research in neurobiology, infection biology or cardiovascular disease (Figure).



Network biology in action: Platelets boost the immune network in dendritic cells against fungal spores (Kaltdorf-M *et al.* 2023)

Selected Publications

R Salihoglu, J Balkenhol, G Dandekar *et al.* (2024). Cat-E: A comprehensive web tool for exploring cancer targeting strategies. **Comput Struct Biotechnol J** 23:1376-1386

A Akash, E Bencurova, T Dandekar (2024). How to make DNA data storage more applicable. **Trends Biotechnol** 42(1):17-30

Ö Osmanoglu, M Khaled AlSeiari, HA AlKhoori *et al.* (2021). Topological Analysis of the Carbon-Concentrating CETCH Cycle ... CO_2-Sequestration by Plants. **Front Bioen. Biotech** 9:708417

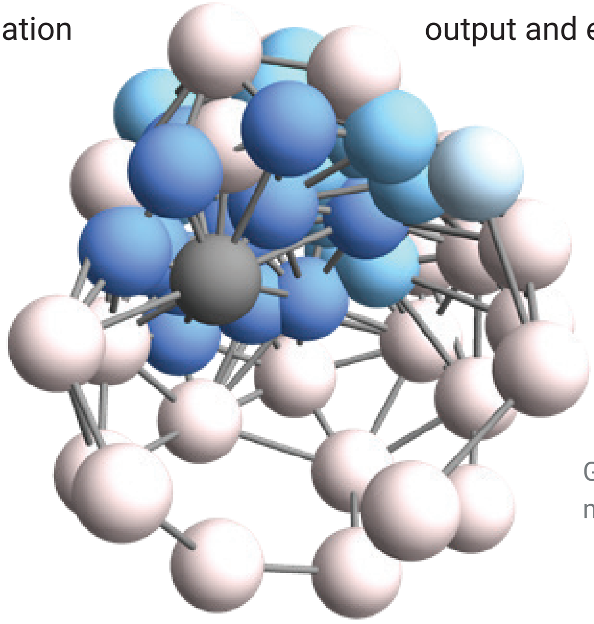
✉ thomas.dandekar@uni-wuerzburg.de ☎ +49 931 31 84551
Chair of Bioinformatics | Theodor Boveri Institute | Faculty of Biology

Data-Driven Spatial Modelling of Multicellular Systems

Are there general mechanisms that drive biological processes across scales and species? This question has been puzzling me since my PhD. The focus of my group is on the link between the morphology of multicellular systems and their functionality. To investigate this connection, we use data-driven, spatially explicit, mechanistic modelling. Our list of projects spans the subcellular, multicellular and multitissue scale. All projects are conducted in close collaboration with experimental experts to ensure that the modelling is relevant to the biology.

One major project is on cell differentiation in mouse embryos. We have been the first to consider detailed quantitative information on the spatial distribution of the cell fates. By doing so, we have identified that only incorporating intercellular communication beyond the nearest neighbours generates the correct cell fate ratio and spatial distribution.

In our future reseach, we are planning to combine our mechanistic modelling approaches with artificial intelligence to obtain even better links between simulation output and experimental data.



Graphs are a fantastic tool to represent multicellular systems such as this mouse embryo.

Prof. Dr. Sabine Fischer

2009
PhD, University of Nottingham

Postdoctoral research at Universities of Cambrigde and Frankfurt

Professor for Supramolecular and Cellular Simulations at JMU Würzburg

since 2025
Professor and Chair of Computational and Theoretical Biology at JMU Würzburg

Selected Publications

A Kuhn, T Krüger, M Schüttler *et al.* (2024). Quantification of *Trypanosoma brucei* social motility indicates different colony growth phases. **J R Soc Interface** 21(221):20240469

K Schmid, AL Olivares, O Camara *et al.* (2024). Inference of alveolar capillary network connectivity from blood flow dynamics. **Am J Physiol Lung Cell Mol Physiol**. 327(6):L852-L866

R Dirk, JL Fischer, S Schardt *et al.* (2023). Recognition and reconstruction of cell differentiation patterns with deep learning. **PLoS Comput Biol** 19(10):e1011582

✉ sabine.fischer@uni-wuerzburg.de ☎ +49 931 31 83961
🏛 Chair of Computational and Theoretical Biology | Theodor Boveri Institute | Faculty of Biology

Evolutionary Dynamics, Learning Eco-Evolutionary Processes

Prof. Dr. Chaitanya Gokhale

2011
PhD, CAU Kiel

Postdoctoral research at Massey University

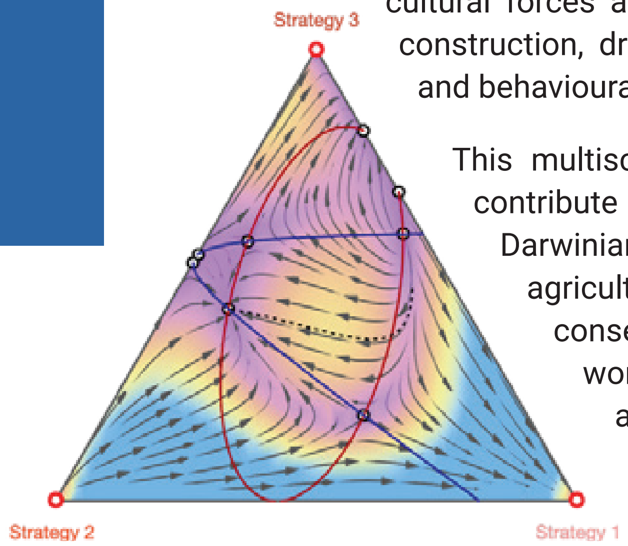
Group Leader at MPI for Evolutionary Biology

since 2023
Professor of Theoretical Evolutionary Biology at JMU Würzburg

Dynamics of living systems unfold across multiple physical and temporal scales — from subcellular processes to societies, and from microseconds to millennia. We study the interactions that generate emergent complexity at and across these levels. Our group focuses on processes within and between hierarchical levels of biological organisation, using and expanding the theoretical biology toolbox. Guided by the principle that “insight precedes application” (Max Planck), we link foundational understanding to translational research.

Our work spans from mathematical models of endosymbiosis and microbial community dynamics, including antibiotic and toxin interactions, to behavioural ecology, where we explore how animals make decisions under risk in response to genetic, abiotic, and social cues. We connect macroecological patterns to macroevolutionary processes using mathematical and phylogenetic tools. At the sociocultural level, we examine how human sociality is shaped by evolutionary and cultural forces and reinforced through niche construction, drawing on social psychology and behavioural economics.

This multiscale approach allows us to contribute to applied fields such as Darwinian medicine, sustainable agriculture, and biodiversity conservation. By grounding our work in theoretical principles and systems thinking, we are better equipped to tackle complex challenges of the future, whether societal, medical, or ecological.



Translating ecology to evolution is conceptually hard but mathematically feasible; the figure depicts evolutionary view of a complex ecological model

Selected Publications

D Lauenroth, CS Gokhale (2023). Theoretical assessment of persistence and adaptation in weeds with complex life cycles. **Nat Plants** 9(8):1267-1279

VR Venkateswaran, CS Gokhale (2019). Evolutionary dynamics of complex multiple games. **Proc Biol Sci** 286(1905):20190900

CS Gokhale, A Traulsen (2010). Evolutionary games in the multiverse. **Proc Natl Acad Sci U S A** 107(12):5500-5504

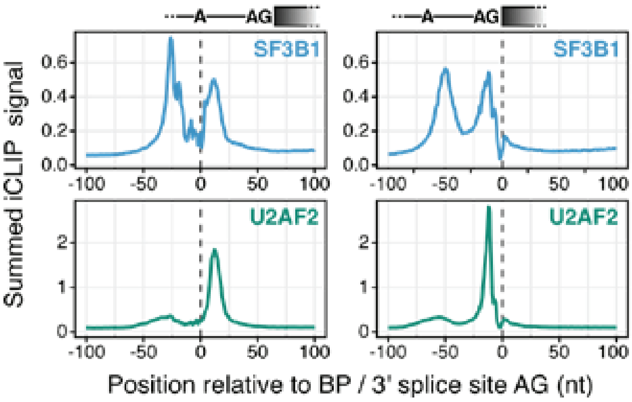
✉ chaitanya.gokhale@uni-wuerzburg.de ☎ +49 931 31 84126 🦋 @gokhalecs.bsky.social
🏛 Chair of Computational and Theoretical Biology | Theodor Boveri Institute | Faculty of Biology

Bioinformatics of RNA Regulation And Gene Expression

The Zarnack group studies the molecular mechanisms that control RNA regulation and genome stability in healthy human cell function and disease. We integrate computational and statistical methods with high-throughput sequencing data and functional genomics to investigate how RNA- and DNA-binding proteins regulate gene expression at multiple levels.

A major focus of the group is understanding post-transcriptional gene regulation. By studying how RNA-binding proteins and sequence variants influence alternative splicing, we seek to elucidate how splicing defects contribute to cancer. Another key area is the regulation of mRNA in the cytoplasm, including its localization, translation, and decay. We recently discovered how m6A RNA modifications in coding regions lead to ribosome pausing and mRNA destabilization—an important mechanism for tuning gene expression. In parallel, we explore how structural features of DNA lead to genomic instability and develop machine learning models to characterize vulnerable regions in the genome.

In our future work, we aim to dissect the dynamic interactions between RNA, DNA, and regulatory proteins in both health and disease, to uncover new regulatory principles and develop predictive models to inform future therapeutic strategies. We place strong emphasis on creating robust, accessible bioinformatics tools for the scientific community, including pipelines for analyzing RNA-protein interactions with nucleotide resolution.



Binding of core splicing factors SF3B1 and U2AF2 at human 3’ splice sites; BP, branchpoint (Pacholewska *et al*., 2024)

Prof. Dr. Kathi Zarnack

2007
PhD, University of Marburg

Postdoctoral research at EMBL EBI Hinxton and CRUK

Junior Group Leader at the University of Frankfurt

since 2025
Professor and Chair of Bioinformatics II at JMU Würzburg

Selected Publications

Y Zhou*, M Ćorović*, P Hoch-Kraft* *et al.* (2024). m6A sites in the coding region trigger translation-dependent mRNA decay. **Mol Cell** 84(23):4576-4593 *shared first authors

A Pacholewska*, M Lienhard*, M Brüggemann* *et al.* (2024). Long-read transcriptome sequencing of CLL and MDS patients uncovers molecular effects of SF3B1 mutations. **Genome Res** 34(11):1832-1848 *shared first authors

L Molitor*, M Klostermann*, S Bacher *et al.* (2023). Depletion of the RNA-binding protein PURA triggers changes in posttranscriptional gene regulation... **Nucleic Acids Res** 51(3):1297-1316 *shared first authors

✉ kathi.zarnack@uni-wuerzburg.de ☎ +49 931 31 81878 🦋 @zarnack-group.bsky.social
🏛 Chair of Bioinformatics II | Theodor Boveri Institute | Faculty of Biology

Ecology & Conservation

Global Change Ecology and Macroecology

Prof. Dr. Christian Hof

2010
PhD, University of Copenhagen

Postdoctoral research at University of Copenhagen and Senckenberg BiK-F Frankfurt

Group Leader at TU Munich

since 2023
Professor and Chair of Global Change Ecology at JMU Würzburg

Humans are changing our planet in many different ways, with profound impacts on biological diversity. In our research we aim to understand how biodiversity varies in space and time across scales, and how interacting anthropogenic drivers, namely climate and land-use change, influence species, ecological communities and biodiversity patterns.

