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GENE CENTER MUNICH

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REPORT 2009-2012

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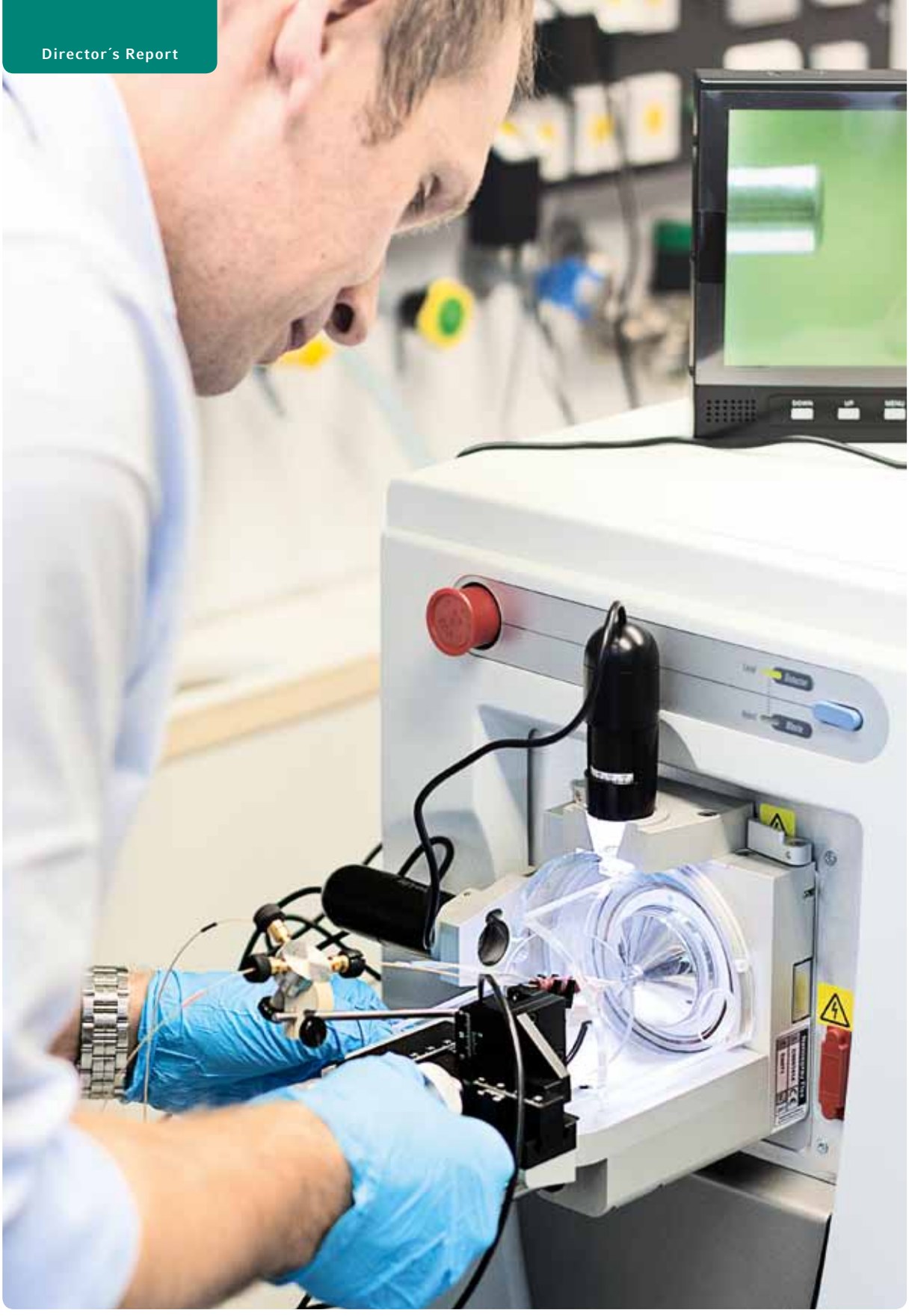


DIRECTOR`S REPORT

Over the last few years, the Gene Center of the Ludwig-Maximilians-Universität (LMU) in Munich has developed into an internationally leading institution for research and teaching in the life sciences. Our success is reflected in many outstanding publications, prestigious awards, and large extramural funding projects. In 2009-2012, scientists who are now at the Gene Center published 429 scientific papers and reviews, including 29 original papers in the leading journals *Nature, Science*, and *Cell*. Amongst the 16 current principal investigators, four received an Advanced Investigator Grant from the European Research Council ERC, one was awarded an Alexander-von-Humboldt-Professorship, and five of the junior group leaders received competitive start-up grants or awards. The extramural funding acquired by Gene Center scientists during the report period amounts to a total of 57 million euros from 25 different sources. In 2012 alone, 28 million euros were acquired, compared to 11 million euros in 2008. The total personnel grew from 158 in 2004 to 224 in 2008 to 324 in 2012. These successes confirm our interdisciplinary interinstitutional strategy.

We extended our research portfolio by recruiting five outstanding junior faculty members from leading research institutions, and by affiliating one investigator. Petra Wendler moved to the Gene Center from Birkbeck College London and studies assisted protein folding by electron microscopy. Mario Halic came from Harvard University and investigates the mechanisms cells use to silence genes. Franz Herzog moved from the ETH in Zurich, and develops mass spectrometry methods to analyze large protein assemblies. Fabiana Perocchi moved here from Harvard Medical School after a short stay at the CRG in Barcelona and studies cellular signaling pathways and mitochondrial metabolism. Julien Gagneur is a computational genome biologist who came from the European Molecular Biology Laboratory. Last but not least, we affiliated Christoph Klein, who is a leading pediatrician and researcher in the fields of immunology and gene therapy. He has won many awards, including the Gottfried Wilhelm Leibniz Prize of the Deutsche Forschungsgemeinschaft (DFG).

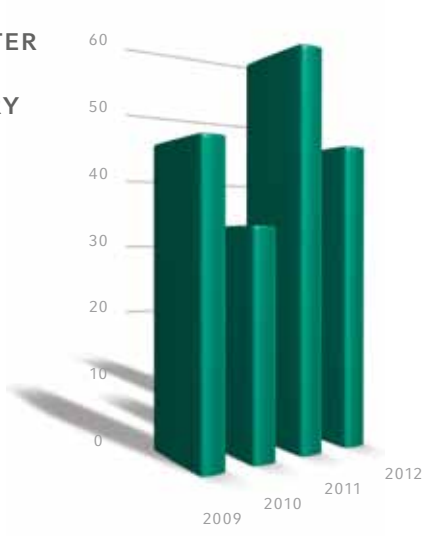
Strong efforts of Gene Center investigators enabled us to extend our research into complementary fields, in particular molecular systems biology. The Center was instrumental in establishing the Bavarian Research Network for Molecular Biosystems, which brings together 24 junior and senior research groups at four locations in Bavaria and is coordinated by Horst Domdey. Ulrike Gaul is establishing a Graduate School of Quantitative Biosciences Munich (QBM) that is funded by the National Initiative for Excellence in Research. Karl-Peter Hopfner coordinates a new DFG-funded Graduate Program on Integrated Analysis of Macromolecular Complexes and Hybrid Methods in Genome Biology. Eckhard Wolf acquired 5 million euros from the Bavarian State Ministry of Sciences, Research and the Arts to set up a new animal facility that will be opened in 2013. Funding could be renewed for major research programs with strong participation of Gene Center groups, including the National Cluster of Excellence in Protein Science CIPSM and the research grant network on genome expression and maintenance SFB646.

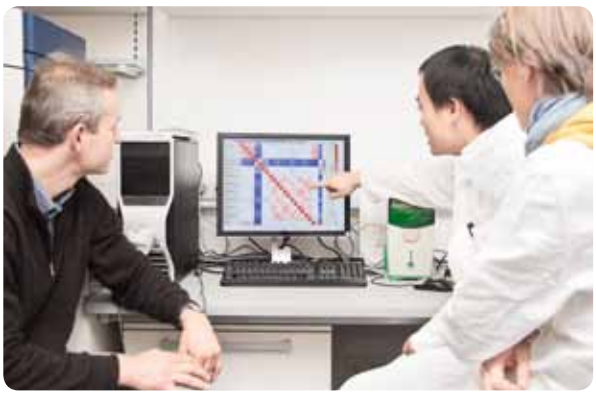
These positive developments generated a high demand for additional space. With support from CIPSM, we obtained a total of 28.8 million euros of funding to construct a new building next door, the Research Center for Molecular Biosystems (BioSys^{M}). The Bavarian Minister of Sciences, Research and the Arts, Wolfgang Heubisch, laid the foundation stone in November 2012. The building will be completed in 2015. Our research facilities are being extended and new technology platforms are being established which form the basis for bringing to life BioSys^{M}. These and other measures let us once again fulfill our role as the engine for development of the life science campus Großhadern-Martinsried.

The Gene Center has also served as a vivid meeting place for scientific exchange. Over the last four years, 84 speakers from 14 different countries have lectured in our research seminar series and several scientific symposia have been organized. A highlight was the 25th anniversary of the Center in 2009. At this occasion, our new DNA artwork in the foyer was dedicated to the founder of the Gene Center, Ernst-Ludwig Winnacker. Interdisciplinary exchange amongst research groups at the Center is fostered by our annual retreats at Wildbad Kreuth in the Bavarian Alps. An annual meeting at Castle Ringberg that we organize together with Bio-M puts investigators in contact with industry leaders. Social events included summer, Halloween and Christmas parties and the annual Römer Foundation graduation and award ceremony that we celebrate together with the Chemistry Department.

The teaching of undergraduate students in Bachelor and Master courses is a key part of our work. To respond to the increased number of undergraduate students in practical courses, new well-equipped teaching labs were set up in a building in Martinsried under the leadership of Heidi Feldmann. This also freed up laboratory space at the Center for the new research groups. Our Master program in Biochemistry that we conduct in English developed into a great success. During the last four years, 182 students have been selected for this advanced course, almost 40% of whom spent part of their time doing research abroad, mostly in the United States. A new minor subject in systems biology complements existing courses.

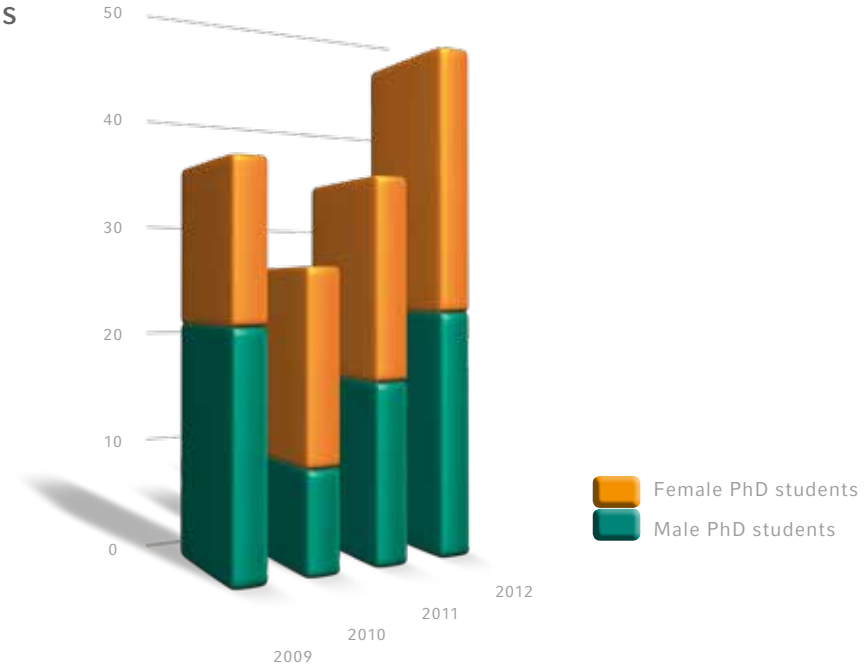
ACCEPTED MASTER STUDENTS IN BIOCHEMISTRY

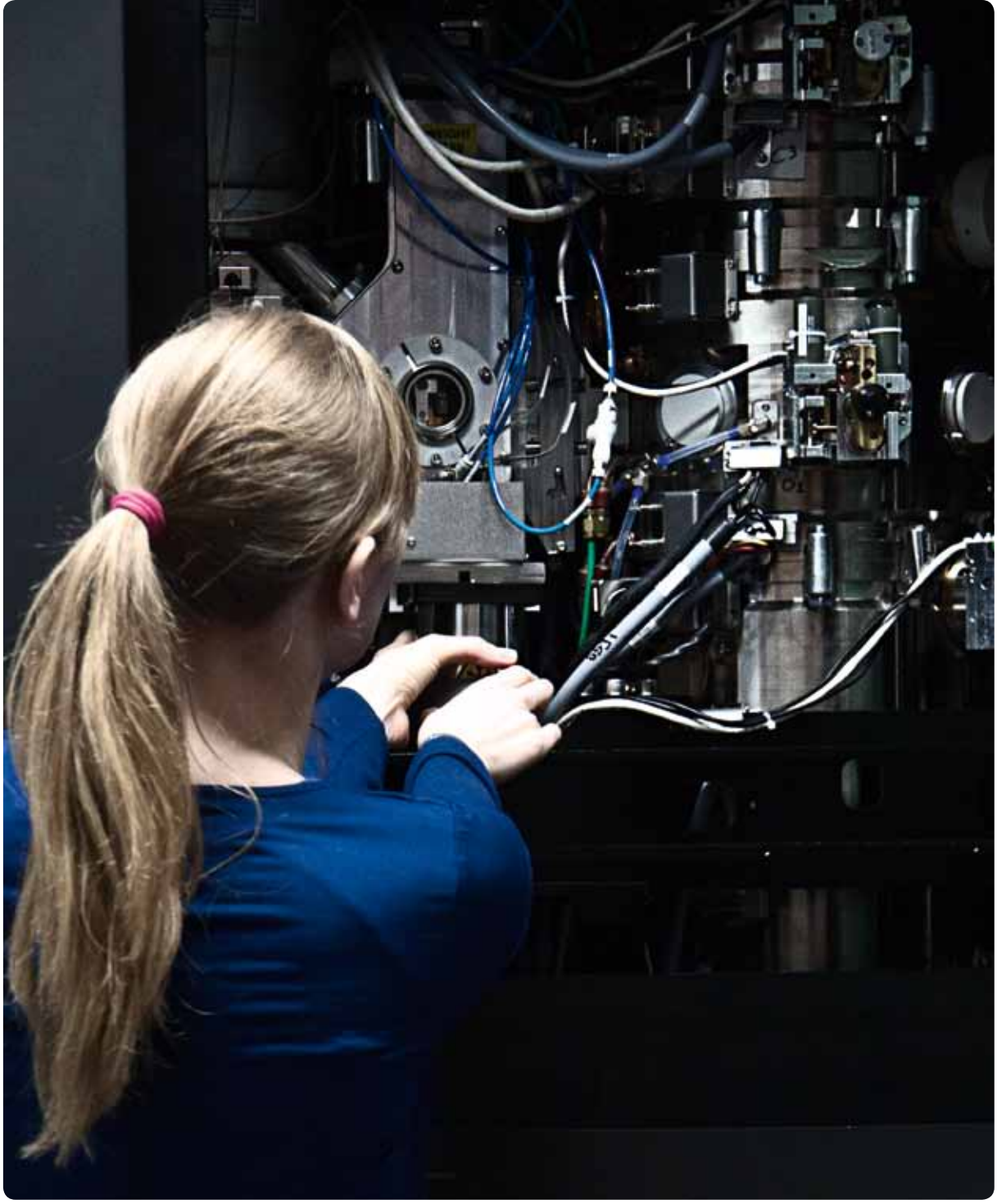




Successful training of PhD students is of central importance to us. During the report period, 122 PhD students graduated in Biochemistry, 56% of whom were female. Students participate in the general graduate program of the Gene Center, which includes weekly institute seminars where PhD students and postdoctoral fellows present their work. Many PhD students also participate in specialized graduate schools and programs which foster exchange between the Gene Center and research groups at other LMU institutions, the Technical University of Munich, the Max Planck Institute of Biochemistry, and the Helmholtz Center.