Our main research approaches cover the fields of macroecological modelling, functional macroecology via extensive data analyses, as well as experimental and field-based approaches studying species' responses to environmental change. Recent highlights of our work include assessments of the past trends of dragonflies, butterflies and grasshoppers at the regional scale of Bavaria using occupancy modelling, where we found a clear signal of climate change; analyses of how the colour of dragonfly communities varies seasonally, which revealed that due to energetic constraints darker dragonflies tend to fly early and late in the season; and the experimental investigation of thermal tolerances of thousands of insect individuals along elevational gradients in Bavaria and Pakistan, illustrating the importance of physiological data for understanding climate change impacts.

In our current research we emphasize even more the integration of data and methods across disciplines and scales in order to provide better answers to some of the current key research questions and to help developing solutions for the grand planetary challenges of our times.

The Black Darter (*Sympetrum danae*) is a dragonfly that has decreased a lot in its occupancy across Bavaria, probably also due to climate change.

Selected Publications

R Novella-Fernandez, R Brandl, S Pinkert *et al.* (2023). Seasonal variation in dragonfly assemblage colouration suggests a link between thermal melanism and phenology. **Nat Commun** 14(1):8427

EK Engelhardt, MF Biber, M Dolek *et al.* (2022). Consistent signals of a warming climate in occupancy changes of three insect taxa over 40 years in central Europe. **Glob Chang Biol** 28(13):3998-4012

C Hof (2021). Towards more integration of physiology, dispersal and land-use change to understand the responses of species to climate change. **J Exp Biol** 224(Suppl 1):jeb238352

✉ christian.hof@uni-wuerzburg.de ☎ +49 931 31 87965 🦋 @christianhof.bsky.social
🏛 Chair of Global Change Ecology | Theodor Boveri Institute | Faculty of Biology

Multitrophic Interactions Under Global Change

Prof. Dr. Malte Jochum

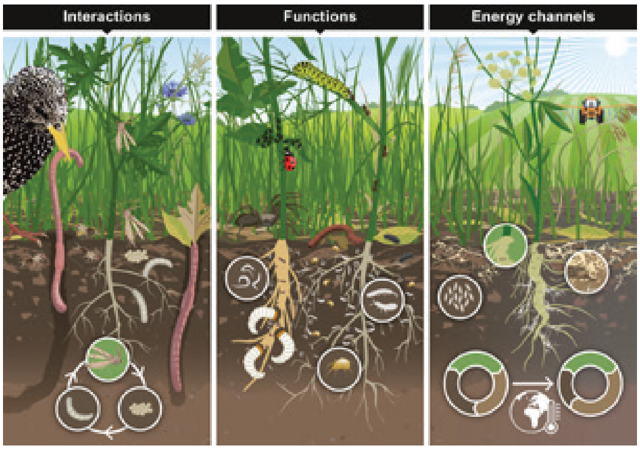
2016
PhD, University of Göttingen

Postdoctoral research at University of Göttingen, University of Bern, and iDiv & Leipzig University

since 2023
Junior Professor of Above-belowground Interaction Ecology at JMU Würzburg

Global change alters Earth's ecosystems with consequences for ecological communities and the ecosystem processes they maintain. We study how combined global-change drivers, such as climate change, land use intensification, or invasions, alter ecological interaction networks and the flux of matter and energy through ecosystems. Our work typically focuses on terrestrial above- and belowground ecosystems, but occasionally includes freshwater and marine realms.

Our current work aims at tackling three questions: How do multitrophic communities and ecosystem processes respond to multiple, simultaneously acting stressors? How does global change alter trophic interactions and food webs? Do above- and belowground communities respond similarly? To answer these questions, we are using a range of approaches involving field experiments and large-scale observational studies. For example, we are using the Global Change Experimental Facility (UFZ, Bad Lauchstädt) to test how climate change and land use intensification jointly alter above- and belowground biodiversity and ecosystem processes. Similarly, we are using the Biodiversity Exploratories to assess how land-use intensity alters the integrity of above- and belowground invertebrate communities and ecosystem multifunctionality across 150 German grasslands.



Global change alters interactions, ecosystem functions, and energy channels across the above-belowground interface (Jochum & Eisenhauer, 2021).

In the near future, we are planning to establish a Würzburg-based global change field experiment and study biodiversity in solar parks and across elevational gradients.

Selected Publications

M Jochum, M Fischer, F Isbell *et al.* (2020). The results of biodiversity-ecosystem functioning experiments are realistic. **Nat Ecol Evol** 4(11):1485-1494

N Eisenhauer, H Schielzeth, AD Barnes *et al.* (2019). A multitrophic perspective on biodiversity-ecosystem functioning research. **Adv Ecol Res** 61:1-54

AD Barnes*, M Jochum*, S Mumme *et al.* (2014). Consequences of tropical land use for multitrophic biodiversity and ecosystem functioning. **Nat Commun** 5:5351 *shared first authors

✉ malte.jochum@uni-wuerzburg.de ☎ +49 931 31 80482 🦋 @maltejochum.bsky.social
🏛 Chair of Global Change Ecology | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Jörg Müller

2005
PhD, TU Munich

Postdoctoral research at the Bavarian Forest Institute and National Park and TU Munich

Associated Professor at TU Munich

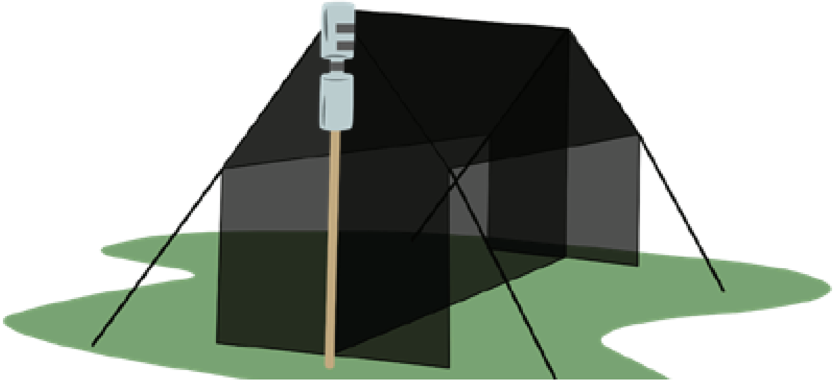
since 2024
Professor and Chair of Conservation Biology and Forest Ecology at JMU Würzburg

Evidence-Based Conservation Ecological Principals

Understanding ecological principles is the basis for a more sustainable approach to our environment. Our research combines the field of animal ecology and conservation biology, further enriched by the experience and expertise we gain through our close collaboration with the Bavarian National Park. Through joined projects and shared insights, we strive towards new and research-based conservation concepts in Germany and abroad.

Our current research focuses on the importance of forest structures at various scales and their influence on biodiversity and ecosystem functions; the study of the recovery capacity of animal communities in tropical forests; and the mechanisms behind the phenomenon of insect decline. We work with a wide range of methods in field surveys of biodiversity, supported by AI methods and metabarcoding, but also with statistical approaches that allow us to overcome limitations of empirical data.

In the future, we will focus even more on linking experimental and theoretical approaches at various scales.



Malaise traps are the most comprehensive technique to sample above ground insect communities.

Selected Publications

J Müller, T Hothorn, Y Yuan *et al.* (2024). Weather explains the decline and rise of insect biomass over 34 years. **Nature** 628(8007):349-354

S Seibold, W Rammer, T Hothorn *et al.* (2021). The contribution of insects to global forest dead-wood decomposition. **Nature** 597(7874):77-81

L Heidrich, S Bae, S Levick S *et al.* (2020). Heterogeneity-diversity relationships differ between and within trophic levels in temperate forests. **Nat Ecol Evol** 4(9):1204-1212

✉ joerg.mueller@uni-wuerzburg.de ☎ +49 931 31 83378
Chair of Conservation Biology and Forest Ecology | Theodor Boveri Institute | Faculty of Biology

Mechanisms Controlling Honey Bee Behavior

Prof. Dr. Ricarda Scheiner

2001
PhD, TU Berlin

Postdoctoral research at TU Berlin

Heisenberg Group Leader and Professor at University of Potsdam

since 2014
Professor of Neuroethology of Arthropods at JMU Würzburg

Our research focuses on the ecology and evolution of pheromones, kairomones and defensive secretions in insects. In particular, we study the evolution of cuticular hydrocarbon (CHC) profiles and their various functions, such as providing a desiccation barrier or acting as signals for intra- and interspecific communication

We investigate the evolutionary trajectories and mechanisms that shape these profiles, using them as a model for complex traits to understand how these traits evolve under different ecological conditions. Current projects include: (1) investigating the evolution of CHC profiles in the context of chemical mimicry and parasite-host interactions; (2) examining the impact of climatic conditions and microbiomes on CHC composition; and (3) exploring the effects of phylogeny and spatial isolation on cuticular profiles. Our main study subjects are Hymenoptera, but we have also started studying mosquitoes, flies, stick insects and beetles in various climate zones around the world, with a focus on the tropics.

Future plans include conducting comparative studies of semiochemicals of insect groups with different phylogenetic, ecological and biogeographical backgrounds to reconstruct their evolutionary past and better understand the selection factors shaping different types of chemical profiles. Additionally, we collaborate with neurobiologists to investigate the perception of chemical signals and the co-evolution of sender and receiver of sex pheromones.

Honey bee foraging at a flower. These social insects have amazing learning abilities.

Selected Publications

DS Rodríguez-León, T Schmitt, MA Pinto *et al.* (2025). Expression of Elongase- and Desaturase-Encoding Genes Shapes the Cuticular Hydrocarbon Profiles of Honey Bees. **Mol Ecol** 34(8):e17716

F Schilcher, R Scheiner (2023). New insight into molecular mechanisms underlying division of labor in honeybees. **Curr Opin Insect Sci** 59:101080

A Schuhmann, R Scheiner (2023). A combination of the frequent fungicides boscalid and dimoxystrobin with the neonicotinoid acetamiprid in field-realistic concentrations... **Ecotoxicol Environ Saf** 256:114850

✉ ricarda.scheiner@uni-wuerzburg.de ☎ +49 931 31 84745
🏛 Chair of Behavioral Physiology and Sociobiology | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Thomas Schmitt

2004
PhD, JMU Würzburg

Assistant Professor at ALU Freiburg and TU Darmstadt

since 2013
Professor of Chemical Ecology at JMU Würzburg

Evolution of Semiochemicals and Cuticular Hydrocarbons

Our research focuses on the ecology and evolution of pheromones, kairomones and defensive secretions in insects. In particular, we study the evolution of cuticular hydrocarbon (CHC) profiles and their various functions, such as providing a desiccation barrier or acting as signals for intra- and interspecific communication

We investigate the evolutionary trajectories and mechanisms that shape these profiles, using them as a model for complex traits to understand how these traits evolve under different ecological conditions. Current projects include: (1) investigating the evolution of CHC profiles in the context of chemical mimicry and parasite-host interactions; (2) examining the impact of climatic conditions and microbiomes on CHC composition; and (3) exploring the effects of phylogeny and spatial isolation on cuticular profiles. Our main study subjects are Hymenoptera, but we have also started studying mosquitoes, flies, stick insects and beetles in various climate zones around the world, with a focus on the tropics.

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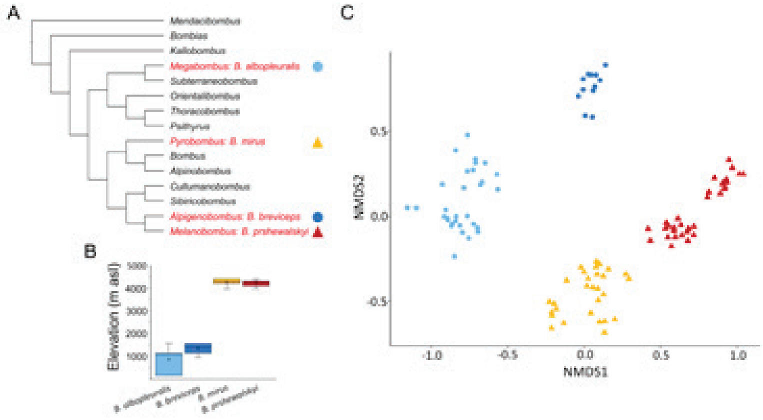


CHC profile diversity of four Himalayan bumble bee species with different elevational ranges. A) Phylogenetic position, B) Elevetional ranges, C) NMDS

Selected Publications

SP Vandenabeele, T Schmitt (2023). Olfaction is essential for nest recognition in solitary Hymenoptera. **Proc Natl Acad Sci U S A** 120(25):e2304703120

F Menzel, BB Blaimer, T Schmitt (2017). How do cuticular hydrocarbons evolve? Physiological constraints and climatic and biotic selection pressures act on a complex functional trait. **Proc Biol Sci B** 284(1850):20161727

O Niehuis, J Buellesbach, JD Gibson *et al.* (2013). Behavioural and genetic analyses of *Nasonia* shed light on the evolution of sex pheromones. **Nature** 494(7437):345-348

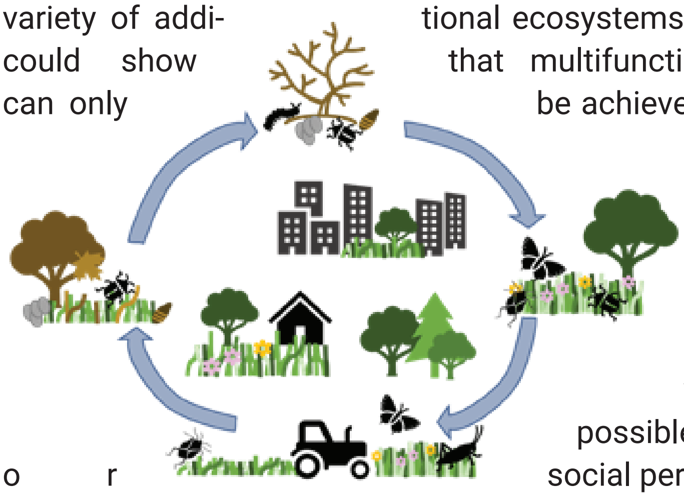
✉ thomas.schmitt@uni-wuerzburg.de ☎ +49 931 31 84188
🏛 Chair of Animal Ecology and Tropical Biology | Theodor Boveri Institute | Faculty of Biology

Biodiversity in Managed Habitats: From Mechanisms to Solutions

In temperate regions, landscapes are shaped by historical and current management. Within these anthropogenic systems, forests and grasslands provide important habitats for biodiversity. Our research focuses on effects of management on arthropod communities, in particular their (functional) diversity and their interactions in the ecosystem. In addition, we ask how biodiversity and ecosystem services are and can be integrated into decision-making processes.

Previous research in agriculturally managed grasslands showed that management intensity affects arthropod diversity and community stability through changes in resource availability, a fundamental insight into the causes of insect decline in Europe. We found that the same underlying mechanism shapes arthropod diversity in urban greenspaces, highlighting the potential for biodiversity-friendly management in cities. In forests, management and especially the promotion of fast-growing tree species has been viewed as contradictory to conservation. We investigated this potential trade-off across common forest types in Europe, including a variety of additional ecosystems services and could show that multifunctional forestry can only be achieved at the landscape level.

Integrating biodiversity-friendly management practices into established land-use systems needs multidisciplinary perspectives and close collaboration with stakeholders. Therefore, we use transdisciplinary approaches whenever possible and link our ecological expertise with economic or social perspectives.



Habitat type and management shape biodiversity as they affect the presence and survival of arthropods throughout the year.

Prof. Dr. Nadja Simons

2015
PhD, TU Munich

Postdoctoral research at TU Munich and TU Darmstadt

since 2023
Junior Professor of Applied Biodiversity Sciences at JMU Würzburg

Selected Publications

- MM Gossner, F Menzel, NK Simons (2023). Less overall, but more of the same: drivers of insect population trends lead to community homogenization. **Biol Lett** 19(3):20230007
- NK Simons, MR Felipe-Lucia, P Schall *et al.* (2021). Forest inventories capture the multifunctionality of managed forests in Germany. **Forrest Ecosyst** 8, 5
- NK Simons, WW Weisser (2017). Agricultural intensification without biodiversity loss is possible in grassland landscapes. **Nat Ecol Evol** 1(8):1136-1145

✉ nadja.simons@uni-wuerzburg.de ☎ +49 931 31 80258 in nadja-simons
🏛 Chair of Conservation Biology and Forest Ecology | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Ingolf Steffan-Dewenter

1997
PhD, University of Göttingen

Postdoctoral research at University of Göttingen

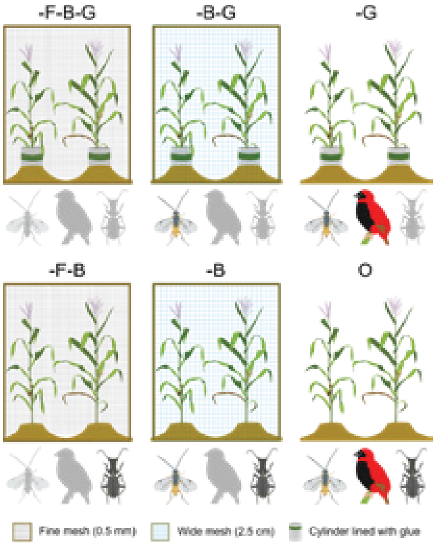
Assistant Professor at University of Göttingen

Professor at University of Bayreuth

since 2010
Professor and Chair of Animal Ecology and Tropical Biology

Animal and Landscape Ecology Ecosystem Functioning

Ingolf Steffan-Dewenter is focusing in his research on how land-use, habitat fragmentation, climate change, environmental pollution and invasive species impact biodiversity and ecosystem functioning. He aims to understand ecological processes at population, community, and ecosystem levels, with a focus on insects and their biotic interactions such as pollination, herbivory, and host-antagonist dynamics. Combining experimental, observational, and comparative approaches across temperate and tropical ecosystems, he investigates the role of species, functional, phylogenetic, and interaction diversity in ecosystem resilience. Key areas include landscape management, plant-pollinator interactions, biological pest control, and elevational gradients as model systems for climate change. Further he studies resource partitioning of honey bees in space and time making use of their unique communication behaviour. By initiating transdisciplinary collaborations and coordinating large international projects, he has contributed extensively to nature conservation in the face of global environmental change.



Field cage experiment to reveal the contributions of different natural enemy guilds to natural pest control in northern Malawi (image: Georg Küstner)

In his future research he aims to better understand the interactive effects of multiple global change drivers on ecosystems, reveal the underlying ecological, behavioural, physiological and evolutionary mechanisms, and implement long-term transformative experiments at landscape scales to restore biodiversity, maintain ecosystem services, and increase ecosystem resilience in changing climates.