COMPLETED PHD THESES
IN BIOCHEMISTRY
PER ACADEMIC YEAR





We had to say goodbye to three principal investigators who left during the period of the report. Ulrich Koszinowski, a distinguished virologist and member of the medical faculty, retired in 2012. Achim Tresch took up a professorship at the University of Cologne. Dierk Niessing now holds a tenured laboratory head position at the Helmholtz Center in Neuherberg. I would like to thank all three colleagues for their great work and many important contributions and wish them all the best for the future.

The successes described in this report are due to the hard work of my dedicated colleagues and many highly motivated researchers and students. Also of critical importance is our supportive infrastructure and administrative personnel, coordinated by our head of administration, Katja Ketterle. I would like to cordially thank all those who made this possible and also all of our supporters!

Many exciting opportunities are ahead of us. I hope this report piques your interest in our Center and we hope to work with you in the future.

Patrick Cramer

ROLAND BECKMANN

PROTEIN SORTING, TRANSLATION AND REGULATION

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1995	PhD from Free University Berlin, Germany
1995-2000	Postdoc at Rockefeller University, USA
2001-2006	Group Leader of the VolkswagenStiftung, Charité, Berlin, Germany
2006-present	Professor, Gene Center and Department of Biochemistry, LMU

GOAL

To determine the molecular mechanisms and regulatory principles of co-translational events such as protein sorting and mRNA decay.

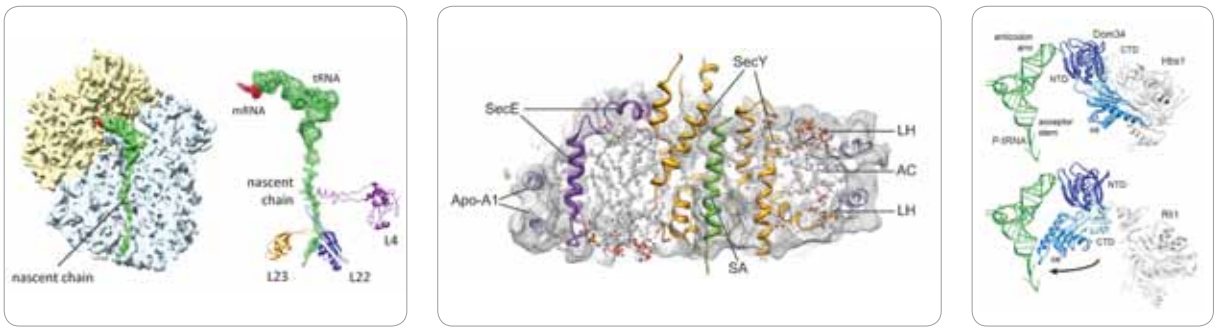
INTRODUCTION

Our research group has for a long time been interested in elucidating the mechanistic principles of cotranslational secretory and membrane protein sorting and translocation. As the main tool we use cryo-electron microscopy (cryo-EM) in combination with single particle analysis. One focus has been the structural analysis of the translating and translocating ribosome-Sec-complex. We are particularly interested in understanding the biogenesis of membrane proteins and how the protein-conducting channel or translocon, the Sec complex, is capable of switching between translocation activity for hydrophilic nascent chains and membrane insertion activity for hydrophobic domains. Moreover, we are also interested in the behavior of the nascent polypeptide chain on the ribosome and the steps guiding the translating ribosome to the membrane, i.e. signal sequence-driven recognition of the ribosome-nascent chain complex by signal recognition particle (SRP) and transfer to the translocon by SRP receptor (SR).

A second important topic of our lab is the structural basis of ribosomal stalling, mRNA decay and ribosomal recycling. Interestingly, the phases of termination, recycling and (re-)initiation of translation appear to be functionally coupled in eukaryotes. We thus started to structurally investigate the different complexes involved in these processes.

RESEARCH HIGHLIGHTS

Over the last few years, we have succeeded in visualizing a number of active ribosomal complexes, with the best structures being now in the resolution range of 5 Å. We could for the first time visualize stalling nascent polypeptide chains (TnaC, SecM, APP, CMV) in the tunnel of the ribosome. Moreover, we observed that α-helices already fold in this environment. After achieving secondary structure resolution for the ribosome-bound mammalian Sec61 complex we were also able to reconstitute the bacterial counterpart, the SecYEG complex, into a lipid environment, so-called Nanodiscs. A cryo-EM based molecular model revealed a signal anchor helix coordinated in the open lateral gate of the



Left: Cryo-EM structure of the stalled TnaC nascent polypeptide chain.

Center: Model of the engaged ribosome-bound SecYEG complex in a Nanodisc.

Right: Switching of Dom34 between delivery by Hbs1 and recycling by ABCE1 (Rli1).

active ribosome-bound translocon. Furthermore, we visualized an intermediate of the No-go mRNA decay pathway, a Dom34-Hbs1 containing 80S ribosome, that suggested how such a stalled ribosome is primed for further mRNA processing. A structural analysis of eukaryotic and archaeal ribosome recycling complexes that engaged with the unique ATPase ABCE1 led to a proposal of a mechanistic model of highly conserved ribosome recycling.

FUTURE DIRECTIONS

In the future, we wish to further improve the resolution of our cryo-EM reconstructions towards 3-4 Å in order to build molecular models *ab initio*. We plan to solve structures of the more complex ribosomes from higher eukaryotes such as from fruit fly or humans. We will continue our efforts to visualize active translocons and co-translational membrane protein biogenesis by using small proteoliposomes and nanodiscs for single particle analysis. We will also extend our studies on ribosome recycling and coupled processes in eukaryotes, i.e. termination, initiation and in particular the different modes of ribosome- dependent mRNA decay pathways.

SELECTED PUBLICATIONS

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- Becker, T., Bhushan, S., Jarasch, A., Armache, J.P., Funes, S., Jossinet, F., Gumbart, J., Mielke, T., Berninghausen, O., et al. and **Beckmann, R.** (2009). Structure of monomeric yeast and mammalian Sec61 complexes interacting with the translating ribosome. Science *326*, 1369-373.
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AWARDS AND MEMBERSHIPS

- Elected member, EMBO, 2010
- Elected member, National Academy of Science, Leopoldina, 2010
- ERC Advanced Grant, 2012

KARL-KLAUS CONZELMANN

MOLECULAR BIOLOGY OF RNA VIRUSES

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1988	PhD, University of Tübingen
1989-1998	Post-Doc, PI, Provisional Director, Institute of Clinical Virology, Federal Research Center for Virus Diseases of Animals, Tübingen
1999-present	Professor, Gene Center and Max von Pettenkofer-Institute, LMU
since Oct 2012	Interim Chair of Virology, LMU

GOAL

To understand the molecular interplay of RNA viruses and the host cell system

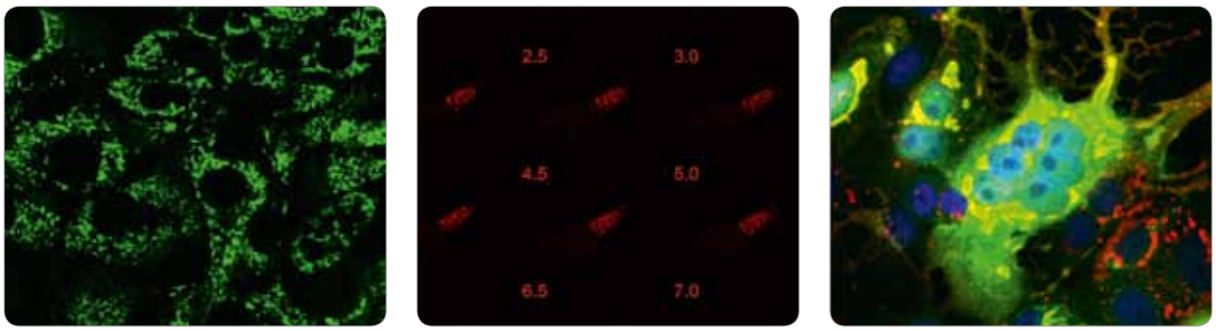
INTRODUCTION

Co-evolution with their hosts has made viruses experts in cell biology and biochemistry. They have found tricks to sneak into cells, switch off alarm systems, re-program cell gene expression, and transform cells into virus factories. We are studying negative strand RNA viruses *(Mononegavirales)* to learn how they exploit cellular machineries for virus replication and assembly, trick host innate immune defenses, and how newly emerging viruses can adapt to new host species. A key technology is the genetic engineering of these RNA viruses (reverse genetics) which was developed in our laboratory. Recombinant viruses with defined genetic changes are being used to reveal the contribution of individual virus proteins to virus-host cell interplay. This involves the full range of up-to-date cell biology and biochemistry methods. Knowledge of the mechanism involved not only tells us how cellular protein machineries and signaling networks function, but also provides means to re-program the viruses in order to use them as valuable biomedical tools.

RESEARCH HIGHLIGHTS

A major topic in the laboratory is the recognition of viruses by immune pattern receptors and the viral mechanisms counteracting cellular defense mechanisms. We have identified proteins of rhabdo- and paramyxoviruses that can switch off both production and effects of the antiviral interferons and of proinflammatory cytokines by targeting IRF, NF-kB, or STAT transcription factors. Engineering of these viral proteins renders viruses highly immunogenic and attenuated, making them promising live vaccine candidates.

Another major interest is to elucidate and exploit the molecular mechanisms of virus entry, intracellular trafficking, assembly and budding. Hallmarks of the neurotropic rabies virus are retrograde infection of neurons, and exclusive transmission via synapses. These traits make rabies an ideal vector for neurons and tracer of synaptic connections. We have previously engineered viruses which can only



Left: Recombinant rabies virus tracer staining mitochondria with autofluorescent GFP protein

Center: Live imaging of a fluorescent viral protein located in the nucleus of an infected cell

Right: Formation of cell syncytia after infection with measles virus (green)

spread from an initially infected neuron to directly connected (2nd order) neurons, but cannot be further transmitted. This first "mono-synaptic" viral tracing system ever is being used widely by neurobiologists to study the wiring of neuronal circuits. Within a collaborative research center (SFB 870 Neuronal Circuits) we are developing novel tracing and gene expression vectors for studies on neuronal connectivity and activity.

FUTURE DIRECTIONS

We aim to further learn from viruses how the network of cellular signaling pathways can be controlled and modified. Biochemical characterization of how viral antagonists interact with components of signaling pathways may lead to the development of substances for immune-stimulatory and -suppressive regimens, as well for antiviral therapies. Elucidating the details of rabies virus gene expression in neurons and trans-synaptic transmission greatly helps in uncovering the complexity of brain wiring and neuron function.

SELECTED PUBLICATIONS

- Motz C., Schuhmann K.M., Kirchhofer A., Moldt M., Witte G., **Conzelmann K.-K.**, Hopfner K.-P. Paramyxovirus V proteins disrupt the fold of the innate immune sensor MDA5 to inhibit antiviral interferon response. Science, in press.
- Sparrer K.M., Pfaller C.K., **Conzelmann K.-K.** (2012). Measles virus C protein interferes with beta interferon transcription in the nucleus. J Virol. 86(2):796-805.
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- Rieder M., **Conzelmann, K.-K.** (2011). Interferon in rabies virus infection. Adv Virus Res. 79:91-114.

AWARDS AND MEMBERSHIPS

- Member, Munich Center for Neurosciences – Brain & Mind (MCN) 2011-present
- Associated faculty Graduate School of Systemic Neuroscience (GSN) 2011-present

PATRICK CRAMER

GENE TRANSCRIPTION AND GENOMIC REGULATION

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1998	PhD from the European Molecular Biology Laboratory in Grenoble, France, and Heidelberg University, Germany
1999-2001	Postdoc at Stanford University, USA
2001-2003	Tenure-track Professor, Gene Center and Department of Biochemistry, LMU
2004-present	Professor and Director, Gene Center and Department of Biochemistry, LMU

GOAL

To determine the molecular mechanisms and systemic principles of gene transcription and its regulation in eukaryotic cells

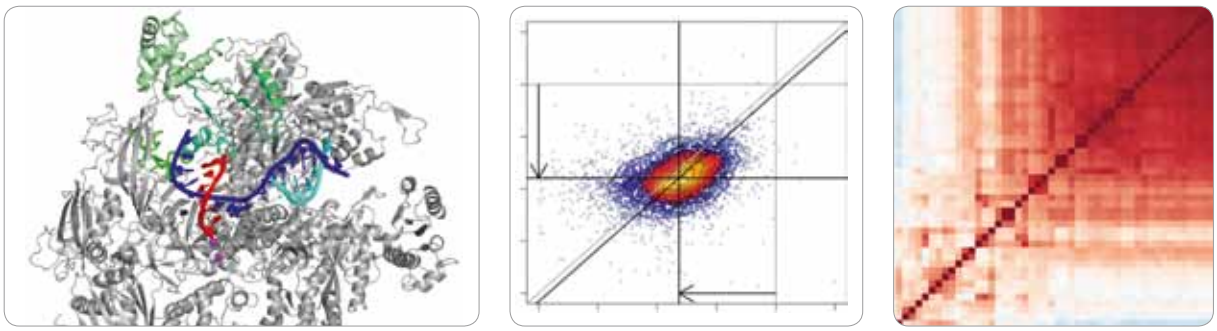
INTRODUCTION

Our research aims at understanding the molecular mechanisms of gene transcription and the cellular principles of genomic regulation. Regulated gene transcription governs organism development and cell differentiation, and its disregulation underlies diseases such as cancer. In eukaryotic cells, gene transcription is carried out by three related multisubunit enzymes, RNA polymerases I, II, and III, which produce mainly ribosomal, messenger, and transfer RNA, respectively. The polymerases transiently bind to many different protein factors for the initiation, elongation, termination and regulation of transcription. To elucidate transcription mechanisms we use various structural biology methods and complementary functional assays. To study the principles of gene regulation on a systems level in living cells we also develop functional genomics techniques and use computational biology methods. These two major efforts complement each other. Our work helps to develop the field of molecular systems biology which aims at an understanding of cellular behavior based on the underlying molecular mechanisms.