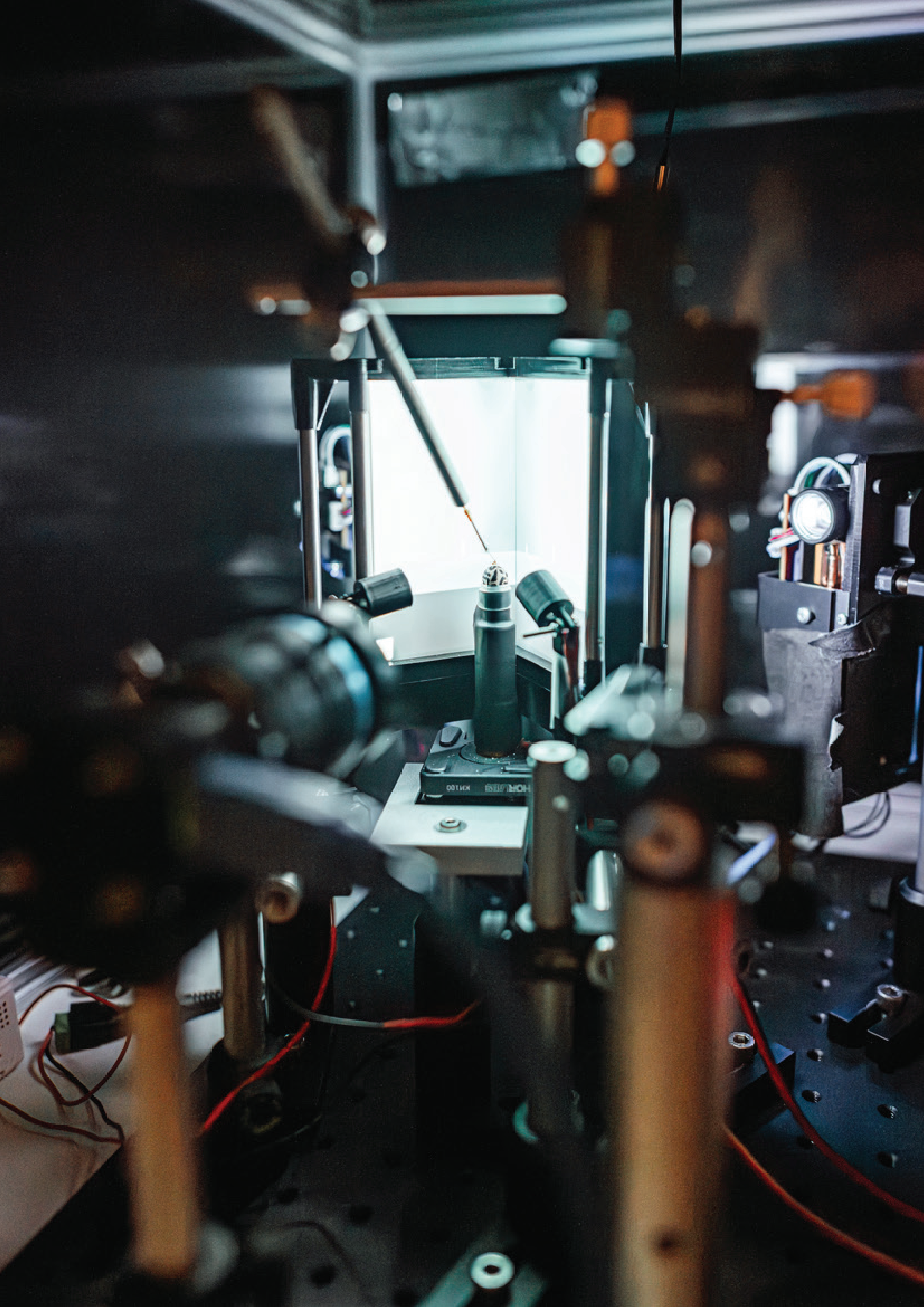
Selected Publications

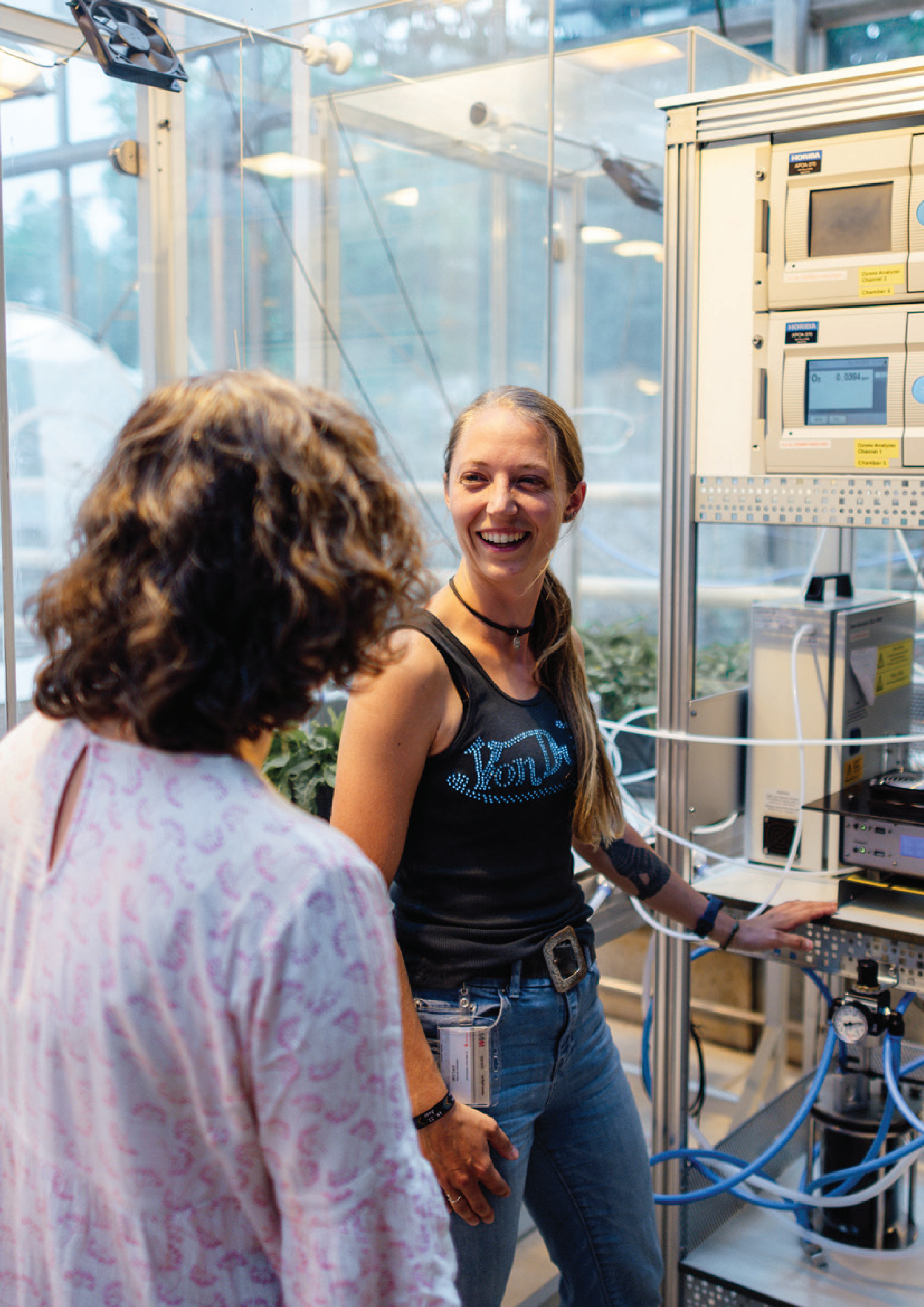
I Steffan-Dewenter, R Bezner Kerr, MK Peters (2024). Insect diversity for agroecosystem resilience in a changing climate. **One Earth** 7(4): 541-544

MK Peters, A Hemp, T Appelhans *et al.* (2019). Climate-land-use interactions shape tropical mountain biodiversity and ecosystem functions. **Nature** 568(7750):88-92

M Dainese, EA Martin, MA Aize *et al.* (2019). A global synthesis reveals biodiversity-mediated benefits for crop production. **Sci Adv.** 5(10):eaax0121

✉ ingolf.steffan@uni-wuerzburg.de ☎ +49 931 31 86947
🏛 Chair of Animal Ecology and Tropical Biology| Theodor Boveri Institute | Faculty of Biology

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Ozone Analyzer Channel 1
Chamber 1

Neurobiology & Behavioural Sciences

Dr. Jan M. Ache

2015
PhD, University of Bielefeld

Postdoctoral research at HHMI Janelia Research Campus

Junior Group Leader at JMU Würzburg

since 2020
Emmy Noether Group Leader at JMU Würzburg

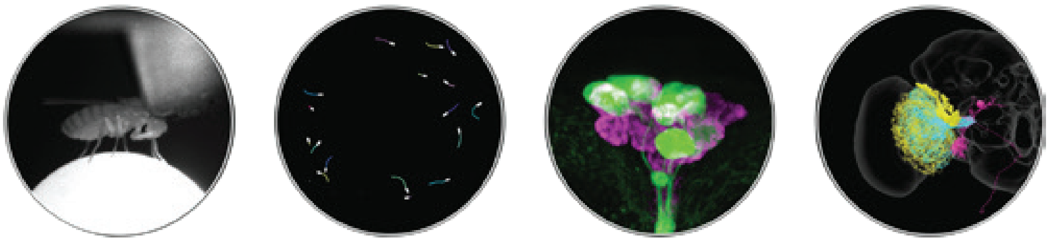
Neuronal Mechanisms for Sensorimotor Flexibility

In order to successfully navigate the complex and ever-changing world we live in, animals and humans need to be capable of initiating and controlling a plethora of flexible and adaptive behaviors. We study the neuronal mechanisms underlying behavioral flexibility in *Drosophila* and other insects. Insects are great model systems to investigate the neuronal circuits controlling behavior because they have numerically small nervous systems that consist of uniquely identifiable neurons.

In one line of research, we dissect neuronal circuits controlling different aspects of innate behaviors, such as walking, flying, and feeding, and the transitions between them. For instance, several projects in the lab focus on the neuronal circuits controlling the initiation, speed, and termination of walking. In a complementary line of research, we investigate modulatory circuits that allow anatomically constrained and synaptically defined circuits to process information in a flexible, state- and context-dependent way. Here, we currently focus on two modulatory systems that are conserved across the animal kingdom: the insulin system, and the dopamine system.

Ultimately, this work allows us to unravel how internal states shape behavior and vice versa - a fundamental, open question in neuroscience. We use a variety of cutting-edge techniques in the lab to tackle this challenging question, including in-vivo patch-clamp recordings and calcium imaging in behaving animals, optogenetics, automated behavioral analyses, and connectomics.

The images represent approaches that we use to analyze individual and group behavior, dissect neuronal circuits, and quantify neuronal activity.



Selected Publications

A Büschges, JM Ache (2025). Motor control on the move: from insights in insects to general mechanisms. **Physiol Rev** 105(3):975-1031

S Liessem, M Held, RS Bisen *et al.* (2023). Behavioral state-dependent modulation of insulin-producing cells in *Drosophila*. **Curr Biol** 33(3):449-463

M Ache, S Namiki, A Lee *et al.* (2019). State-dependent decoupling of sensory and motor circuits underlies behavioral flexibility in *Drosophila*. **Nat Neurosci** 22(7):1132-1139

✉ jan.ache@uni-wuerzburg.de ☎ +49 931 31 88577 @jan-ache.bsky.social
Chair of Neurobiology und Genetics | Theodor Boveri Institute | Faculty of Biology

Spatial Memory in Insects

Dr. Jerome Beetz

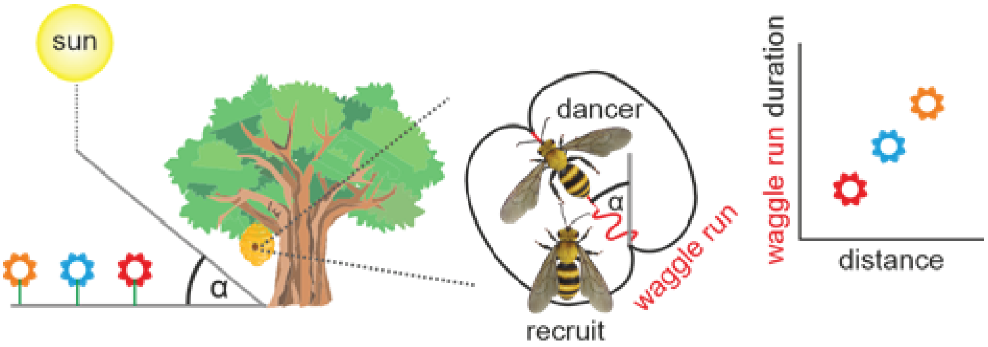
2018
PhD, University of Frankfurt

Postdoctoral research at JMU Würzburg

since 2025
Emmy Noether Group Leader at JMU Würzburg

Whether it is a honeybee piloting between the hive and flower patches or migratory monarch butterflies that keep a constant flight direction for thousands of kilometres, every navigating animal must know where it is located in space with respect to a spatial goal.

My lab focuses on bees that navigate in the same habitat on a daily basis. This site fidelity requires a sophisticated spatial memory. Aside from humans, honeybees are the only known species that communicates spatial information to conspecifics. A bee returning from a foraging trip often performs a stereotypic waggle dance on vertical combs inside the dark hive. From this dance, follower bees (recruits) extract distance and direction of the food source. Because dancers retrieve and recruits acquire spatial memory, the dance represents a unique chance to get a glimpse into the bee's spatial mind. Through a combination of behavioral experiments and brain recordings (tetrode recordings) in behaving honeybees, we study the neural mechanisms underlying spatial memory and place coding. To dissect the neural circuit of the waggle dance, we record intracellularly from neurons that are anatomically traced through dye injections. This enables us to study how waggle-dance related spatial information gets translated into vision-based spatial information that flying bees experience outside the hive.



Waggle dance: Food direction relative to the sun is encoded by the waggle angle relative to gravity. Waggle run duration increases with food distance

Selected Publications

MJ Beetz, C Kraus, B el Jundi (2023). Neural representation of goal direction in the monarch butterfly brain. **Nat Commun**. 14(1):5859

MM Konnerth, JJ Foster, B el Jundi *et al.* (2023). Monarch butterflies memorize the spatial location of a food source. **Proc Biol Sci**. 290(2013):20231574

MJ Beetz, C Kraus, M Franzke *et al.* (2022). Flight-induced compass representation in the monarch butterfly heading network. **Curr Biol** 32(2):338-349

✉ jerome.beetz@uni-wuerzburg.de ☎ +49 931 31 84528 @beetzjerome.bsky.social
Chair of Behavioral Physiology and Sociobiology | Theodor Boveri Institute | Faculty of Biology

Social Wound Care in Animals

Dr. Erik T. Frank

2018
PhD at JMU Würzburg

Postdoctoral research at the
University of Lausanne (UNIL)

since 2022
Emmy Noether Group Leader at
JMU Würzburg

Injuries are common in animals and often pose a serious risk of lethal infections. In social insects, specialized wound care behaviours have evolved to mitigate these dangers. The emerging field of social wound care, a subdiscipline of social immunity, investigates how injured individuals are treated within insect colonies. Such injuries may involve severed limbs or predators attached to the body.

Our research aims to uncover the evolutionary pathways that gave rise to rescue and wound care behaviours in social insects. Current projects explore why some ant species amputate infected limbs while others apply antimicrobial secretions; how mutualistic ants tend to wounds on their host plants; how wound care dynamics shift in ant species with social hierarchies, such as *Dinoponera grandis*; whether bumblebees and honeybees care for injured nestmates; and why chimpanzees apply insects to their own wounds.

We combine behavioural observations in the field (Latin America and Africa) with laboratory experiments on ants, bumblebees, and honeybees. These studies are complemented by chemical analyses of pheromones and antimicrobial compounds involved in wound care, as well as mathematical modelling to identify the selective pressures and ecological factors driving the evolution of these behaviours. We also seek to identify novel wound treatment strategies, antimicrobial compounds, and wound healing mechanisms inspired by these systems.

A *Camponotus maculatus* ant cleaning the wound of an injured conspecific (picture by Bart Zijlstra)

Selected Publications

ET Frank, D Buffat, J Liberti *et al.* (2024). Wound-dependent leg amputations to combat infections in an ant society. **Curr Biol** 34(14):3273-3278

ET Frank, L Kesner, J Liberti *et al.* (2023). Targeted treatment of injured nestmates with antimicrobial compounds in an ant society. **Nat Commun** 14:8446.