RESEARCH HIGHLIGHTS

Over the last few years, we have strongly advanced our understanding of transcription mechanisms by all three RNA polymerases. We found how the central initiation factor TFIIB bridges between the polymerase and a gene promoter and how it stimulates RNA synthesis (*Nature* 2009, 2012). We also located on the polymerase surface the initiation factor TFIIF (*EMBO J.* 2011), the elongation factor Spt4/5 (*EMBO J.* 2012), and the RNA product after polymerase backtracking and arrest (*Nature* 2011). Together with published data this information resulted in a first movie of Pol II transcription that captures key aspects of transcription initiation and elongation (*Cell* 2012).

Additional structural and functional studies showed that many aspect of transcription are conserved in the Pol I and Pol III systems (*Cell* 2010, *Mol. Cell*



Left: Structure of the initially transcribing RNA polymerase II (silver) with initiation factor TFIIB (green), DNA (blue) and RNA (red).

Center: Changes in mRNA metabolism of a eukaryotic cell upon mutation (each mRNA is represented by one dot).

Right: Correlation analysis of transcriptome profiles identifies genes that work together.

2011, *Genes Dev.* 2012, *Mol. Cell* 2012), but not in the mitochondrial transcription system (*Nature* 2011). Our long-standing analysis of the coactivator complex Mediator has now led to a breakthrough. We solved the structure of the essential Mediator head module, which resembles the head of a crocodile and serves as a starting point for analyzing gene regulation (*Nature* 2012).

To analyze the coordination of the transcription cycle in cells, we used genome-wide analysis. We characterized the transition from transcription initiation to elongation that occurs on all genes (*NSMB* 2010). We also found that a new polymerase modification is involved in the transition from transcription elongation to termination (*Science* 2012). Finally, we developed methods to globally monitor mRNA metabolism in eukaryotic cells (*Mol. Sys. Biol.* 2011). With the use of metabolic labeling, microarray analysis, and computational modeling, we uncovered a feedback loop between mRNA synthesis in the nucleus and mRNA degradation in the cytoplasm that can buffer mRNA levels in living cells (*Genome Res.* 2012).

FUTURE DIRECTIONS

We will continue our structural analysis of the RNA polymerase II transcription machinery and extend our initial molecular movie of transcription. A combination of X-ray crystallography, electron microscopy, crosslinking, and modeling will unravel the architecture of multicomponent transcription complexes. This work will be complemented by functional analysis in yeast and human cells, to elucidate the mechanisms underlying genomic regulation. Genome-wide crosslinking and immunoprecipitation will map protein-DNA and protein-RNA landscapes. Together with a systemic analysis of mRNA synthesis and degradation this will elucidate the principles of cellular mRNA metabolism.

SELECTED PUBLICATIONS

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- Lariviere, L., Plaschka, C., Seizl, M., Wenzeck, L., Kurth, F., and **Cramer, P.** (2012a). Structure of the Mediator head module. Nature 492, 448-451.
- Sainsbury, S., Niesser, J. and **Cramer P.** (2012b). Structure and function of the initially transcribing RNA polymerase II-TFIIB complex. Nature, published online November 14.

AWARDS AND MEMBERSHIPS

- Jung Prize for Medicine, 2009
- Familie Hansen Award of the Bayer Science and Education Foundation, 2009
- Member of the German Academy of Sciences Leopoldina, 2009
- Member of the European Molecular Biology Organization EMBO, 2009
- Medal of Honour of the Robert Koch Institute, 2010
- Member of the Max Planck Society, 2010
- Advanced Investigator of the European Research Council ERC, 2010
- Feldberg Foundation Prize, 2011
- Vallee Foundation Visiting Professorship, 2012
- Paula und Richard von Hertwig Prize, 2012
- Cross of Merit of the Federal Republic of Germany (Bundesverdienstkreuz), 2012

KLAUS FÖRSTEMANN

BIOLOGY OF mi/siRNA MEDIATED REGULATION

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2002	PhD from Swiss Cancer Research Institute (ISREC) and University of Lausanne
2002	Postdoc at ISREC in Lausanne, Switzerland
2003-2006	Postdoc at UMASS Medical School in Worcester, USA
2006-2011	Tenure-track Professor, Gene Center and Department of Biochemistry, LMU
2012-present	Professor, Gene Center and Department of Biochemistry, LMU

GOAL

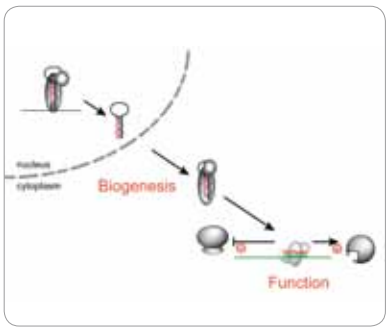
To examine small RNA-mediated regulation in organismic networks

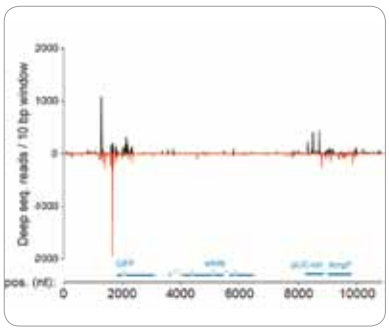
INTRODUCTION

Small RNAs have a profound impact on gene expression. In addition to controlling the stability and translation rate of mRNAs, they can also instruct and maintain specific chromatin structures, thereby affecting transcription rates as well. Developmental processes were among the first phenotypes ascribed to miRNA-mediated regulation, while siRNAs are likely to represent a defense pathway against foreign genetic material. This can be viruses or transposable elements, both of which need to be controlled efficiently to protect the genome. A common theme that emerges for all small RNAs is that they ensure robustness of the organism against environmental challenges. To this end, they implement thresholds in regulatory circuits, relay information between signaling cascades, sharpen decisions for e.g. cell-fate determination and contribute to epigenetic inheritance. We want to place the small RNA-mediated regulation into the biological context, ideally describing the input (= induction or activation of the small RNA) and the consequences in a quantitative manner. Of particular interest to us is how cells sense the need for small RNA regulation and how their deployment is achieved. We reconstruct key events in cultured cells to verify molecular mechanisms, but also try to test the hypotheses we derive *in vivo*.

RESEARCH HIGHLIGHTS

Starting out from the biochemistry of small RNA maturation, we identified a novel co-factor for *Drosophila* Dcr-2, one of the enzymes that process small RNA precursors during biogenesis. This co-factor, Loqs-D, is particularly important for the repression of selfish DNA by siRNAs in somatic cells. We could model transposon recognition and defense with reporter genes in cell culture, which allows for dissection of the necessary elements. This system helped to demonstrate that transposon defense does not require passage through germ line and allows us to decipher how foreign genetic elements are recognized by the host. We also discovered that a double-strand break in DNA triggers





Left: Biogenesis and function of small RNAs is at the heart of our research

Center: Eye-color pigments can be harnessed as an indicator of siRNA function

Right: Modern sequencing technologies allow the detection and interpretation of millions of small RNA sequences

the production of siRNAs if it occurs within a transcribed gene. This raises the question of how transcription, which is necessary to generate the small RNAs, is coordinated with the access of DNA repair enzymes that need to act on the same substrate. We established an assay system to determine direct and indirect regulatory targets for miRNAs by specifically measuring their influence on RNA decay and transcription rates. This technique has allowed us to describe post-transcriptional co-regulation of an entire metabolic cascade. This regulation affects lifespan in flies and may be helpful to understand human pathologies.

FUTURE DIRECTIONS

Regulatory events are best interpreted in the network context, a fascinating but complex endeavor. We will use biological paradigms, e.g. the induction of specific metabolic programs such as diapause, to acquire quantitative data on miRNA and mRNA expression as well as metabolite profiling. Our goal is to infer important regulatory network-motifs, then test them in cell culture reconstructions. Furthermore, we are analyzing the molecular mechanisms that generate siRNAs in transposon defense and in response to DNA double-strand breaks. Here we focus on the events that relay recognition of the damage to the production of siRNAs.

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› **Förstemann K.** (2010): Transposon defense in Drosophila somatic cells: A model for distinction of self and non-self in the genome. RNA Biol. 7, 158-161

› Hartig, J.V., **Förstemann, K.** (2011): Loqs-PD and R2D2 define independent pathways for RISC generation in Drosophila. Nucleic Acids Res. 39, 3836-3851

› Helfer S., Schott J., Stoecklin G. and **Förstemann K.** (2012): AU-rich Element Mediated mRNA Decay can occur independently of the miRNA machinery in Mouse Embryonic Fibroblasts and Drosophila S2-cells. PLoS One 7, e28907

› Dittmer A., **Förstemann K.** (2012): MCMV infection of cultured mouse cells induces expression of miR-7a. J Gen Virol. 93, 1537-1547

› Aumiller V.A., Graebsch A., Kremmer E., Niessing, D., **Förstemann K.** (2012): Drosophila Pur-α binds to trinucleotide-repeat containing cellular RNAs and translocates to the early oocyte. RNA Biol. 9, 633-643

› Michalik K., Böttcher R., **Förstemann K.** (2012): A small RNA response at DNA ends in Drosophila, Nucleic Acids Research 40, 9596-603

AWARDS AND MEMBERSHIPS

› Preis für gute Lehre 2012, Bay. Staatsministerium

JULIEN GAGNEUR

COMPUTATIONAL GENOMICS

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2004	PhD thesis from Ecole Centrale Paris, Paris
2005-2012	Staff scientist, European Molecular Biology Laboratory, Heidelberg
2012-present	Group Leader, Gene Center, LMU

GOAL

To quantitatively understand genetic and phenotypic variation on a genome-wide scale

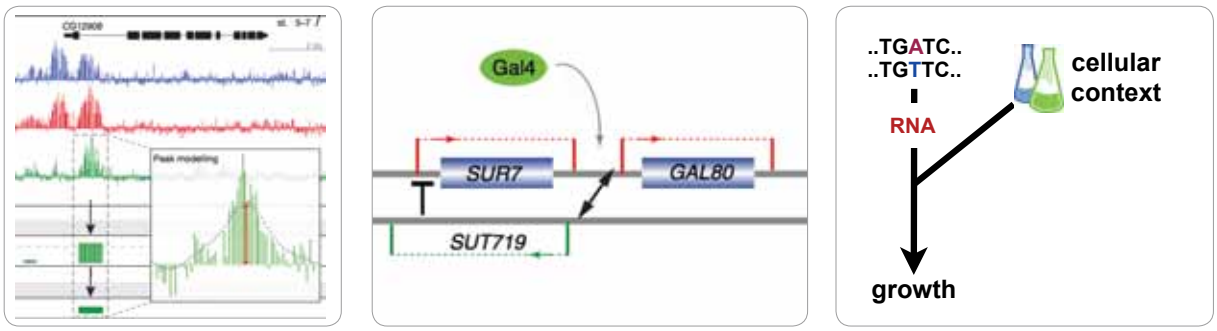
INTRODUCTION

Genomics technologies provide extremely rich datasets covering genome sequence variations, gene expression, as well as metabolic and proteomic quantifications. The challenge now lies in identifying mechanistic and causal relationships across these multiple levels.

We combine computational and experimental approaches to further understand genetic and phenotypic variation on a genome-wide scale. Our research is articulated along three axes: advancing our understanding of gene regulation through quantitative modeling; developing methods to study the mechanisms by which genetic variants condition phenotypes; and providing the community with computational methods for genomics research.

RESEARCH HIGHLIGHTS

Over the past few years we have worked on understanding gene regulation principles from genome-wide datasets. Our results include in yeast the first report of allele- and strand-specific expression genome-wide and the finding that promoters are typically bidirectional. We also developed predictive models of spatio-temporal enhancer expression patterns in the developing fly embryo. The predictions, confirmed experimentally, demonstrated a surprising plurality of transcription factor binding patterns on enhancers with similar expression profiles. More recently, we have turned our interest on functional characterization of non-coding RNAs. We found that expression of non-coding RNAs antisense to genes (a class that represents the majority of stable uncharacterized non-coding RNAs in yeast and affects more than a quarter of genes in humans) induces ultrasensitivity or threshold behavior on gene regulation.



Left: Pinpointing transcription factor binding sites from ChIP signal genome-wide (Zinzen et al., 2009)

Center: Antisense expression confers a switch-like regulation of sense gene expression (Xu et al., 2011)

Right: Defeating genetic defects: Bayesian model of genotype, environment, and phenotype

In combination with these efforts on deriving biological insights, we have also developed computational methods for genomics. Our most relevant contribution in the past few years in this field has been a method called Model-based Gene Set Analysis (MGSA). MGSA is a ayesian approach to gene set enrichment analysis that returns high-level and summarized views of biological processes enriched in a gene list and efficiently limits redundant and confounding enrichments.

FUTURE DIRECTIONS

In the future, we wish to derive mathematical models of the transcription machinery to quantify the contribution of its components and predict its dynamic behavior genome-wide. Along with our systems biology effort on transcription, we will develop systems genetics methodologies for unraveling the causal chain of molecular events linking naturally occurring genetic variations to phenotype by integrating multiple layers of genome-wide data from the DNA sequence up to organismal phenotypes. Medically relevant projects are particularly appealing to us. On both fronts we will tightly integrate mathematical modeling together with experimental approaches either done in our wet lab or through collaborations.

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- Xu Z.*, Wei W.*, **Gagneur J.**, Perocchi F., Clauder-Münster S., Camblong J., Guffanti E., Stutz F., Huber W., and Steinmetz L.M. (2009) Bidirectional promoters generate pervasive transcription in yeast. Nature, 457 (7232), 1033-7.
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MEMBERSHIPS

- Member, Graduate school of Quantitative Biosciences Munich (QBM)

ULRIKE GAUL

SYSTEMS BIOLOGY OF GENE REGULATION AND FUNCTION OF GLIA IN THE NERVOUS SYSTEM

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1988	PhD University of Tübingen
1989	Postdoc, University of Washington, Seattle, USA
1989-1993	Postdoc, University of California, Berkeley, USA
1993-2000	Assistant Professor, Rockefeller University, New York, USA
2000-2009	Associate Professor, Rockefeller University, New York, USA
2009-present	Alexander von Humboldt-Professor, Gene Center and Department of Biochemistry, LMU

GOAL

To achieve a systems-level understanding of gene regulation during animal development and to characterize the role of glia in the nervous system

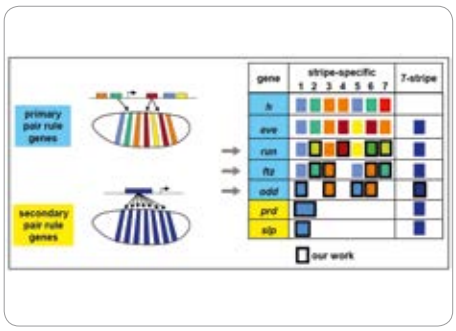
INTRODUCTION

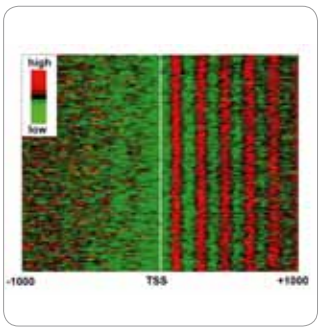
The establishment of complex spatio-temporal patterns of gene expression lies at the heart of animal development. Our lab has a long-standing interest in deciphering the underlying 'regulatory code', from the interaction between regulatory factors and DNA or RNA to their interplay in complex networks. Combining experimental and computational approaches, we seek to develop appropriate methods and concepts to analyze these processes at a systems level. Our previous work focused on the *Drosophila* segmentation gene network: We identified and characterized many unknown *cis*-regulatory elements and developed a novel thermodynamic model that predicts observed expression patterns as a function of *cis*-element sequence and of the affinity and distribution of participating transcription factors.

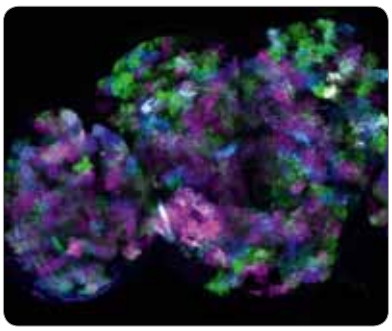
A second line of research in the lab focuses on the function of glial cells in nervous system development and homeostasis. Glia constitute the majority of cells in the CNS of all higher animals, but their contribution has long been neglected. We have discovered numerous novel glial genes, including a GPCR pathway involved in blood-brain barrier formation and a family of phagocytic receptors required for apoptotic clearance.

RESEARCH HIGHLIGHTS AND FUTURE DIRECTIONS

Since moving to the Gene Center in 2009, we have extended and deepened our research in several ways, with a focus on achieving higher throughput and on tracking key regulatory events at higher quantitative resolution. We established techniques to measure the binding affinity landscapes of relevant transcription factors, to map factor binding to DNA genome-wide, and to measure enhancer/promoter activity in high throughput. We completed a systems-level analysis of the key transition from non-periodic to periodic expression patterns within the segmentation network and began to inves-







Left: Transcriptional control of stripe formation in Drosophila segmentation

Center: Clustering of genes by nucleosome pattern around transcription start site (TSS)

Right: Multi-color mosaics of astrocytic glia in Drosophila adult brain.

tigate the regulatory role of nucleosomes, finding more complex occupancy patterns and correlations with genic features than previously thought. In addition, we have launched a major effort to dissect the *Drosophila* core promotor, using both genomic and large-scale synthetic biology approaches. The long-term goal of these studies is an integrated quantitative model of gene regulation that realistically captures the underlying molecular mechanisms.

In our glial studies, we completed a genome-wide RNAi screen for genes required in glia for the long-term survival of the animal, and embarked on a detailed molecular and genetic analysis of some of the 4,000 genes we identified. Two recently concluded studies push forward our investigation of the blood-brain barrier and pinpoint PKA as a key antagonistic effector of GPCR signaling. In a second large screen, we characterized all glial subtypes in the adult *Drosophila* brain. This work, together with other genetic tools we developed, will enable us to systematically assess the role of glia in brain homeostasis and neurodegeneration.

Aside from our own research, we have worked to strengthen the environment for systems biological research in Munich. At the Gene Center, we set up or improved key instrumentation facilities (bioimaging, robotics, FACS, deep sequencing). We contributed to important initiatives such as the new research building BioSysM and took the lead in establishing the new Graduate School of Quantitative Biosciences Munich.

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- Iovino, N., Pane, A., and **Gaul, U.** (2009). miR-184 has multiple roles in *Drosophila* female germline development. Dev Cell 17, 123-133.
- Schroeder, M., Greer, C., and **Gaul, U.** (2011). How to make stripes - deciphering the transition from non-periodic to periodic patterns in *Drosophila* segmentation. Development 138, 3067-3078.

AWARDS AND MEMBERSHIPS

- Alexander von Humboldt-Professor, 2009
- Visiting Scientist, Janelia Farm Research Campus, HHMI, Ashburn, 2009-11
- Member, Strategy committee, LMU Munich, 2009-present
- Member, Center for Advanced Studies (CAS), LMU Munich, 2009-present
- Member, DFG Excellence Cluster "Center for Integrated Protein Science Munich", 2009-present
- Member, International Max-Planck-Research School "From Biology to Medicine", Munich, 2009-present
- Member, Center for NanoScience Munich (CeNS), 2009-present
- Elected Member, European Molecular Biology Organization (EMBO), 2012-present
- Speaker, Graduate School of Quantitative Biosciences Munich (QBM), 2012-present

MARIO HALIC

RNAi AND HETEROCHROMATIN FORMATION

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2005	PhD from Humboldt University in Berlin, Germany
2005 - 2007	Postdoc at Humboldt University in Berlin and Gene Center in Munich, Germany
2007 - 2011	Postdoc at Harvard University in Boston, USA
2011 - present	Tenure-track Professor, Gene Center and Department of Biochemistry, LMU

GOAL

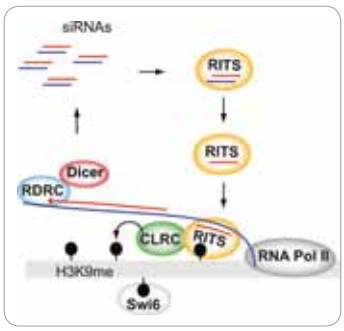
To determine the molecular mechanisms of small RNA mediated heterochromatin formation

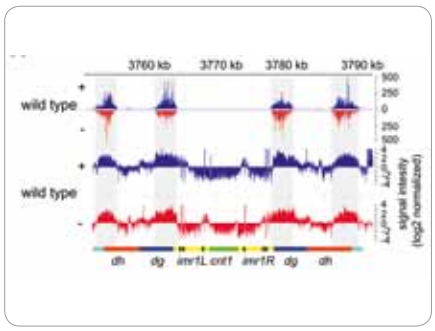
INTRODUCTION

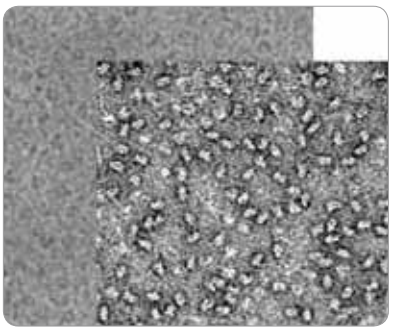
Our research group is interested in small RNA mediated silencing pathways. Small RNAs are involved in the cellular control of gene expression and in the protection of the genome against mobile repetitive DNA sequences, retroelements and transposons. In the fission yeast *Schizosaccharomyces pombe* small RNAs are required for formation of centromeric heterochromatin, for deposition of centromere specific nucleosomes and proper chromosome segregation. Small interfering RNAs (siRNAs) are generated by enzyme Dicer from double-stranded RNA (dsRNA) and loaded onto Argonaute protein. siRNAs direct the inactivation of target RNAs by guiding the Argonaute complex (RITS) to complementary target sequences. At the target RNA RITS recruits two complexes to amplify siRNAs and induce heterochromatin formation. First, RNA-dependent RNA polymerase complex (RDRC) will be recruited to centromeric transcripts to synthesize new dsRNAs that will be processed by Dicer into siRNAs. Second, RITS complex recruits the histone 3 lysine 9 (H3K9) methyltransferase complex CLRC to centromeric chromatin (Figure 1). CLRC methylates H3K9 on neighboring nucleosomes which leads to recruitment of heterochromatin protein HP1 and to heterochromatin formation. Efficient silencing of pericentromeric repeats in fission yeast requires both RNAi and heterochromatin.

RESEARCH HIGHLIGHTS

We sequenced Argonaute-associated small RNAs in various fission yeast mutant strains (Figure 2). Small RNA profiling showed that generation of a subclass of siRNAs occurred independently of H3K9 methylation and HP1 protein indicating that heterochromatin is not essential for siRNA generation and that siRNAs precede and guide heterochromatin formation in fission yeast. Furthermore, Argonaute slicer activity was essential for generation of first siRNAs suggesting that Argonaute-associated small RNAs guide RNAi to centromeric transcripts to synthesize first dsRNA and first siRNAs. We have uncovered a distinct class of







Left: Model of small RNA mediated heterochromatin formation in fission yeast

Center: Small RNA and transcription profile showing centromeric region in fission yeast

Right: Negative stain and cryo EM images of nucleosomes.

small RNAs called primal small RNAs (priRNAs) which are generated independently of RNAi machinery and could guide Argonaute to centromeric transcripts to initiate silencing and heterochromatin formation. The basis of this specificity lies in the prevalence of bidirectional transcription within centromeric repeats, which generates both sense and antisense priRNAs. Once antisense priRNAs initiate siRNA generation, RNAi machinery will target centromeric transcripts to induce heterochromatin formation. Our results suggest that a transcriptome surveillance mechanism based on the random association of small RNAs with Argonaute triggers RNAi-mediated heterochromatin formation within DNA repeats.

FUTURE DIRECTIONS

In the future, we wish to determine how cells recognize foreign genetic elements and initiate their silencing. Our results suggest that transcription patterns and priRNAs might be involved in initial recognition of transposable and repetitive elements. In our work we use genetic, biochemical and systemic approaches to determine how small RNAs recognize specific genetic elements to induce chromatin modifications. We are also interested in structural characterization of complexes involved in RNAi and chromatin mediated silencing.

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- **Halic M** and Moazed D. (2010) Dicer-Independent priRNAs and Argonaute Trigger RNAi and Heterochromatin Formation. Cell. 140, 504-516
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- **Halic M**, Moazed D. (2009) 22G-RNAs in transposon silencing and centromere function. Mol Cell. 36, 170-1.
- **Halic M**, Moazed D. (2009) Transposon silencing by piRNAs. Cell. 138, 1058-60.

AWARDS AND MEMBERSHIPS

- ERC Starting Grant, 2012
- Charles King Trust Postdoctoral fellowship, 2010-2011
- EMBO Postdoctoral fellowship, 2007-2009

FRANZ HERZOG

BIOLOGICAL MASS SPECTROMETRY

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2006	PhD from the Research Institute of Molecular Pathology and University of Vienna, Austria.
2007	Postdoc at the Research Institute of Molecular Pathology, Vienna.
2008-2012	Postdoc at the Swiss Federal Institute of Technology, Zurich, Switzerland.
since 2012	Group Leader, Gene Center, LMU

GOAL

To investigate the architecture and regulated assembly of cellular protein structures, we establish structural and quantitative mass spectrometric approaches.

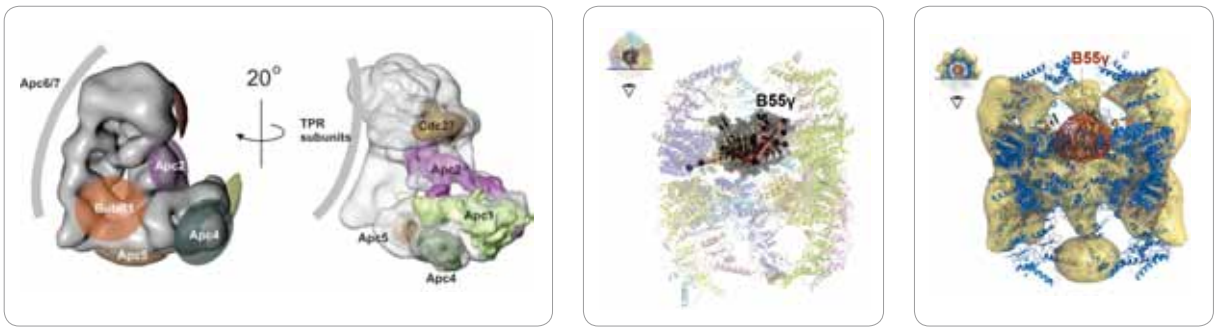
INTRODUCTION

Cellular processes can rarely be attributed to the activity of a single protein. Instead, proteins act in functional modules, such as signal transduction pathways or macromolecular complexes. Understanding how proteins cooperate to achieve the specific function of a multi-subunit complex requires its structural elucidation. In rare cases, the structures of macromolecular protein complexes like the ribosome or RNA polymerase II were solved by x-ray crystallography as they could be isolated as stable and homogeneous particles.

Chemical labeling of surface-exposed reactive groups has been applied as a complementary structural method for decades. Recent advances in mass spectrometric instrumentation and bioinformatic analysis tools facilitate the identification of spatially proximate amino acid residues that are cross-linked by a bi-functional reagent. The combination of chemical cross-linking and mass spectrometry provides distance information based on the length of the cross-linker. So called hybrid structural biology approaches apply these distance restraints to integrate high resolution subunit structures and low resolution density maps of the holo complex to elucidate its domain architecture. We showed that in contrast to high resolution structural biology techniques, cross-linking together with mass spectrometry has the potential to acquire spatial restraints from heterogeneous protein samples revealing the topology of protein complexes in a signaling network.