ET Frank, M Wehrhahn, KE Linsenmair (2018). Wound treatment and selective help in a termite-hunting ant. **Proc R Soc B** 285(1872): 20172457

✉ erik.frank@uni-wuerzburg.de ☎ +49 931 31 82183 🦋 @etf1989.bsky.social
🏛 Chair of Animal Ecology and Tropical Biology | Theodor Boveri Institute | Faculty of Biology

Chronobiology Neurobiology

Chronobiology is the study of biological rhythms, i.e., recurring events that occur in a regular sequence and continue even without external influences. Such biological rhythms are controlled by the body's own (endogenous) clocks, which run on different time scales: daily (circadian), monthly (circalunar), and annually (circa-annual). These clocks adapt behavior, physiology, and metabolism to the optimal time of day, month, and year and are important for overall fitness and survival.

My goal is to understand how these clocks work in animals at the neurobiological level. I want to understand how they perceive daily changes in the environment, how they adapt to seasonal changes, and how they control behavior, physiology, and metabolism. The focus of my work is on daily (circadian) clocks, and my group uses the fruit fly *Drosophila melanogaster* as the main model organism. However, we also studied the circadian clocks of other arthropods such as Antarctic krill, aphids, flies living in the far north, and bees, as these animals show fascinating seasonal or social adaptations.

Prof. Charlotte Förster

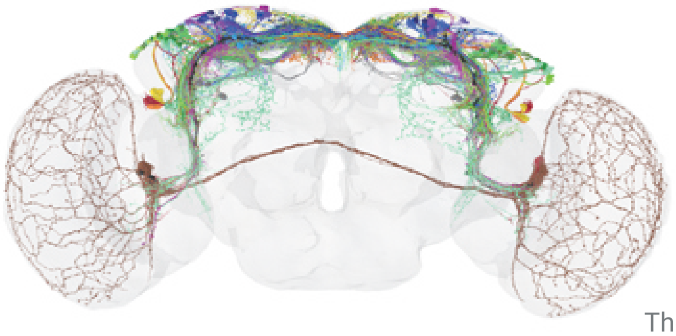
1985
PhD, EKU Tübingen

Postdoctoral research at MPI for Biology Tübingen

Professor at University of Regensburg

Professor and Chair of Neurobiology and Genetics at JMU Würzburg

since 2025
Senior Professor of Chronobiology at JMU Würzburg



The neuronal clock network in the fly brain

My current work focuses on annual (seasonal) rhythms in flies and lunar rhythms in humans. Lunar rhythms in reproduction occur in almost all marine animals, and there is growing evidence that terrestrial animals also respond to the periodic changes caused by the moon on Earth.

Selected Publications

N Reinhard, A Fukuda, G Manoli *et al.* (2024). Synaptic connectome of the *Drosophila* circadian clock. **Nat Commun** 15(1):10392

C Helfrich-Förster, S Monecke, I Spiousas et al. (2021). Women temporarily synchronize their menstrual cycles with the luminance and gravimetric cycles of the Moon. **Sci Adv** 7(5):eabe1358

P Menegazzi, E Dalla Benetta, M Beauchamp *et al.* (2017). Adaptation of Circadian Neuronal Network to Photoperiod in High-Latitude European *Drosophilids*. **Curr Biol** 27(6):833-839

✉ charlotte.foerster@uni-wuerzburg.de ☎ +49 931 31 88823
Chair of Neurobiology und Genetics | Theodor Boveri Institute | Faculty of Biology

Dr. Hannah Haberkern

2018
PhD, University of Cambridge

Postdoctoral research at HHMI
Janelia Research Campus

since 2023
Emmy Noether Group Leader at
JMU Würzburg

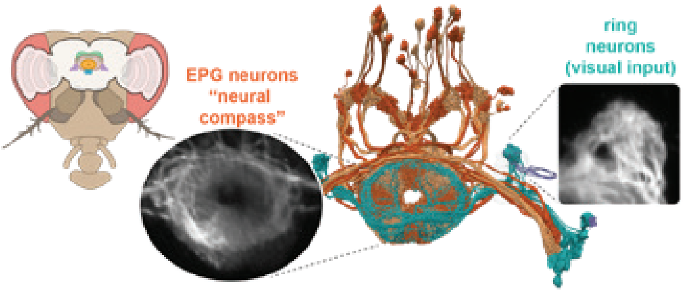
Behavioral and Neural Mechanisms For Robust Navigation

Navigating through diverse and dynamic environments is a fundamental and complex problem. To achieve robust navigation, our brains need to generalize knowledge across ever changing environmental conditions. This can be achieved by generating abstract representations that extract relevant information from the environment. One such abstract representation that is found from insects to humans, is a head direction estimate or neural compass. We investigate how the brain processes the sensory environment to update this compass, and we aim to identify the circuit mechanisms that ensure the compass stability in dynamic environments. We also study how the environment affects the choice between different navigational strategies and how circuits can be adapted to environmental conditions through structural plasticity.

We study two species that each bring unique experimental advantages. In fruit flies we can use genetic tools and imaging techniques to monitor and perturb defined populations of neurons. Desert ants show robust navigation behavior, which has been characterized in a defined ethological context. We compare these models across multiple axes: neuroanatomy, behavior and physiology.

To understand how neural activity drives behavior, we combine a range of cutting-edge techniques:

- immersive virtual reality to simulate natural environments in the lab
- in-vivo 2-photon calcium imaging
- volume electron microscopy for connectomics



Neurons of the visual input pathway to the insect head direction system. The two insets show stills from calcium imaging.

Selected Publications

H Haberkern, SS Chitnis, PM Hubbard *et al.* (2022). Maintaining a stable head direction representation in naturalistic visual environments. **bioRxiv** 2022.05.17.492284

BK Hulse, H Haberkern, R Franconville *et al.* (2021). A connectome of the *Drosophila* central complex reveals network motifs suitable for flexible navigation and context-dependent action selection. **Elife** 10:e66039

H Haberkern, MA Basnak, B Ahanonu *et al.* (2019). Visually Guided Behavior and Optogenetically Induced Learning in Head-Fixed Flies Exploring a Virtual Landscape. **Curr Biol** 29(10):1647-1659

✉ hannah.haberkern@uni-wuerzburg.de ☎ +49 931 31 88604 🦋 @hannah-haberkern.bsky.social
🏛 Chair of Behavioral Physiology & Sociobiology | Theodor Boveri Institute | Faculty of Biology

Neuroethology of Spatial Orientation

Insects show a broad repertoire of spatial orientation behaviors. This includes simple behaviors, like straight-line orientation, as well as long-range navigation and the ability to return to a nest on a direct path at any time (vector navigation or path integration). All these behaviors are facilitated through sensory information, especially from the visual and olfactory system.

Bees use an internal sky compass, which allows them to orient themselves with respect to the position of the sun. Both the direct sunlight as well as the polarization pattern of the sky and its spectral gradient can be used as reference cues for orientation. Beyond the sky compass, landmarks and the visual panorama play an important role in the orientation of bees. In addition to directional information, the animals need to evaluate distance information, which they extract from optic flow, i.e. the perceived movement of the environment.

Our group studies how information from these different reference systems is being used, how they are interconnected, how the different sources of information information are integrated and processed in the brain, and what influence temperature has on these processes. Our studies are carried out on bumblebees and honeybees using anatomical, physiological and ethological methods. This includes dye injection into neurons, immunocytochemistry, electrophysiology, and behavioral experiments.

Prof. Dr. Keram Pfeiffer

2006
PhD, University of Marburg

Postdoctoral research at Dalhousie University Halifax and Sokendai, Hayama

since 2017
Professor of Neurobiology at JMU Würzburg

The navigation center of the insect brain, is called central complex. The image shows a standard 3D-model of the honeybee's central complex

Selected Publications

B Jaske, K Pfeiffer (2025). Temperature-induced shifts and temperature compensation in the tuning of motion-sensitive neurons of bumblebees. **J Neurophysiol** 133(6):1675-1691

B Jaske, K Tschirner, MF Strube-Bloss, K Pfeiffer (2024). Velocity coding in the central brain of bumblebees. **J Neurophysiol** 132(6):1986-2001

L Rother*, R Müller*, E Kirschenmann *et al.* (2023). Walking bumblebees see faster. **Proc Biol Sci** 290(1999):20230460

✉ keram.pfeiffer@uni-wuerzburg.de ☎ +49 931 31 88510
🏛 Chair of Behavioral Physiology and Sociobiology | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Wolfgang Rössler

1990
PhD, University of Marburg

Postdoctoral research at University of Arizona

Assistant Professor at University of Göttingen

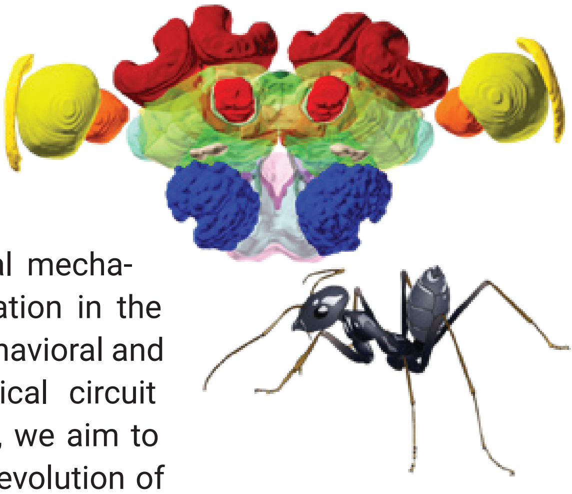
Professor of Neuroethology at JMU Würzburg

since 2011
Professor and Chair of Zoology II at JMU Würzburg

Neuroethology of Social Insects

The ecological importance and evolutionary success of social Hymenoptera (ants, bees, wasps) is enormous. What are the neuronal mechanisms underlying behavioral adaptations that promote insect sociality?

To address this overarching question, our current research focuses on adaptations in olfactory systems, mechanisms underlying complex navigation, and the cellular and molecular bases of behavioral plasticity. We use select species of ants and bees as experimental models and combine behavioral experiments and manipulations in the field and laboratory with brain imaging (confocal, 2-photon, EM), computer-generated 3D-brain models, neurocircuit tracing, molecular neuroanatomy, and single- or multi-unit electrophysiology. In recent years, we discovered the function of a dual olfactory pathway in the honeybee brain, a polarity sensitive magnetic compass in desert ants important for neuronal calibration of sun-compass based navigation, and plasticity of synaptic microcircuits in learning and memory centers of the insect brain promoting behavioral flexibility important for social organization.



3D-computer reconstruction of a desert ant brain comprising 33 compartments (neuropils) and image of the North African desert ant *Cataglyphis fortis*

Our future work focusses on neuronal mechanisms underlying multisensory integration in the insect brain. Using combinations of behavioral and physiological methods, neuroanatomical circuit analyses, and biophysical approaches, we aim to unravel the neuronal foundations and evolution of adaptations constituting a “social-insect brain”.