RESEARCH HIGHLIGHTS

Since my PhD work in the lab of Jan-Michael Peters I have been fascinated by the intricate regulatory mechanisms that precisely control the timing of mitosis in order to achieve faithful chromosome segregation. We investigated how proteins of the spindle checkpoint inhibit the ubiquitin-protein ligase activity of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is essential for the or-



Left: Subunit architecture of the APC/C interacting with the checkpoint protein, BubR1, using electron microscopy and subunit labeling

Center: Topology of the human TRiC chaperonin in complex with the PP2A subunit B55γ based on cross-links

Right: Topology of the human TRiC chaperonin in complex with the PP2A subunit B55γ using electron microscopy

dered proteolysis of cell cycle regulators. We revealed that inhibition is achieved by a significant reduction in substrate binding and electron microscopic studies indicated that checkpoint proteins inhibit APC/C by blocking the substrate acceptor site and by displacing its coactivator Cdc20.

As the solution to pathbreaking biological problems often depends on innovative technologies, I joined the lab of Ruedi Aebersold where I developed a mass spectrometric approach to probe the topology of protein complexes. Combining chemical cross-linking and mass spectrometry facilitated the structural analysis of modular protein phosphatase 2A (PP2A) complexes which unveiled the interaction with a multitude of adaptor proteins that control PP2A's activity and cellular localization. The cross-link derived spatial restraints guided molecular modeling of the topology of a TRiC chaperonin bound to its substrate B55γ and provided a structural model for the recruitment of the PP2A inhibitor SET to the active site of the phosphatase by shugoshin.

FUTURE DIRECTIONS

In the future, we will exploit the potential of chemical cross-linking and mass spectrometry to elucidate the protein architecture of macromolecular complexes and organelles that can be isolated from their cellular context. We are specifically interested in the large protein structure of the kinetochore that provides a structural framework for the segregation of sister chromatids along the mitotic spindle. Structural analysis of endogenous kinetochore complexes will help to understand its role as central integration site for feedback regulatory mechanisms that ensure faithful chromosome segregation. Defects in this process can lead to aneuploidy, which is associated with tumorigenesis, congenital trisomies, and aging.

SELECTED PUBLICATIONS

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AWARDS AND MEMBERSHIPS

- EMBO Long-term Fellowship, 2009
- Marie Curie Fellowship, 2010-2011

KARL-PETER HOPFNER

STRUCTURAL GENOME BIOLOGY

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1997	PhD Max-Planck-Institute for Biochemistry and Technical University Munich
1998-2001	Postdoc at The Scripps Research Institute, USA
2001-2005	Tenure-track Professor, Gene Center, LMU
2005-present	Professor, Gene Center and Department of Biochemistry, LMU

GOAL

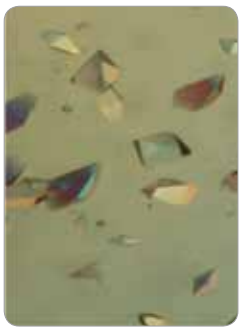
To understand how cells maintain their genome and distinguish self from non-self.

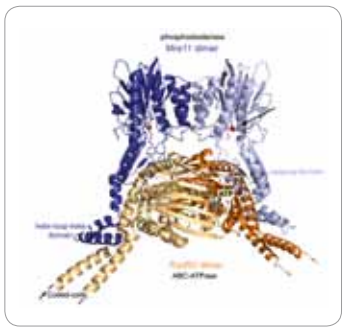
INTRODUCTION

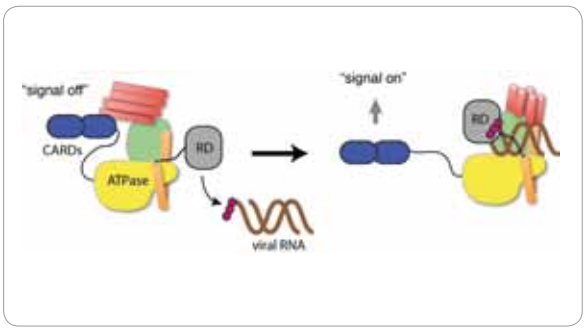
All cells must maintain the integrity of the genome and respond to threats by damaged or pathogenic nucleic acids. Cells possess complex, highly specific protein machineries that sense and signal the presence of damaged chromosomes or foreign nucleic acids and trigger appropriate host responses. For instance, DNA double-strand breaks trigger complex signaling cascades and response mechanisms that lead to cell either restoration of the genomic and epigenomic information, or alternatively apoptosis to prevent formation of oncogenic chromosomal aberrations. Inactivation of the cellular response to DNA double-strand breaks is intimately linked to familial and sporadic cancer susceptibility while the inhibition of these pathways is a promising route to selectively kill cancer cells. Cytoplasmic viral RNA and DNA are likewise recognized and induce cellular responses such as interferon or inflammation. We combine structural biology methods with in vitro biochemical and cell-based approaches to reveal how non-self (damaged and foreign) nucleic acids are sensed and distinguished from normal cellular RNA and DNA. Detailed mechanistic insights into these processes provide e.g. an understanding of the molecular pathology of cancer associated with DNA double-strand breaks and genome aberrations.

RESEARCH HIGHLIGHTS

In the past few years, we have had several breakthroughs on the structural mechanism of molecular machines implicated in genome maintenance and host defense. We could determine structures of the Mre11-Rad50-Nbs1 DNA double-strand break sensor, show by structural biology hybrid methods that it forms an ATP-dependent molecular clamp at DNA double-strand breaks and reveal the molecular pathology associated with cancer susceptibility mutations in Mre11. Collaborative X-ray crystallography and electron microscopy work enabled us to determine the first structure of a Swi2/Snf2 remodeler bound to a protein substrate and we could formulate a model how these ATP-dependent DNA trans-







Left: Protein crystals

Center: Crystal structure of the Mre11-Rad50 DNA damage sensor

Right: Model for viral RNA sensing by the innate immune receptor RIG-I.

locases remodel protein-nucleic acid complexes in genome biology. With respect to sensing for viral RNA, we could determine several high-resolution structures of RIG-I like RNA sensors (RIG-I, MDA5 and LGP2) and show by collaborative single-molecule studies that RIG-I is an ATP-driven translocase on dsRNA activated by 5′ triphosphates on RNA. These results showed that RIG-I integrates two distinct molecular patterns associated with viral RNA to elicit a sensitive yet robust and failsafe host response. All in all, in the past few years we have made several critical advancements regarding the basal structure and mechanism of sensors for damaged and non-self nucleic acids.

FUTURE DIRECTIONS

In the future, we want to specifically address how recognition of damaged and pathogenic nucleic acids results in the formation of active signaling complexes. This goal will require an integrated structural and functional approach and developments towards the analysis of transient and regulated macromolecular assemblies. To this end, we particularly implement and improve hybrid approaches through the combination of high resolution X-ray crystallography with electron microscopy and high-resolution mass spectrometry. The structural studies will be combined with functional in vitro and in vivo approaches to obtain a detailed mechanistic understanding of how cells distinguish self from non-self.

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AWARDS AND MEMBERSHIPS

- Elected EMBO Member, 2010
- m4 Award for personalized Medicine, 2011
- ERC Advanced Grant, 2012

CHRISTOPH KLEIN

MONOGENETIC DISORDERS OF THE BLOOD AND IMMUNE SYSTEM – DEVELOPMENTAL BIOLOGY AND NOVEL THERAPIES

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1991	MD from University Ulm
2000	PhD from Université Paris V and Institut Pasteur, Paris
1995-2000	Fellow and Instructor, Harvard Medical School, Boston
2000-2008	Associate Professor, MHH, Hanover
2008-2011	Professor and Chair, Department of Ped. Hem/Onc, MHH
2011-present	Professor and Chair, Department of Pediatrics, LMU

GOAL

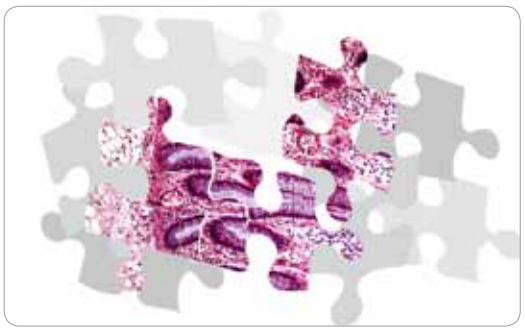
To delineate the molecular pathophysiology of monogenetic human diseases and to develop novel therapeutic strategies

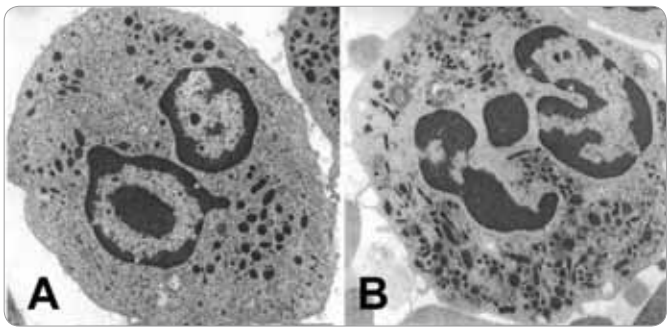
INTRODUCTION

Our research group is interested in defining molecular mechanisms governing development and function of the blood and immune system. We look at the "human model" to highlight relevant pathways controlling differentiation and function of immune cells. Our investigations start with children suffering from rare diseases. We try to unravel mechanisms of disease by discovering underlying genetic mutations, generating appropriate in vitro and/or in vivo models and to develop novel therapeutic strategies such as stem cell gene therapy.

RESEARCH HIGHLIGHTS

Over the last few years, we have established a global network of clinical and scientific collaborators sharing our mission. We have discovered several new human diseases and have identified underlying genetic defects. Our work on G6PC6 deficiency has highlighted a central role of glucose metabolism on viability of neutrophil granulocytes. Our discovery of children with mutations in the IL10-receptor genes has not only determined the central role of IL10 for immune homeostasis in the human gut but also opened up new therapeutic strategies in selected patients with severe and refractory inflammatory bowel diseases. With respect to hematopoietic stem cell gene therapy, our group was the first to study the use of gene transfer to cure children with Wiskott-Aldrich Syndrome, a rare primary immunodeficiency caused by defective rearrangement of the actin cytoskeleton.





Left: Like pieces of a puzzle each novel human genetic defect causing inflammatory bowel disease tells us more about the complex immunoregulation in the human intestinal system

Right: Transmission electron microscopy of neutrophil granulocytes reveal abnormal granules in patients (B) in comparison to healthy individuals (A).

FUTURE DIRECTIONS

In the future, we wish to continue our scientific journey building bridges between clinical medicine and science. We follow our mission to unravel molecular mechanisms of disease and to design innovative therapies for children with life-threatening disorders. We expand our focus to study the immune-pathophysiology of intestinal and pulmonary diseases and to develop new computational tools for genomic medicine. We employ novel genome-engineering tools using designer-nucleases and study new disease-relevant pathways in human cells. Animal models based on mice and zebrafish are being studied in collaboration with expert laboratories.

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AWARDS AND MEMBERSHIPS

- Gottfried-Wilhelm-Leibniz Prize, 2010
- Eva Luise Köhler Prize, 2011
- Paul Martini Award, 2011
- William-Dameshek Prize 2011
- ERC Advanced Grant, 2011

FABIANA PEROCCHI

FUNCTIONAL GENOMICS OF MITOCHONDRIAL PHYSIOLOGY AND PATHOPHYSIOLOGY

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2007	PhD from European Molecular Biology Laboratory in Heidelberg and Heidelberg University
2008-2011	Postdoc at Harvard Medical School and Massachusetts General Hospital, USA
2011-2012	Postdoc at the Centre for Genomic Regulation in Barcelona, Spain
2012-present	Group Leader, Gene Center, LMU

GOAL

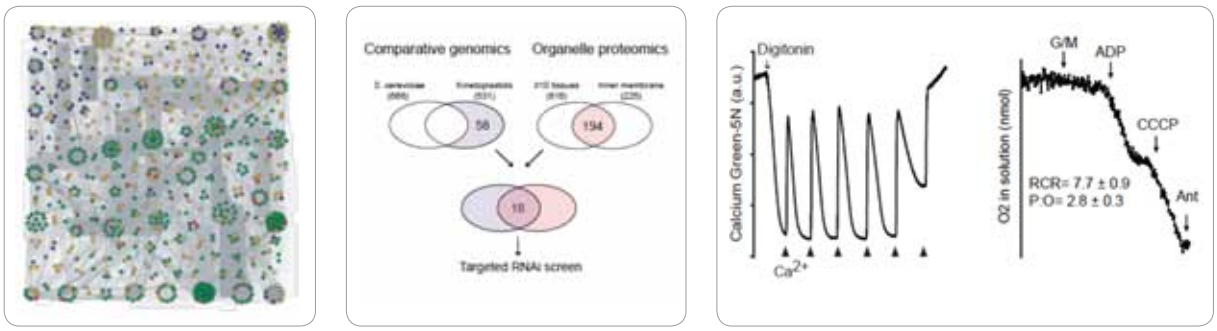
To identify, characterize and target the molecular components of signaling networks in human mitochondria.

INTRODUCTION

Our research group is interested in understanding the molecular basis of mitochondrial function in human physiology and pathophysiology. Mitochondria are double membrane organelles found in virtually all eukaryotic cells and are central to energy production, ion homeostasis, intermediary metabolism, and cell death. Inherited defects in mitochondria cause the most common inborn errors of metabolism, but a growing body of evidence links them to virtually all age-associated diseases, ranging from diabetes and cancer to neurodegeneration. Human mitochondria contain a tiny genome encoding 13 well-studied proteins, while all the remaining estimated 1,500 mitochondrial proteins are encoded from nuclear genes, translated in the cytosol, targeted and imported into the organelle. As a consequence of the dual genetic origin of mitochondrial proteins, mitochondrial biogenesis and function require a robust coordination between cellular and mitochondrial machineries. Bi-directional signaling exists between mitochondria and other cellular components that regulate the dynamic and complex remodeling of mitochondrial shape, motility, metabolism, and proteome in response to environmental stimuli and energetic requirements during growth and development. However, in many instances, the molecular links between intracellular signals and mitochondrial responses remain unknown. What are the mitochondrial proteins that sense, modulate, and propagate intracellular signals? How is the mitochondrial signaling "toolkit" regulated? How do mitochondria integrate into signal transduction cascades? What happens when mitochondrial signaling networks are compromised and how can we prevent deleterious effects?

RESEARCH HIGHLIGHTS

Over the last few years, we have applied integrative strategies that blend systems-level approaches with genetic, biochemical, and physiological studies toward major unsolved problems in mitochondrial biology. One such question is how calcium enters into mitochondria. Mitochondrial calcium import has been shown to regulate key processes



Left: Functional network of yeast mitochondria

Center: Integrative approach to predict human mitochondrial proteins involved in mitochondrial calcium uptake

Right: Mitochondrial Physiology

including ATP synthesis, cell death, and signal transduction. The basic mechanisms have been firmly established for decades, since their first discovery in the 1960s and 1970s, but the molecular identity of the calcium channel, the so-called uniporter, has remained a mystery. We cracked open this mystery integrating clues from comparative physiology, evolutionary biology, and organelle proteomics. We observed that the biophysical properties of mitochondrial calcium uniporter activity are evolutionarily conserved in vertebrates and in kinetoplastids, yet not measurable in the yeast S. *cerevisiae*. Human genes encoding for the uniporter should therefore share this unique evolutionary profile. Of a proteomic inventory of 1,098 human mitochondrial proteins, only 58 proteins were conserved in all sequenced vertebrates and in kinetoplastids, but absent in budding yeast. Using RNAi, we discovered two proteins that we showed represent the pore and regulatory subunits of the uniporter. These studies – published in *Nature* in 2010 and 2011 – now for the first time offer a genetic tool to characterize the role of mitochondrial calcium signaling in human pathophysiology and a potential pharmacological target in numerous calcium-related disorders.

FUTURE DIRECTIONS

The long-term goal of our laboratory is to achieve a systems-level understanding of human mitochondria to advance basic and disease biology. To achieve this goal, we combine large-scale, computational and experimental strategies with focused genetic, biochemical, and physiological studies of mitochondrial functions in fungi, mouse, and human cells. Computational strategies and loss-of-function genetic and chemical screens will be developed to predict, test, and reverse the effects of genetic and environmental perturbations on mitochondrial calcium signaling and to spotlight key signaling checkpoints that could be targeted pharmacologically. Comprehensive and quantitative measurements of metabolites, proteins, and their post-translational modifications will be performed to decipher the mitochondrial calcium footprint on cell metabolism and protein regulation. In light of the fundamental roles of calcium signaling in development, learning, metabolism, and neuromuscular function and the ability of mitochondria from virtually all tissues to regulate calcium homeostasis, we hope our research will have implications for understanding the pathological mechanisms of several human disorders.

SELECTED PUBLICATIONS

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- Xu, Z., Wie, W., Gagneur, J., **Perocchi, F.**, Clauder-Münster, S., Camblong, J., Guffanti, E., Stutz, F., Huber, W., Steinmetz, L.M. (2009). Bidirectional promoters generate pervasive transcription in yeast. Nature 457, 1033-7.

AWARDS AND MEMBERSHIPS

- Mass General Hospital Partners in Excellence Award for outstanding performance and commitment to excellence, 2010
- Mass General Hospital Martin Prize for an outstanding published article in Basic Research, 2010
- FEBS Return-to-Europe Fellowship, 2011
- Bavarian Molecular Biosystems Research Network Grant, 2012
- Emmy Noether Research Grant, 2012

JOHANNES SÖDING

COMPUTATIONAL GENOME AND PROTEIN BIOLOGY

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1996	Ph.D. in Physics at the Max Planck Institute for Nuclear Physics in Heidelberg
1997 -1998	Postdoc at the École Normale Supérieure in Paris
1999-2002	Management Consultant, Boston Consulting Group
2002-2007	Staff scientist, Max Planck Institute for Developmental Biology in Tübingen
Since 2007	Group Leader, Gene Center and Department of Biochemistry, LMU

GOAL

To develop the standard tools of tomorrow for protein sequence searching, structure and function prediction and to derive quantitative predictive models for transcriptional regulation and transcriptional networks using statistical modeling approaches.

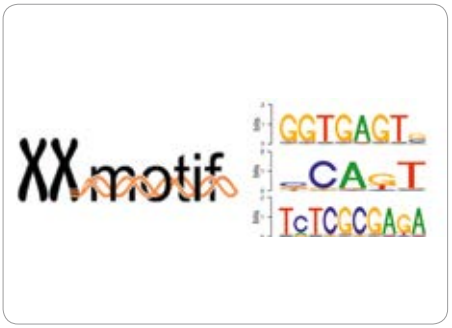
INTRODUCTION

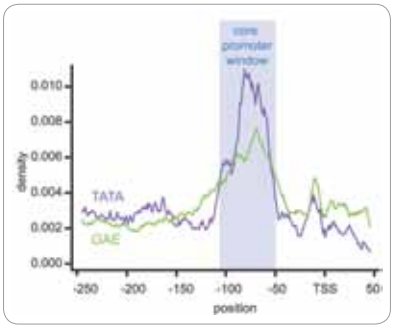
We are interested in two broad areas of research. First, we develop computational methods for predicting the structure, function, and evolution of proteins from sequence. We develop statistical methods that enable us to make use of the vast amount of sequence information that is becoming available at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

We develop and employ machine learning, statistical, and algorithmic methods, both to create tools for the wider biological community, and to investigate biological questions in the above areas.

RESEARCH HIGHLIGHTS

Two key innovations have allowed us to considerably improve the performance of protein sequence search methods and hence the prediction of protein structure and functions. First, by utilizing the local sequence context (13 residues) around each amino acid we can better predict the amino acids likely to be found at homologous positions in related proteins (Biegert et al., PNAS 2009). Second, we have developed an iterative sequence search method that represents both query and database proteins by profile hidden Markov models (HMMs). Thus, pairwise comparison of sequences is replaced by pairwise comparison of profile HMMs. Our result-





Left: The galaxy of folds, a 2D map of homology relationships between protein structural folds.

Center: Our de-novo motif discovery method XXmotif can find rare and weak motifs.

Right: The yeast GAE box is a new core promoter element.

ing software HH-suite is faster, more sensitive and more accurate than the widely used BLAST and PSI-BLAST programs (Remmert et al., Nat. Methods 2011). In the last community-wide blind benchmark, Critical Assessment of Techniques for Protein Structure Prediction (CASP9), our server HHpred produced the most accurate 3D homology models on average while being over 50 times faster than the other top 10 servers.

We also developed a method (XXmotif) for the de-novo discovery of motifs enriched in a set of nucleotide sequences, such as binding motifs of protein factors in sequences returned by ChIP-seq or DNase I hypersensitivity experiments. We devised a very fast way to calculate enrichment P-values that allows us to optimize the enrichment P-value of PWMs instead of their likelihood, as other methods do (Hartmann et al., Genome Res. 2012). Using this method, we analyzed core promoters and could show at the example of D*rosophila melanogaster* that core promoters can be considered to be mixtures of four classes with distinct sets of motifs, typical nucleotide positioning, and in particular distinct regulatory properties such as basal transcription rate, degree of regulation, and maximum strength.

FUTURE DIRECTIONS

We will pursue two broad goals. First, we aim to develop the standard tools for protein structure and function prediction. We are going to devise machine learning approaches to exploit subtle conserved sequence patterns, to score alignments nonlinearly, to predict protein structures de-novo using the inference of causal links between residues, and to reorganize and annotate the protein universe based on their structural and functional domains.

Second, we want to decipher the cis-regulatory code of transcriptional regulation, by developing quantitative models that are able to predict the transcriptional output of a gene given its cis-regulatory sequences and the concentrations of regulatory factors that bind them. This will include modeling the cross-talk between chromatin states, chromatin modifiers, and activators and repressors. In close collaboration with experimentalists we will analyze high-throughput quantitative measurements for large libraries of synthetic or native regulatory elements.

SELECTED PUBLICATIONS

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- **Söding J.** and Remmert M. (2011) Protein sequence comparison and fold recognition: progress and good-practice benchmarking. Curr. Opin. Struct. Biol. 21, 404-411.
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- Alva V., Remmert M., Biegert A., Lupas A. N., and **Söding J.** (2010) A galaxy of folds. Protein Sci. 19, 124-130.
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AWARDS AND MEMBERSHIPS

- Best template-based modeling server in the 9'th community-wide protein structure prediction competition "Critical Assessment of techniques for protein Structure Prediction" (CASP9)
- Member of the International Society for Computational Biology (ISCB)

KATJA STRÄßER

POST-TRANSCRIPTIONAL GENE REGULATION

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2001	PhD from Heidelberg University
2001-2003	Postdoc at Heidelberg University
2003-present	Group Leader, Gene Center, LMU

GOAL

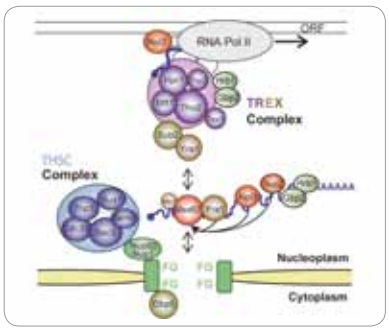
To determine the intricate network of gene expression in eukaryotic cells on a molecular as well as a systems level with a focus on transcription and mRNA export.

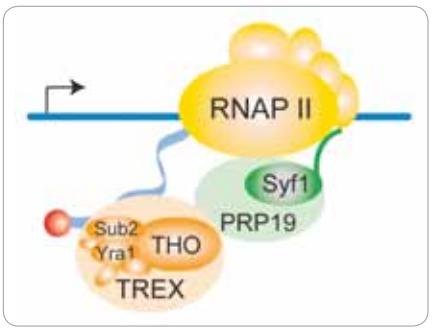
INTRODUCTION

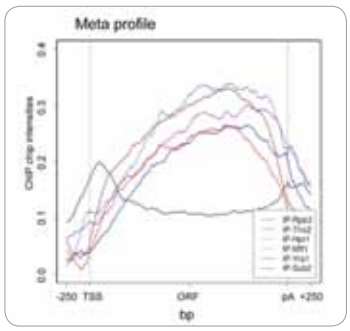
In eukaryotic cells, the messenger RNA (mRNA) is synthesized by RNA polymerase II during transcription, processed, packaged into a messenger ribonucleoprotein (mRNP) by RNA-binding proteins and exported from the nucleus to the cytoplasm. Here, the ribosomes decode the information contained in the mRNA and synthesize a protein in a process called translation. My group focuses on the formation of mRNPs. To do this we determine, for example, the recruitment of mRNA-binding proteins during transcription on a genome-wide level and the requirements of different mRNA-binding proteins on a transcriptom-wide level. In addition, we unravel the molecular function of these mRNA binding proteins. A second focus in the lab is the control of translation. Translation is highly regulated; however, the function of phosphorylation sites on ribosomal proteins is only poorly understood. Thus, we aim to elucidate the functions of ribosomal phosphorylation sites, recently identified by us, in translation.

RESEARCH HIGHLIGHTS

TREX is a large protein complex coupling transcription to nuclear mRNA export and necessary for mRNP formation. We answered the long-standing question how TREX is recruited to the transcription machinery. First, Prp19C, a complex known for its function in splicing, is required to keep TREX at genes. Thus, we identified the first factor necessary for TREX occupancy at transcribed genes, but also a novel transcription elongation factor. In addition, using a genome-wide approach we showed that TREX is recruited to all transcribed genes and that TREX occupancy increases with the length of the gene, *i.e.* during transcription elongation. We show that this is due to phosphorylation of the CTD, a "landing platform" on RNA polymerase II. Sro9, another mRNA-binding protein, is also recruited to the mRNP during transcription and shuttles with the mRNA to the cytoplasm for its function







Left: Proteins and protein complexes involved in transcription and mRNA export in *S. cerevisiae*

Center: Function of the protein complex Prp19C in recruiting TREX to genes

Right: Transcription profiles of TREX components and RNAPII (Rpb3)

in translation. A second major research focus of the lab is the regulation of translation by phosphorylation of ribosomal proteins. We identified about 300 phosphorylation sites on ribosomal proteins and now aim to unravel their biological function. Importantly, we already showed for two ribosomal phosphorylation sites that they are needed for two different steps in translation initiation.

FUTURE DIRECTIONS

In the future, we aim to elucidate the intricate network of mRNP proteins at a systems level. To do this we will apply systems approaches combined with genetics, biochemistry, and cell biology. While *S. cerevisiae*, amenable to many techniques, but also simpler and thus easier to study at a systems level, will remain our main model organism, we will extend our research to mammalian cells. In addition, we will pursue our novel project to unravel the function of translation by phosphorylation of ribosomal proteins adding a novel paradigm for the regulation of this fundamental cellular process.

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AWARDS AND MEMBERSHIPS

- ERC Starting Grant, 2008-2012
- Therese von Bayern-Preis, 2009
- Medaille für besondere Verdienste um Bayern in einem Vereinten Europa", 2009
- Member of the Young Center of Advanced Studies (CASY), LMU, 2010-present

PETRA WENDLER

PROTEIN REMODELING AND AAA+ ASSEMBLIES

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2004	PhD at Humboldt University Berlin
2004-2009	Postdoc at Birkbeck College London, UK
2009-present	Emmy-Noether Group Leader, Gene Center, LMU

GOAL

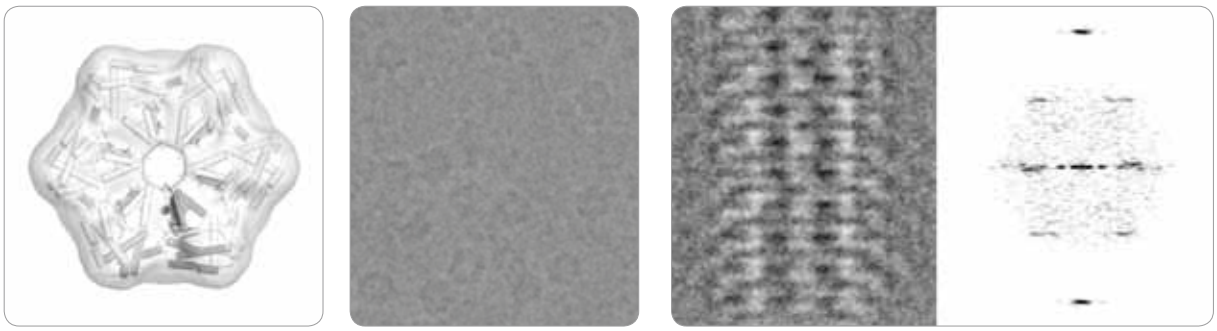
To understand the mechanism by which AAA+ ATPases exert force on protein substrates during various protein remodeling events

INTRODUCTION

During my academic career in engineering, biochemistry and structural biology I have developed a strong interest in molecular machines, particularly in the mechanisms and regulation of members of the ubiquitous AAA+ (ATPases associated with various cellular activities) family. AAA+ proteins form one of the largest superfamilies and are at the core of many essential multi-protein assemblies involved in re-organisation and recycling processes of proteins, membranes or DNA in the cell. Despite a great number of known three-dimensional structures obtained by X-ray crystallography, a structural view on the conformational dynamics of these fascinating molecular machines is still missing. Cryo-electron microscopy (EM) is an essential tool for visualizing assemblies of this complexity, size and dynamic properties in their different physiological states. We aim to integrate structural data obtained by cryo-electron microscopy and X-ray crystallography with mutational analysis and biophysical experiments to understand i) how allosteric interactions between AAA+ modules in the active oligomer regulate ATPase activity, ii) how ATP hydrolysis is transmitted into mechanical work on the substrate iii) how accessory factors influence complex activity and iv) which mechanisms define specificity or are intrinsic to all AAA+ proteins.