Selected Publications

R Grob, VL Müller, K Grübel *et al.* (2024). Importance of magnetic information for neuronal plasticity in desert ants. **Proc Natl Acad Sci U S A** 121(8):e2320764121

PN Fleischmann, R Grob, VL Müller *et al.* (2018). The Geomagnetic Field Is a Compass Cue in Cataglyphis Ant Navigation. **Curr Biol** 28(9):1440-1444

MF Brill, T Rosenbaum, I Reus *et al.* (2013). Parallel processing via a dual olfactory pathway in the honeybee. **J Neurosci** 33(6):2443-2456

✉ wolfgang.roessler@uni-wuerzburg.de ☎ +49 931 31 84306
🏛 Chair of Behavioral Physiology and Sociobiology (Zoology II) | Theodor Boveri Institute | Faculty of Biology

Neural Mechanisms of Olfaction

Prof. Dr. Silke Sachse

2002
PhD, FU Berlin

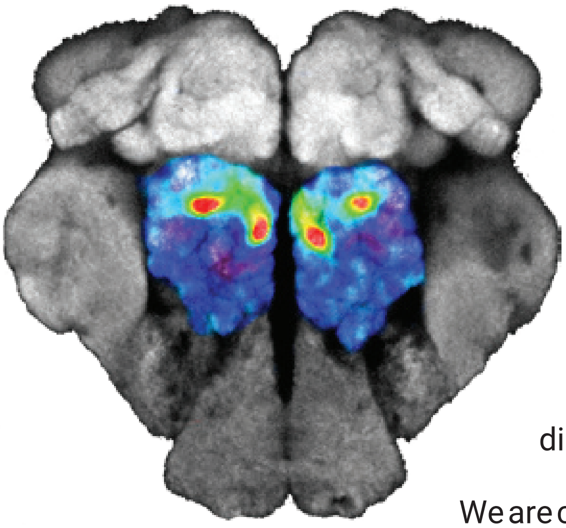
Postdoctoral research at
Rockefeller University New York

Group Leader at MPI for
Chemical Ecology

since 2025
Professor and Chair of
Neurobiology and Genetics at
JMU Würzburg

Animals rely on their sensory systems to navigate their environment in ways that enhance survival and reproduction. The olfactory system plays a key role in encoding chemical information and translating the outside world into neural representations in the brain, enabling an organism to thrive in its surroundings. My lab is interested in the neural mechanisms that allow animals to encode and interpret the vast array of odors that drive behavior.

By combining a sophisticated suite of neurogenetic, physiological and behavioral approaches, we dissect the neural circuitry of *Drosophila melanogaster* to elucidate its role in odor coding and processing. My lab has uncovered fundamental neuronal mechanisms in olfaction. We have identified the neuronal correlates of behavioral responses to odor mixtures and demonstrated that each olfactory glomerulus has a unique neural composition that correlates with its functional relevance. Furthermore, we have shown that higher brain centers decode the behavioral significance of an odor. Recently, we discovered a novel odor coding rule in the migratory locust.



Odor-evoked activities in the fly brain visualized with calcium imaging

We are currently investigating how olfactory circuits are modulated by internal states, previous experiences, and associative learning. Additionally, we study the olfactory code in non-model organisms, including species of *Drosophila* that exploit different ecological niches, as well as the yellow fever mosquito. We are also interested in multimodal sensory processing and integration.

Selected Publications

X Jiang, E Dimitriou, V Grabe *et al.* (2024). Ring-shaped odor coding in the antennal lobe of migratory locusts. **Cell** 187(15):3973-3991

AAM Mohamed, T Retzke, S Das Chakraborty *et al.* (2019). Odor mixtures of opposing valence unveil inter-glomerular crosstalk in the *Drosophila* antennal lobe. **Nat Commun** 10(1):1201

S Das, T Trona, MA Khallaf *et al.* (2017). Electrical synapses mediate synergism between pheromone and food odors in *Drosophila melanogaster*. **Proc Natl Acad Sci U S A** 114(46):e9962-e9971

✉ silke.sachse@uni-wuerzburg.de ☎ +49 931 31 89893 🦋 @silkesachse.bsky.social
🏛 Chair of Neurobiology and Genetics | Theodor Boveri Institute | Faculty of Biology

Prof. Dr. Christian Wegener

2000
PhD, FSU Jena

Postdoctoral research at
Stockholm University and
University of Leeds

Emmy Noether Group Leader at
Marburg University

since 2011
Professor of Neurogenetics at
JMU Würzburg

Neuropeptide Signalling and Circadian Clocks

Neuropeptides are the most diverse group of neuronal messengers. They act as neuromodulators or neuroendocrine hormones. In addition, non-neuronal endocrine cells in the gut and other tissues hormonally release neuropeptides. In particular, the circadian system relies on peptidergic signalling to temporally coordinate behaviour, physiology and development.

Using peptidomic techniques, our group has significantly contributed to the chemical characterisation of insect neuroendocrine and brain-gut peptides and their post-transcriptional processing. At the centre of current research is the role of neuroendocrine peptides in the circadian control of behaviour, metabolism and development, and its significance for the ability of insects to adapt to a daily changing environment.

Major specific aims are to understand the mechanisms underlying the circadian timing of insect development and emergence (eclosion) and the role of neuropeptide hormones in the communication between central and peripheral clocks. Further, in collaboration with the metabolomics core unit at the Biocenter, we are investigating the roles of central and peripheral clocks and neuropeptides in the control of feeding and energy metabolism.

The central nervous system of the vinegar fly *Drosophila*, stained against the neuropeptide allatostatin A (magenta) and a GFP marker

Our main model is the vinegar fly *Drosophila* which allows us to use powerful genetic tools, connectomics, imaging and automatised behavioural assays to gain a systemic understanding of the circadian regulation of the neuroendocrine system and its functions.

Selected Publications

D Pauls, M Selcho, J Räderscheidt J *et al.* (2021). Endocrine signals fine-tune daily activity patterns in *Drosophila*. **Curr Biol** 31(18):4076-4087

M Selcho, C Millán, A Palacios-Muñoz *et al.* (2017). Central and peripheral clocks are coupled by a neuropeptide pathway in *Drosophila*. **Nat Commun** 8:15563

C Wegener, A Gorbashov (2008). Molecular evolution of neuropeptides in the genus *Drosophila*. **Genome Biol** 9(8):R131

✉ christian.wegener@uni-wuerzburg.de ☎ +49 931 31 85380
Chair of Neurobiology and Genetics | Theodor Boveri Institute | Faculty of Biology

Plant Sciences

Prof. Dr. Wolfgang Dröge-Laser

1992
PhD, University of Bielefeld

Postdoctoral research at the Salk Institute La Jolla

Group Leader at University of Göttingen

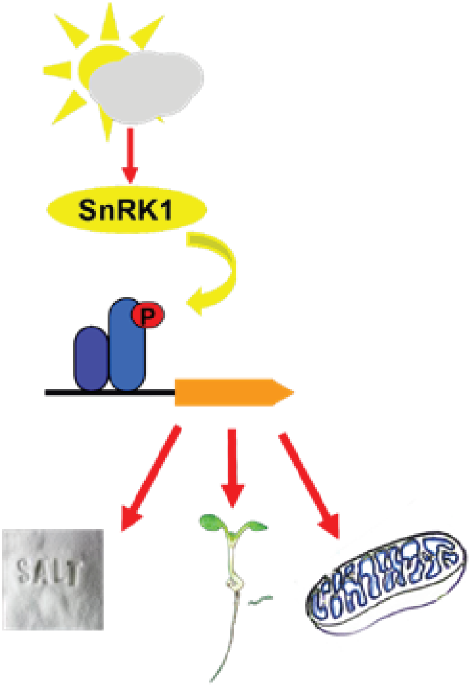
since 2010
Professor of Pharmaceutical Biology at JMU Würzburg

Plant Stress Signalling

Rapid adaptation to ever changing environmental conditions is crucial for plant survival. Our lab is focusing on signalling networks governing plant stress response with particular interest on gene expression.

Similarly to TOR (TARGET OF RAPAMYCIN) and AMPK (AMP-ACTIVATED PROTEIN KINASE) in mammals, two evolutionarily conserved central kinases act in plants. Depending on available resources, they facilitate fine-tuning of metabolism and development. We have identified transcription factors downstream of the *Arabidopsis thaliana* kinase SnRK1 (Snf1 RELATED PROTEIN KINASE1) and studied their impact on development (e.g. lateral root initiation, seedling establishment) and abiotic and biotic stress response. Our future research aims at understanding SnRK1 activation mechanisms, as well as identifying downstream phosphorylated targets and their functions.

A second topic deals with the pathogenic fungus *Verticillium longisporum*, a model to study root infection processes. Using Translating Ribosome Affinity Purification (TRAPseq), we studied root cell-layer specific defences. As this fungus is a threat to oilseed rape, we test novel strategies to establish resistance mechanisms based on secondary metabolites. Currently, we compare RNAseq and RIBOseq data to define post-transcriptional regulatory mechanisms in plant pathogen defence. Here, we aim at identifying consensus sequences or structural motives in the UTR regions.



SnRK1 function in metabolic and developmental control

Selected Publications

C Fröschel, J Komorek, A Attard *et al.* (2021). Plant roots employ cell-layer-specific programs to respond to pathogenic and beneficial microbes. **Cell Host Microbe** 29(2):299-310

P Muralidhara, C Weiste, S Collani *et al.* (2021). Perturbations in plant energy homeostasis prime lateral root initiation via SnRK1-bZIP63-ARF19 signaling. **Proc Natl Acad Sci U S A** 118(37):e2106961118

C Weiste, W Dröge-Laser (2014). The *Arabidopsis* transcription factor bZIP11 activates auxin-mediated transcription by recruiting the histone acetylation machinery. **Nat Commun** 5:3883

✉ wolfgang.droege-laser@uni-wuerzburg.de ☎ +49 931 31 80955
Chair of Pharmaceutical Biology | Julius von Sachs Institute | Faculty of Biology

Plant Signaling and Transport In a Constantly Changing World

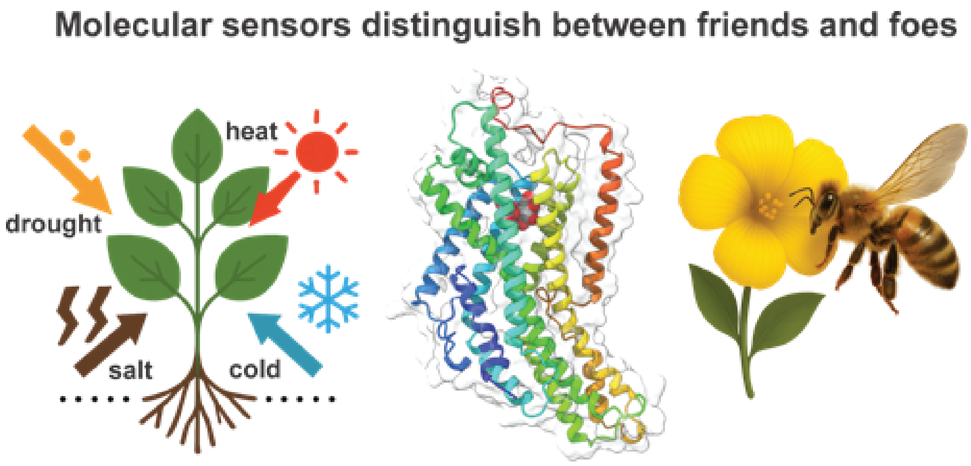
Prof. Dr. Dietmar Geiger

2005
PhD, JMU Würzburg

since 2011
Professor of Plant Physiology at JMU Würzburg

Plants absorb nutrient salts from the soil and produce photoassimilates in photosynthetically active leaves. We are interested in the uptake and distribution of nutrient salts from the soil, as well as the redistribution of energy-rich hydrocarbon compounds produced during photosynthesis. Biophysical techniques allows us to gain profound insights into the transport mechanism, the thermodynamics, and the structure of ion channels and substrate transporters. These transport processes are subject to tight regulation by signaling pathways that control the activity of the transport proteins depending on demand and environmental influences. Reconstructing these signaling pathways in heterologous expression systems allows us to gain insights into the regulation of individual transporters independent of the plant background.

Within a close collaboration between the lab of Prof. Dr. Ricarda Scheiner and the Geiger lab, we recently focused on the mutualistic relationship between honey bees and flowering plants. Thereby, we investigate gustatory receptors expressed at peripheral taste organs of honey bees and how the perception of sugar-rich nectar influences the decision-making of individual bees and the foraging strategy of the colony. We are also interested in the question of how bitterness in sugary foods is perceived and how toxic exposure can be effectively avoided.