RESEARCH HIGHLIGHTS

Over the last few years, I have established my Emmy Noether group at the Gene Center. We apply genetic, biochemical and biophysical methods to isolate and characterize multiprotein AAA+ assemblies from yeast and bacteria. Ultimately, we aim to resolve the structures of these complexes at the highest possible resolution using cryo-EM in combination with single particle reconstruction. We constantly adapt our image processing and EM procedures to new challenges posed by different AAA+ assemblies. By de novo structural characterization of the Pex1/Pex6 ATPase complex we obtained first substantial insights into the novel



Left: Hexameric EM structure of red-type rubisco activase CbbX with fit of crystal structure

Center: Cryo EM image of the 500 kDa AAA+ complex of the DeltaN Hsp104 hexamer.

Right: Class average of type VI secretion system tubulus and its fourier transform

domain organization of a hetero-hexameric ATPase complex. Initial functional data help to understand the distribution of labor between the subunits. Furthermore, we determined the structure of the ClpV ATPase complex involved in the type VI secretion system (T6SS). We resolved the tubular structure of the T6SS ejection tunnel at 8Å and we are currently elucidating the interaction between the ClpV AAA+ complex and its substrate. Finally, we determined the hexameric structures of red- and green-type rubisco activase. In collaboration with Manajit Hayer-Hartl we revealed an AAA+ protein architecture that requires binding of the co-factor ribulose 1,5-bisphosphate for hexameric assembly and activation of rubisco.

FUTURE DIRECTIONS

In the future, we want to further enhance the structural characterization of the AAA+ assemblies and aim to explore the interaction of different complexes with their substrate. In particular the peroxisomal and T6SS ATPase assemblies have to be captured in different physiological states at subnanometer level in order to deduce their mode of action. Mutational studies of the hetero-hexameric Pex1/6 complex will complete the functional analysis of subunit interplay. For interaction studies between AAA+ complexes and their usually weakly bound substrates we will have to establish novel biochemical and/or biophysical protocols in the lab.

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- **Wendler, P.**, Shorter, J., Snead, D., Plisson, C., Clare, D.K., Lindquist, S., and Saibil, H.R. (2009). Motor mechanism for protein threading through Hsp104. Mol Cell 34, 81-92.

AWARDS AND MEMBERSHIPS

- Emmy Noether Fellowship , 2009

DANIEL WILSON

REGULATION OF GENE EXPRESSION: THE RIBOSOME AND PROTEIN SYNTHESIS

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1999	PhD from University of Otago, Dunedin, New Zealand
2000-2002	Alexander von Humboldt fellow, AG Ribosomen (Nierhaus), Max-Planck-Institute for Molecular Genetics, Berlin, Germany
2002-2006	Postdoc, X-ray crystallography group, Max-Planck-Institute for Molecular Genetics, Berlin, Germany
2007-present	Group Leader, Gene Center, LMU

GOAL

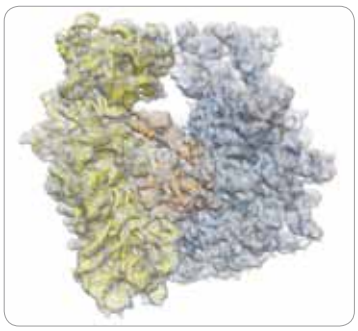
To investigate the mechanism by which the ribosome and protein synthesis is regulated in response to interaction with protein factors and small molecules such as antibiotics.

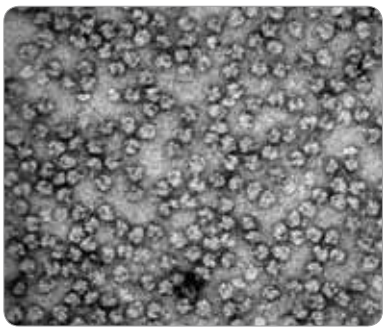
INTRODUCTION

In all cells, the accurate conversion of the genetic information within messenger RNA (mRNA) into a corresponding polypeptide sequence occurs on large macromolecular machines called ribosomes. Regulation of translation is critical for cells and bacteria to respond rapidly to stimuli and changes in environmental factors. Our group uses biochemical and structural (X-ray crystallography and cryo-electron microscopy) approaches to determine the distinct mechanisms by which diverse ligands, such as translation factors and antibiotics, interact with the ribosome to modulate its function.

RESEARCH HIGHLIGHTS

In the past four years, we have investigated the mechanism of action of a diverse range of antibiotics, such as macrolides, ketolides, thiopeptides, hygromycins, orthosomycins and tetracyclines. Recently, we have determined the structure of the ribosome protection protein TetM bound to the ribosome, revealing how TetM dislodges the antibiotic tetracycline from the ribosome to confer tetracycline resistance to bacteria. In collaboration with the Beckmann group (Gene Center), we have determined cryo-EM structures of ribosomes stalled during translation of specific regulatory nascent polypeptide chains, such as TnaC, SecM, CMV and AAP. These structures provide insights into how the nascent polypeptide chains interact with components of the ribosomal tunnel to induce translational stalling. Recently, in collaboration with the





Left: Structure of TetM on the ribosome

Center: Crystals of translation factors

Right: Negative-stain EM images of ribosomes.

group of Prof. Jung (LMU), we have discovered that translation of polyproline stretches in nascent polypeptide chains also leads to translational stalling, and that in the cell this stalling is alleviated through the action of the universally conserved translation elongation factor EF-P. The presence of polyproline stretches in a number of important virulence regulators explains why disruption of the *efp* gene leads to attenuation of virulence in pathogenic bacteria.

FUTURE DIRECTIONS

With the problem of ever-emerging multi-drug resistant bacteria, the development of new and improved antimicrobial agents will be essential. To this end, one of the major goals for the future will be to utilize our biochemical and structural insights into how various antibiotics interact with the ribosome, as well as how bacteria obtain resistance to antibiotics, to aid the development of successive generations of more potent inhibitors. Our future direction encompasses characterization of small molecules that target novel sites on the ribosome in order to avoid cross-resistance, as well as the identification of compounds with novel targets, such as within the EF-P pathway, which is critical for virulence in pathogenic bacteria.

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AWARDS AND MEMBERSHIPS

- Römer-Prize of Dr. Klaus Römer-Stiftung, München, 2010
- EMBO Young Investigator Award, 2010
- GlaxoSmithKline Foundation Prize for Medical Research, 2011

ECKHARD WOLF

GROWTH, METABOLISM AND REPRODUCTION IN MAMMALS

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1990	Dr. med. vet. from the LMU
1991-1993	Postdoc at the Institute of Animal Breeding, LMU
1994	Assistant Professor, University of Veterinary Sciences, Vienna, Austria
1995-present	Professor, Gene Center and Department of Veterinary Sciences, LMU

GOAL

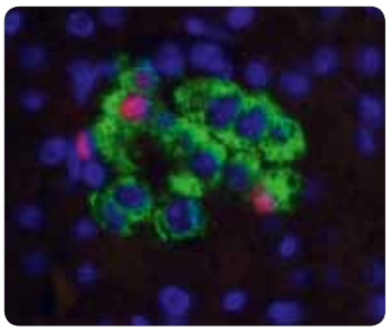
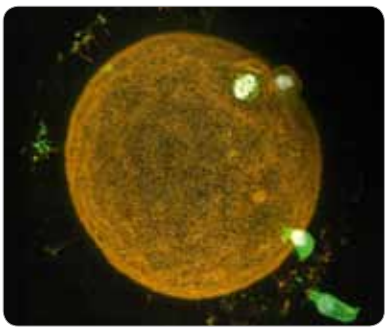
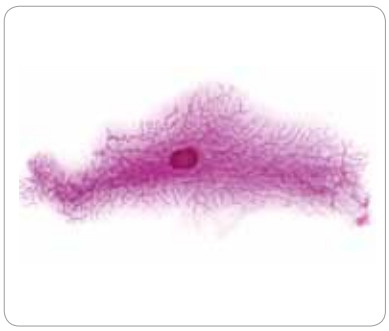
To dissect mechanisms of growth regulation, metabolism and fertility in mammalian model systems

INTRODUCTION

Our research group uses genetically designed mouse and large animal models to address mechanisms of growth regulation, metabolism and fertility, and their disturbances. The laboratory studies key steps of reproduction, such as age-dependent changes in oocyte quality, the dynamics of preimplantation development as a predictor of developmental potential, and the interaction between early embryos and their maternal environment. Both mouse and large animal models (cattle, pig) are used to unravel common and species-specific features in normal and assisted reproduction and consequences for growth and development. In addition, components of growth factor systems, such as EGF receptor ligands, that regulate pre- and postnatal growth processes are systematically characterized by forward and reverse genetics approaches in the mouse. A more recent field of interest is diabetes mellitus, a metabolic disease with dramatically increasing global prevalence. Based on tailored mouse and pig models for diabetes research, we study interactions between metabolic disease and reproduction, such as developmental consequences of maternal diabetes. Within BioSysNet, oocytes and embryos exposed to a diabetic environment are characterized on molecular (collaboration with LAFUGA), structural and functional levels to identify windows in development which may be particularly vulnerable to maternal hyperglycemia.

RESEARCH HIGHLIGHTS

Over the last few years, we have extended and refined the arsenal of technologies for the generation of genetically designed pig models for translational biomedical research. Technical advances include the first pig models with inducible transgene expression and the first gene targeting in the pig by using bacterial artificial chromosome vectors. Transgenic pigs expressing a dominant-negative receptor for the incretin hormone GIP (glucose-dependent insulinotropic polypeptide) in the pancreatic beta-cells mimic important aspects of human type 2 diabetes mellitus, such as impaired incretin effect, reduced glucose tolerance as well

Left: Islet of Langerhans with insulin-producing beta cells (green) in a pig pancreas (Photo: Simone Renner)

Center: Bovine oocyte in metaphase II (Photo: Felix A. Habermann)

Right: Whole-mount preparation of a mouse mammary gland (Photo: Maik Dahlhoff)

as reduced insulin secretion and beta-cell mass. This model was successfully used to identify metabolic signatures characteristic of the pre-diabetic period and of progression towards clinical disease. Expression of mutant INS^{C94Y} in pigs resulted in the first large animal model for permanent neonatal diabetes, with a plethora of potential research applications, including regenerative medicine, bariatric surgery, and developmental consequences of maternal diabetes. However, pigs cannot only serve as models for diabetes research but also as donors for pancreatic islet xenotransplantation to insulin-dependent diabetic patients. In this context, we demonstrated that islet clusters from transgenic pigs expressing the T cell co-stimulation blocking molecule LEA29Y are protected against human T cells in a humanized mouse model.

FUTURE DIRECTIONS

In the future, we wish to expand our research towards both basic and translational directions. Within BioSysNet and QBM we will analyze quantitative molecular profiles on the RNA and protein level of oocytes and early embryos to identify pathways involved in the activation of the embryonic genome, the loss of totipotency and the first events of cell lineage differentiation. Within the Leading-Edge Cluster "m^4 - Personalized Medicine and Targeted Therapies" and ongoing collaborations with pharmaceutical and biotech companies we will address translational questions in the fields of diabetes research and reproductive biotechnology using our tailored large animal models.

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- Dahlhoff, M., Blutke, A., Wanke, R., **Wolf, E.**, and Schneider, M.R. (2011). In vivo evidence for epidermal growth factor receptor (EGFR)-mediated release of prolactin from the pituitary gland. The Journal of biological chemistry 286, 39297-39306.
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- Klymiuk, N., Bocker, W., Schonitzer, V., Bahr, A., Radic, T., Frohlich, T., Wunsch, A., Kessler, B., Kurome, M., Schilling, E., Herbach, N., Wanke, R., Nagashima, H., Mutschler, W., Arnold, G.J., Schwinzer, R., Schieker, M., and **Wolf, E.** (2012). First inducible transgene expression in porcine large animal models. FASEB journal : official publication of the Federation of American Societies for Experimental Biology 26, 1086-1099.
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- Klymiuk, N., van Buerck, L., Bahr, A., Offers, M., Kessler, B., Wuensch, A., Kurome, M., Thormann, M., Lochner, K., Nagashima, H., Herbach, N., Wanke, R., Seissler, J., and **Wolf, E.** (2012). Xenografted islet cell clusters from INSLEA29Y transgenic pigs rescue diabetes and prevent immune rejection in humanized mice. Diabetes 61, 1527-1532.
- Renner, S., Braun-Reichhart, C., Blutke, A., Herbach, N., Emrich, D., Wuensch, A., Kessler, B., Kurome, M., Baehr, A., Klymiuk, N., Streckel, E., Krebs, S., Puk, O., Nagashima, H., Graw, J., Blum, H., Wanke, R., and **Wolf, E.** (2012). Permanent neonatal diabetes in INSC94Y transgenic pigs. Diabetes (accepted).
- Renner, S., Romisch-Margl, W., Prehn, C., Krebs, S., Adamski, J., Göke, B., Blum, H., Suhre, K., Roscher, A.A., and **Wolf, E.** (2012). Changing metabolic signatures of amino acids and lipids during the prediabetic period in a pig model with impaired incretin function and reduced beta-cell mass. Diabetes 61, 2166-2175.