Perception of stressfull environments as well as recognition of their lively environment involves highly specific receptors in plants and insects

Selected Publications

T Maierhofer, S Scherzer, A Carpaneto *et al.* (2024). *Arabidopsis* HAK5 under low K+ availability operates as PMF powered high-affinity K+ transporter. **Nat Commun** 15(1):8558

L Değirmenci, FL Rogé Ferreira, A Vukosavljevic *et al.* (2023). Sugar perception in honeybees. **Front Physiol** 13:1089669

Geiger D (2020). Plant glucose transporter structure and function. **Pflügers Arch** 472(9):1111-1128

✉ dietmar.geiger@uni-wuerzburg.de ☎ +49 931 31 86105
Chair of Molecular Plant Physiology and Biophysics | Julius von Sachs Institute | Faculty of Biology

Metabolite and Hormone Transport Transporter Structure Function

Prof. Dr. Ulrich Z. Hammes

2020
PhD, University of Tübingen

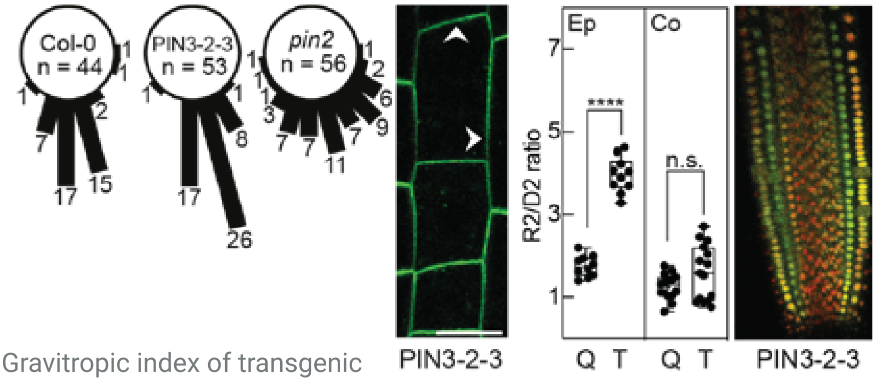
Postdoctoral research at Danforth Center (St. Louis) and FAU Erlangen

Group leader at University of Regensburg and TU Munich

since 2025
Chair of Molecular Plant Physiology at JMU Würzburg

The uptake and export of hormones and metabolites in plants are facilitated by transporters from many different protein families and transport mechanisms. We are interested in understanding the structure and function of these proteins on a biochemical and biophysical level, their posttranslational regulation, as well as their cell biology and physiological roles at the organismal and ecological level. We use electrophysiology, flux studies, various microscopy techniques, and physiological assays to characterize transporters.

Our current research focuses on the role of transporters for the central phytohormone auxin, which enables plants to adapt to environmental stimuli such as light and gravity. We are investigating how substrates and transporters interact, and we engineer these proteins to exhibit enhanced performance under negative selective pressure. Furthermore, we address how transporters and regulatory kinases interact and which structural factors underlie the regulation of transporter activity.



Gravitropic index of transgenic lines and wildtype, localization of an auxin exporter and auxin distribution in a root of *Arabidopsis*.

Our future research will expand to transporters of other phytohormones to unravel the complex and intricate interactions among hormone signaling pathways that enable plants to respond to changing environmental cues with the unparalleled developmental plasticity that characterizes them. Ultimately, we aim to contribute to the development of resilient crop plants for sustainable agriculture.

Selected Publications

L Schulz L, KL Ung KL, L Zuzic *et al.* (2025). Transport of phenoxyacetic acid herbicides by PIN-FORMED auxin transporters. **Nat Plants** 11(5):1049-1059

DP Janacek, M Kolb, L Schulz *et al.* (2024). Transport properties of canonical PIN-FORMED proteins from Arabidopsis and the role of the loop domain in auxin transport. **Dev Cell** 59(24):3259-3271

KL Ung, M Winkler, L Schulz *et al.* (2022). Structures and mechanism of the plant PIN-FORMED auxin transporter. **Nature** 609(7927):605-61

✉ ulrich.hammes@uni-wuerzburg.de ☎ +49 931 31 88849 @uhammes.bsky.social
Chair of Molecular Plant Physiology and Biophysics | Julius von Sachs Institute | Faculty of Biology

Plant Specialized Metabolites Biosynthesis and Evolution

Plants produce a remarkable diversity of specialized metabolites that support their ability to respond to changing environmental conditions. These low-molecular-weight compounds mediate interactions with biotic and abiotic factors and reflect a high degree of structural and functional diversity. Despite their importance, the underlying biosynthetic pathways and their evolutionary origins are still not fully understood.

Our research focuses on the biosynthesis, evolution, and functional analysis of specialized metabolites across different plant families. Using integrative approaches - including transcriptomics, metabolomics, and pathway reconstitution - we aim to identify key biosynthetic pathways and understand how structural diversity arises. By reconstructing selected pathways, we also seek to explore evolutionary patterns and gain insights into the enzymatic logic underlying metabolic complexity.

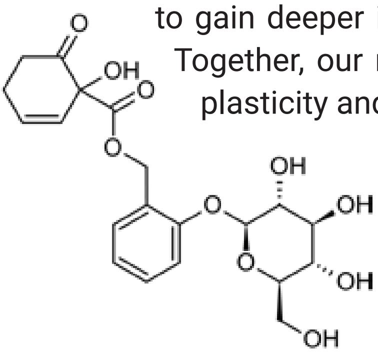
Future work will expand on these findings through comparative studies and synthetic biology approaches to reconstitute and modify biosynthetic pathways. At the same time, we will explore the potential multifunctionality of selected metabolites, such as roles in defense and nutrient homeostasis, to gain deeper insight into their physiological relevance and adaptive significance. Together, our research contributes to a deeper understanding of plant metabolic plasticity and its relevance for both ecological function and applied use.

Prof. Dr. Nathalie Lackus

2020
PhD, FSU Jena/MPI-CE

Postdoctoral research at MPI for Chemical Ecology

since 2022
Junior Professor of Plant Metabolism and Metabolomics



Salicortin, a salicinoid from *Salicaceae*, plays a key role in plant defense against herbivores

Selected Publications

H Gordon, C Fellenberg, ND Lackus *et al.* (2022). CRISPR/Cas9 disruption of UGT71L1 in poplar connects salicinoid and salicylic acid metabolism and alters growth and morphology. **Plant Cell** 34(8):2925-2947

ND Lackus, A Schmidt, J Gershenzon, TG Köllner (2021). A peroxisomal β-oxidative pathway contributes to the formation of C6-C1 aromatic volatiles in poplar. **Plant Physiol** 186(2):891-909

ND Lackus, A Müller, TDU Kröber *et al.* (2020). The Occurrence of Sulfated Salicinoids in Poplar and Their Formation by Sulfotransferase1. **Plant Physiol** 183(1):137-151

✉ nathalie.lackus@uni-wuerzburg.de ☎ +49 931 31 86923
🏛 Chair of Pharmaceutical Biology | Julius von Sachs Institute | Faculty of Biology

Prof. Dr. Katharina Markmann

2008
PhD, LMU Munich

Group Leader at University of Tübingen

Professor of Molecular Genetics, University of Halle

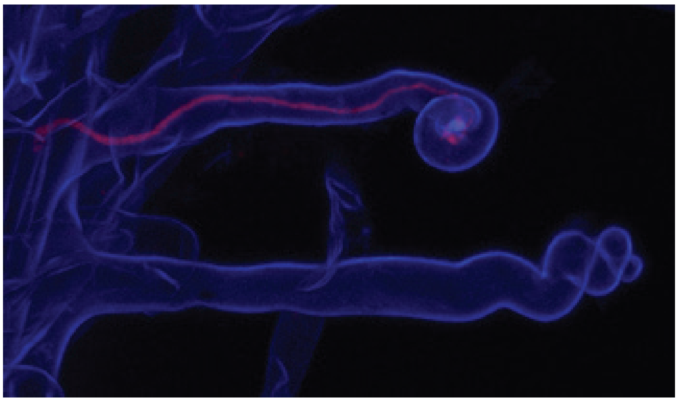
since 2022
Professor and Chair of Plant Ecophysiology at JMU Würzburg and Director of the Würzburg Botanical Garden

RNA Regulators of Symbiosis Systemic Plant Signaling

Plant root interactions with fungal or bacterial soil microbes help hosts alleviate nutrient limitations. Examples are arbuscular mycorrhiza with fungi, an ancient interaction, and the evolutionarily younger nodulation symbiosis with N-fixing bacteria. Both types of interaction are tightly regulated by the plant hosts. For example, legumes plants that are known for their protein-rich seeds (beans, peas, soy) balance symbiotic interactions with nitrogen-fixing bacteria via a systemic feedback system tightly controlling infection rates. This host regulatory system, termed autoregulation of nodulation (AON), prevents nutritional misbalances and is key to maintaining the association at a mutually beneficial state.

In our research, we seek to understand the molecular mechanisms underlying host control of plant root symbioses with both bacteria and fungi, and the role of regulatory small RNAs therein. In particular, we try to elucidate RNA-mediated communication between shoot and root organs in the context of plant responses to microbial interactors.

Aiming to reveal the evolutionary origin of the AON genetic framework as well as its role in shaping plant fitness under changing conditions, we will expand our focus to plant developmental responses to other biotic as well as abiotic stimuli and stresses.



Root hairs of the model legume *Lotus japonicus* forming an entry passage (infection thread) for compatible N-fixing bacteria (*Mesorhizobium loti*)

Selected Publications

M Sexauer, H Bhasin, M Schön *et al.* (2023). A micro RNA mediates shoot control of root branching. **Nat Commun** 14(1):8083

M Sexauer, D Shen, M Schön *et al.*, (2021). Visualizing polymeric components that define distinct root barriers across plant lineages. **Development** 148(23):dev199820

D Tsikou, Z Yan, DB Holt *et al.* (2018). Systemic control of legume susceptibility to rhizobial infection by a mobile microRNA. **Science** 362(6411):233-236

✉ katharina.markmann@uni-wuerzburg.de ☎ +49 931 31 80792
Chair of Plant Ecophysiology | Julius von Sachs Institute | Faculty of Biology

Plant Adaptation to Environment Plant Metabolism & Metabolomics

Prof. Dr. Dr. Martin J. Müller

1992
PhD, LMU Munic

2001
PhD, Karolinska Stockholm

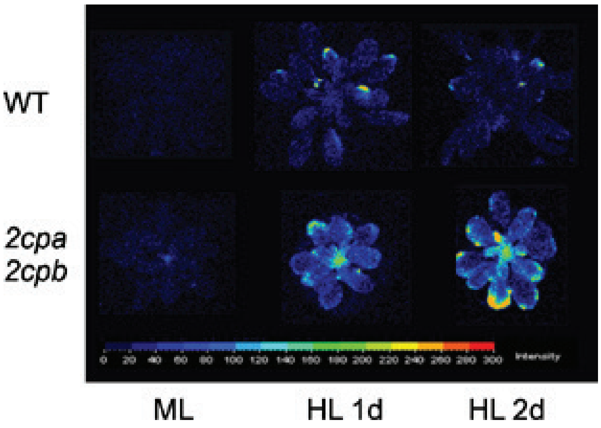
Postdoctoral research at LMU Munich and Karolinska Institute

Group Leader at LMU Munich

since 2000
Professor and Chair of Pharmaceutical Biology at JMU Würzburg

Our research focuses on the metabolic adaptation of plants to abiotic stress. We are particularly interested in rapid lipid signaling and metabolic responses that are not initially transcriptionally regulated in the context of heat, high light and drought stress. We use untargeted metabolomic analyses with high-end mass spectrometers and isotope labeling experiments to identify stress-induced metabolic pathways. The functional relevance of these pathways for stress resilience will be investigated by genetic and physiological means.

We are currently investigating the swift stress-induced remodelling of membrane lipids, which leads to the rapid formation of lipid signals, reactive electrophilic species (RES) and oxidized lipids, as well as the highly dynamic accumulation of storage lipids in lipid droplets. Our work shows that stress-induced lipid remodelling plays an important role in the adaptation of membrane fluidity and the apid provision of energy.



Chemiluminescence indicating elevated lipid peroxidation in wild type and peroxiredoxine-deficient *Arabidopsis* plants exposed to high light stress

The functional significance of lipid catabolism for the provision of carbon building blocks and as an alternative energy source in photosynthetically active plant organs has been little studied to date. It is generally assumed that photosynthesis provides more than sufficient carbon and energy in the form of carbohydrates. The aim of future studies is to identify the importance of alternative metabolic pathways in stress situations where the availability of photosynthesis as a primary energy source is limited.

Selected Publications

P Korte, A Unzner, T Damm *et al.* (2023). High triacylglycerol turnover is required for efficient opening of stomata during heat stress in *Arabidopsis*. **Plant J** 115(1):81-96

E Ferber, J Gerhards, M Sauer *et al.* (2020). Chemical Priming by Isothiocyanates Protects Against Intoxication by Products of the Mustard Oil Bomb. **Front Plant Sci** 11:887

EE Farmer, MJ Mueller (2013). ROS-mediated lipid peroxidation and RES-activated signaling. **Annu Rev Plant Biol** 64:429-450

✉ martin.mueller@uni-wuerzburg.de ☎ +49 931 31 86160
🏛 Chair of Pharmaceutical Biology | Julius von Sachs Institute | Faculty of Biology

Prof. Dr. Thomas Müller

1995
PhD, JMU Würzburg

Postdoctoral research at EMBL Heidelberg, FMP Berlin, and UC Los Angeles

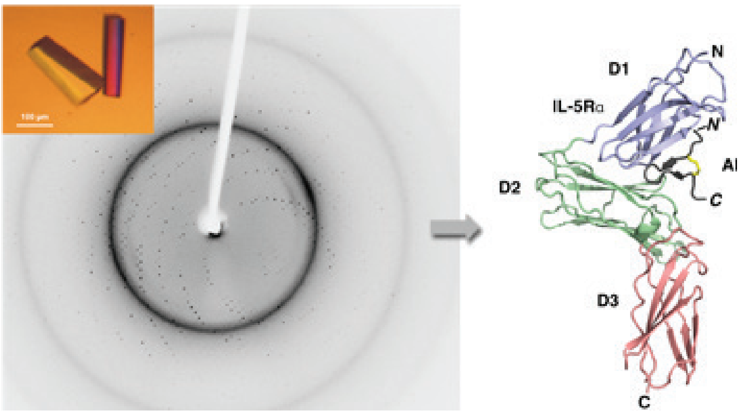
Group Leader at JMU Würzburg

since 2007
Professor of Plant Genetics and Biophysics at JMU Würzburg

Molecular Mechanisms in Protein-Protein Recognition

Intercellular communication is a prerequisite for the existence of multicellular organisms. While genome research has provided insights into cellular and organismic communication in the past decade often allowing detailed predictions about cellular signaling networks, knowledge about the molecular basis of these cell-cell communication, why and how certain proteins do interact whereas others do not, is still lacking. Hence we use structure biology and protein chemistry to determine the molecular mechanisms underlying protein-biomolecule recognition.

We are working on different protein families in plants and animals, in which protein-protein recognition or protein-substrate interaction will be investigated. Interleukin (IL)-5 is a human cytokine, which is involved in the onset of allergic diseases and causes the known symptoms in allergy and asthma. Thus, inhibitors of IL-5 signaling, i.e. small cyclic peptides that block the IL-5 receptor, might offer new therapeutic strategies against atopic diseases. On the basis of structures of IL-5 inhibitory peptides bound to the IL-5 receptor IL5Ra, we are currently trying to improve the inhibitory capacities using peptide design and peptide engineering approaches. In another project we study plant anion channels of the SLAC/SLAH family that are involved in opening and closing of stomata. Using interaction analyses and structural modeling we try to unravel ion selectivity, which can then be used to generate salt-tolerant plants.



X-ray structure analysis of a crystal of a IL5Ra-peptide complex yielding structure insights into peptide recognition and binding

Selected Publications

S Thomas, JE Fiebig, EM Kuhn *et al.* (2023). Design of Glyco-engineered IL-4 Antagonists Employing Chemical and Biosynthetic Glycosylation. **ACS Omega** 8(28):24841-24852

J Lehmann, ME Jørgensen, S Fratz *et al.* (2021). Acidosis-induced activation of anion channel SLAH3 in the flooding-related stress response of Arabidopsis. **Curr Biol** 31(16):3575-3585

T Malinauskas, TV Peer, B Bishop *et al.* (2020). Repulsive guidance molecules lock growth differentiation factor 5 in an inhibitory complex. **Proc Natl Acad Sci U S A** 117(27):15620-15631

✉ thomas.mueller@uni-wuerzburg.de ☎ +49 931 31 89207
🏛 Chair of Molecular Plant Physiology and Biophysics | Julius von Sachs Institute | Faculty of Biology

Scientific Services

Imaging Core Facility

The Imaging Core Facility at the Biocenter Hubland campus provides access to cutting-edge technologies in both light and electron microscopy, along with advanced sample preparation methods such as high-pressure freezing and freeze substitution. Our portfolio of light microscopes ranges from confocal laser scanning systems to super-resolution instruments, enabling high-resolution imaging across a variety of applications.

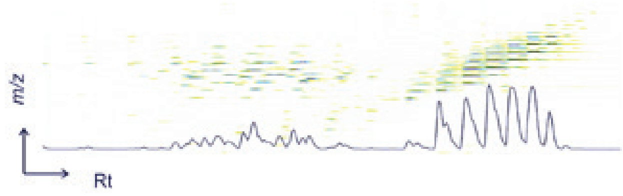
For ultrastructural studies, we offer a comprehensive selection of scanning and transmission electron microscopy technologies. Our electron tomography workflow enables near-isotropic 3D resolution at the nanometer scale. For projects requiring precise molecular localization within the context of cellular ultrastructure, we offer a versatile correlative light and electron microscopy (CLEM) workflow. This adaptable platform supports a wide range of organisms and experimental designs.

To support image processing and data analysis, we provide dedicated workstations equipped with a wide selection of software tools. Our expert staff are available to assist throughout the entire workflow—from sample preparation and imaging to image analysis and quantification.

Metabolomics Core Unit

At the Metabolomics Core Unit located at the Biocenter Dallenberg campus, we aim to identify and quantify all metabolites in a biological sample at a specific time. We use two main approaches: untargeted metabolomics (profiling and fingerprinting) and targeted metabolomics.

Targeted metabolomics enables absolute quantification of predefined metabolites. We use UPLC-MS/MS to analyze hormones (e.g., jasmonates, juvenile hormones), amino acids, alkaloids, and sugars, and can develop custom methods upon request. Untargeted approaches aim to detect metabolites with significantly altered levels—potential biomarkers. Our core expertise lies in untargeted lipidomics, routinely performed using UPLC-qTOF-MS.



Since 2011, we have offered LC-MS-based metabolomics in close collaboration with partner laboratories. Together, we select the most suitable approach and experimental design. Where possible, we also train PhD and MSc students to participate in the analysis in our lab, fostering efficiency and rapid adaptation to unexpected results.

Cryo-Electron Microscopy Facility

Our central facility for cryo-electron microscopy located at the Grombühl campus offers access to a state-of-the-art Titan Krios G3 electron microscope equipped with an X-FEG source, Selectris energy filter, and a Falcon IVi camera with direct electron detection. The setup is optimized for high-resolution image acquisition with high throughput for structure determination by single-particle image analysis. Data collection is automated with EPU and can run continuously for several days without user intervention. Typical sessions take one to two 24 hour slots with an acquisition rate of some 350–450 movies/hour. In most cases, a single 24-hour slot is sufficient to obtain enough data to solve a structure of a biological complex with better than 3 Å resolution.

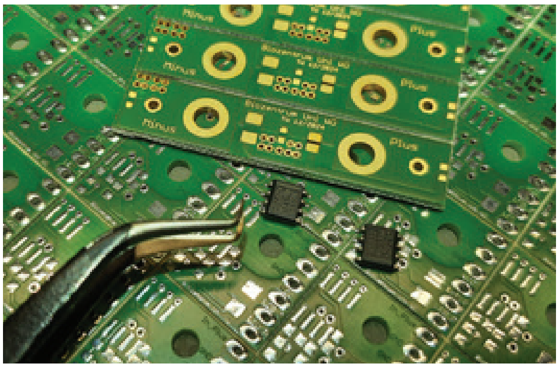
Access to the microscope is arranged in 24-hour slots, with operator-driven setup and acquisition. Users are required to provide a vitrified sample and acknowledge the contribution of the facility in later publications. The service is offered at cost.

Scientific Instrumentation Workshop

Not all scientific instruments can be purchased off the shelf. The Biocenter Instrumentation Facilities at the Hubland and Dallenberg campuses bridge this gap by bringing together experts in electronic and mechanical engineering who collaborate closely with scientists to transform ideas into practical solu-tions. Whether the task is simple or highly complex, a combination of advanced machinery and a dedicated team ensures rapid turnaround times at a reasonable cost.

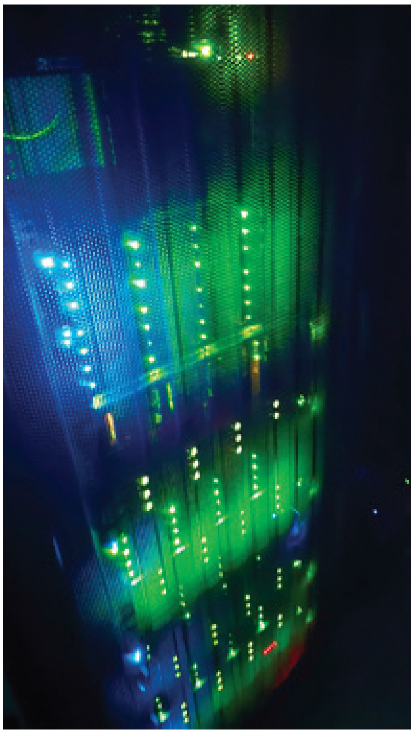
Our facilities are equipped with a wide array of modern tools for working with metal, plastic, and wood, including digitally controlled, high-precision machinery. Services offered by our specialists include the design and construction of experimental setups, 3D modeling, CNC machining, and additive manufacturing using 3D printing technologies.

On the electronics side, our engineers design, build, and implement both analog and digital circuits, as well as embedded systems tailored to scientific needs, particularly in the automation of measurement and control processes. In addition, they offer expert consulting on a range of electrotechnical challenges. The workshop also plays a key role in maintaining the accuracy and reliability of both custom-built and commercially acquired instruments.



IT Services

In today’s biological research, data is a cornerstone of scientific progress—and the IT department plays a vital role in enabling that progress. Our mission is to ensure that scientists can focus fully on their research by maintaining a reliable and secure computing environment.



We deliver tailored IT solutions, such as custom virtual machines configured to meet the specific needs of each research group. Our infrastructure is continuously updated to protect against cybersecurity threats, and we actively collaborate with other universities to stay current with the latest developments in digital security.

Behind the scenes, our team ensures that research data is safely stored and regularly backed up, protecting against data loss or corruption. We also operate a centralized ticketing system to efficiently track, prioritize, and resolve IT support requests, minimizing disruptions to research activities.

In short, we provide the technological foundation that empowers our scientists to carry out world-class research with confidence and efficiency.

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Impressum

Julius-Maximilians-Universität Würzburg
Biozentrum
Am Hubland
97074 Würzburg
Telefon: (0931) 31-84440
www.biozentrum.uni-wuerzburg.de