AWARDS AND MEMBERSHIPS

- LMU-Chairman of the Steering Committee for the Research Collaboration LMU Munich / Sanofi R&D, 2012
- Member, Scientific Board of the Hans Eisenmann-Zentrum for Agricultural Science, TU Munich, 2012
- Associated Member, German Center for Diabetes Research (DZD), 2012

DIERK NIESSING

GENE REGULATION BY mRNA LOCALIZATION

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2000	PhD from Max-Planck Institute for Biophysical Chemistry in Göttingen, Germany, and University of Hohenheim
2000-2002	Postdoc at The Rockefeller University, USA
2003-2005	Postdoc & Staff Scientist at SGX Pharmaceuticals INC, USA
2005-2009	Group Leader of the Helmholtz Zentrum München at the Gene Center, LMU
2009-2011	Tenured Group Leader of the Helmholtz Zentrum München, located at the Gene Center, LMU
2012-present	Tenured Group Leader at the Helmholtz Zentrum München

GOAL

To unravel the molecular mechanisms of the assembly and function of mRNA transport complexes

INTRODUCTION

The molecular motors kinesin, myosin, and dynein play an important role in organizing the inner life of eukaryotic cells. They interact with a range of co-factors to assemble into motile transport particles and mediate subcellular localization of cargos like proteins, mRNAs, vesicles, and organelles. Our research group is interested in understanding molecular mechanisms of cytoplasmic gene regulation by such directional transport processes. In order to unravel principles of motor-cargo interaction and the assembly of active RNA-cargo complexes, we utilize a combination of X-ray crystallography, biophysical and biochemical approaches.

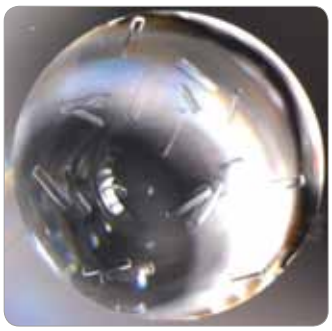
As a primary model, we analyzed the directional transport of *ASH1* mRNA in budding yeast. We determined crystal structures and performed functional analysis on the assembly of this complex. In a parallel approach, we also study transport factors from higher eukaryotes.

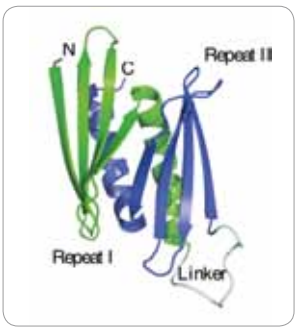
Our long-term goal is to understand how core factors of large multiprotein complexes interact to (i) detect their cargo, (ii) assemble into functional complexes in response to cargo recognition and (iii) translocate their cargo through the cytoplasm.

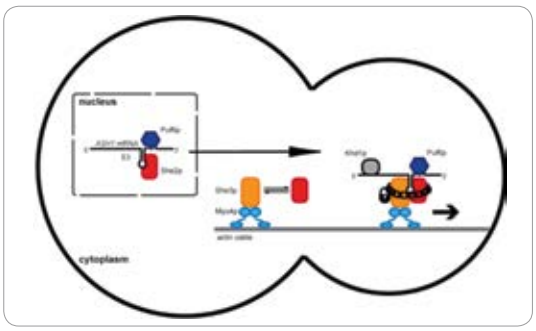
RESEARCH HIGHLIGHTS

Over the last few years, we unraveled the mechanism of specific cargo mRNA recognition for the directional transport of *ASH1* mRNA. Our results suggested that RNA-binding transport factors interact with nascent transcripts already co-transcriptionally, but with only moderate specificity (Müller et al, 2011). In the cytoplasm the interaction of this pre-complex with the motor pre-complex results in highly specific recognition of localizing RNAs (Müller et al, 2011). To our knowledge, this finding constitutes the first example where highly specific RNA recognition for transport could be explained by its faithful recapitulation *in vitro*.

We also assessed the properties of the cytoplasmic pre-complex. By solving the high-resolution X-ray structure of the myosin cargo-binding domain and studying its interaction with its cargo adapter, we







Left: Crystals of a cargo-binding domain from type V myosins

Center: X-ray structure of the RNA- and DNA-binding protein Pur-alpha

Right: Schematic drawing of the molecular events mediating *ASH1* mRNA transport in the budding yeast (image taken from Heym & Niessing, Curr Mol Life Sci, 2012)

provided a mechanistic explanation for the motor coupling to the cargo complex at atomic resolution (Heuck et al. 2010).

Related studies in higher eukaryotes yielded first structures of the Pur-alpha type of RNA- and DNA-binding proteins (Graebsch et al. 2009, 2010). Pur-alpha is found in neuronal transport particles and plays a role in transcriptional regulation of neuronal genes. Furthermore, Pur-alpha has been implicated in the neurodegenerative Fragile X-associated Tremor/Ataxia Syndrome (FXTAS). Our work helped to understand how this protein interacts with nucleic acids and thus provides insights into disease-related molecular events.

FUTURE DIRECTIONS

In the future, we wish to extend our reconstitution experiments in yeast to assess particle motilities and translational control of transported mRNAs. In addition, we aim to continue understanding RNA-transport factors that have been implicated in neurodegenerative diseases.

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- Müller, M.*, Heym, R.*, Mayer, A., Kramer, K., Schmid, M., Cramer, P., Urlaub, H., Jansen, R.P., and N**iessing, D.** (2011). A Cytoplasmic Complex Mediates Specific mRNA Recognition and Localization in Yeast. PLoS Biol 9, e1000611. *equal contribution.
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AWARDS AND MEMBERSHIPS

- Positive tenure decision by the Helmholtz Zentrum München, 2009

ULRICH KOSZINOWSKI

CELL BIOLOGY OF CYTOMEGALOVIRUS INFECTION

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1975	Habilitation at the University of Göttingen
1984	Apl. Professor of Virology and Immunology, University of Tübingen
1980 – 1987	Director of "Bundesforschungsanstalt für Viruserkrankungen der Tiere (BFVT)", Tübingen
1987 – 1992	Professor / Chair of Virology at the University of Ulm
1992 – 1996	Professor / Chair of Virology at the University of Heidelberg
1996 – 2012	Professor / Chair of Virology at the Ludwig-Maximilians-Universität München

GOAL

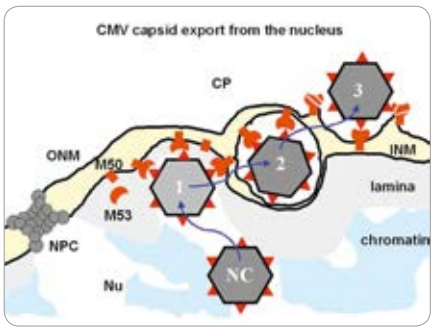
To understand and control transport processes which are essential for cytomegalovirus replication.

INTRODUCTION

Cytomegaloviruses are widespread pathogens of mammals which establish lifelong latency upon a mainly symptom-less primary infection. However, in susceptible individuals such as immunocompromised patients, during pregnancy, or in the elderly the human cytomegalovirus can provoke fatal diseases either in the context of primary infection or after reactivation from latency. Our group is studying core functions in cytomegalovirus entry and egress. We pioneered BAC technology for forward and reverse genetics of large DNA viruses including cytomegaloviruses, and we developed tools which aid dissection of functional sites of essential proteins and identification and characterization of dominant negative mutants as well as new drug targets. We also studied the cytomegalovirus biology utilizing the above mentioned tools in the mouse model to gain access the biology of cytomegaloviruses in their native host. We are investigating the role of individual cell types during infection with mouse cytomegaloviruses well as the importance of virus tropism in the immune control of the host.

RESEARCH HIGHLIGHTS

During productive infection herpesvirus capsids assemble within the nucleus and are exported to the cytoplasm to complete their maturation. As the size of the herpesvirus capsids exceeds the functional limit of the nuclear pores the newly formed particles need to use an alternative pathway to leave the nucleus. This is achieved by budding through the inner nuclear membrane to the perinuclear space followed by a fusion of these primary enveloped particles with the outer nuclear membrane (ONM). This process seems to reflect a newly discovered and not very well understood nuclear export mechanism. In the herpesvirus egress two conserved herpesvirus proteins, the pM/UL50 and pM/UL53 in cytomegaloviruses, form the nuclear egress complex (NEC) at the INM and recruit cellular PKC and many other cellular and probably viral



Nuclear egress of cytomegaloviruses

proteins which lead to alterations of the nuclear architecture which export new capsids to the cytosol. In the past few years we have described that the NEC of cytomegalovirus is also crucial to promote maturation of viral replication compartments at the nuclear periphery and plays an important role in DNA packaging and capsid maturation. In addition, we developed a new protein complementation assay (PCA) which reliably monitors the core interaction of the human cytomegaloviruses in a cell-free system allowing screens for antivirals with a novel mode of action.

The new protein complementation assay (PCA) for the core interaction of the human cytomegalovirus nuclear egress complex will be utilized to find new antiviral drugs. The same approach is planned to be transferred to other essential viral protein-protein interactions in order to identify new drug targets. The basic research of the entry and egress of cytomegaloviruses will be continued towards the identification of essential or contributing host factors such as new receptors and cellular pathways which contribute or control viral transport processes.

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AWARDS AND MEMBERSHIPS

- Honorary Doctor of the University of Rijeka, Croatia, 2009

ACHIM TRESCH

COMPUTATIONAL BIOLOGY OF TRANSCRIPTION REGULATION

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2001	PhD in Mathematics, Johannes Gutenberg University Mainz,
2002-2004	Postdoc, Fraunhofer Institute for Algorithms and Scientific Computing, Bonn
2005-2006	Postdoc, German Cancer Research Center, Division of Molecular Genome Analysis
2006-2008	Junior Professor, Johannes Gutenberg University Mainz
2008-2012	Group Leader, Gene Center, LMU
Since 2012	Jeff Schell endowed Professor for Computational Biology, Max-Planck-Institute for Plant Breeding Research and University of Cologne

GOAL

To reveal the causal relations between molecular components involved in RNA synthesis and decay and to advance the statistical theory of high dimensional data, in particular that of probabilistic graphical models.

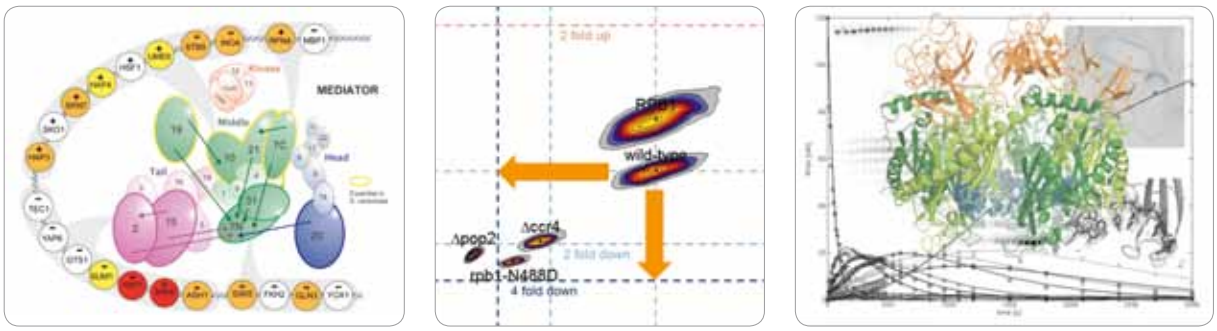
INTRODUCTION

On our way to a mechanistic understanding of the cell we need to analyze and interpret huge amounts of multi-dimensional, incomplete and noise-containing data. To this end, we develop and apply the statistical machinery which is able to cope with these challenges. Our primary research target is RNA regulation. In a joint effort with experimentalists, we impose well-defined perturbations on the cell's transcription (and degradation) machinery, then collect large-scale protein and mRNA expression data and analyze them with our network models to shed light on the processes that balance RNA activity levels. Ultimately, we want to identify novel transcription factors and co-activators/-repressors and characterize their role in transcription regulation.

RESEARCH HIGHLIGHTS

Over the last few years, we have developed probabilistic graphical models that allowed us to infer transcription factor and miRNA activity, and even transcription factor interactions from gene expression data. In particular, we improved the theory of nested effects models and implemented very efficient algorithms for parameter estimation in this model class. This enabled us to reconstruct a signaling network of the Mediator multi-protein complex and its interaction partners.

In collaboration with the Cramer lab, we have developed the dynamic transcriptome analysis (DTA) method, which allows us to measure RNA synthesis and degradation rates on an absolute and genome-wide scale. We could show that RNA synthesis and degradation are coupled such that they mutually compensate global changes and stabilize RNA levels. Using DTA, we monitored the yeast salt stress response and found that such a coupling also exists for dynamically induced stress-specific transcripts. Moreover, we could model the process of



Left: Signaling network of the Mediator complex

Center: Synthesis-decay compensation in a slow RNA polymerase II mutant in *S.cerevisiae*

Right: Model-based fit of the RNA degradation process by the exosome

RNA degradation by the archaeal exosome at single nucleotide resolution using an ordinary differential equation model and RNA digestion time series data from the Hopfner lab.

FUTURE DIRECTIONS

We will improve the statistical models of RNA regulation by dissecting the processes of RNA transcription and degradation into their elementary steps and spotting the relevant factors that interfere at the different stages of transcription and degradation. In particular, we will perform integrative modeling of epigenetic data, chromatin structure and protein-DNA interaction data to discover a "grammar" of transcription. We will also set out to find regulators of RNA decay, and reveal how they couple RNA synthesis and degradation.

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LABORATORY FOR FUNCTIONAL GENOME ANALYSIS (LAFUGA)

GENOMICS – PROTEOMICS – ANIMAL MODELS

GOAL

The functional analysis of biological modules in mammals requires appropriate model systems which are studied by quantitative holistic approaches at all levels of gene expression. The integrated technology platform LAFUGA with the three closely interacting units Genomics, Proteomics, and Animal Models comprises a unique high-end facility for discovery and validation of gene function on an organismic level.

HELMUT BLUM
LAFUGA–GENOMICS

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The genomics unit of LAFUGA has established a platform for next generation sequencing including automated library preparation, data acquisition on an Illumina Genome Analyzer IIx and bioinformatic analysis. The latter is provided by a web-interfaced analysis platform („Galaxy") hosted on a scalable grid computing system. It allows to assemble complex tailored workflows on a user-friendly graphic interface. Our lab uses this platform and microarrays to study transcription in tumor cells, reproductive tissue and early stages of embryonic development. In various collaborations we established procedures like e.g. exome sequencing, PAR-Clip, ChIP-Seq and targeted resequencing.

GEORG J. ARNOLD
LAFUGA–PROTEOMICS

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Gene expression studies at the protein level are an indispensable tool for the comprehensive investigation of complex biological processes. The proteomics unit is focused on quantitative proteome approaches based on nano-HPLC-MS-MS and stable isotope labeling techniques supplemented by the highly sensitive saturation-2D-DIGE technology. For targeted approaches, the SRM technology (Selected Reaction Monitoring) is applied, facilitating protein quantifications in the attomole range. For cellular localization and functional characterization of relevant proteins, we use our iSEPIA technology to generate highly specific peptide-induced antibodies with mono-epitopic binding characteristics. Latest protein mass spectrometry instruments (Orbitrap XL, Q-TRAP 5500) could recently be implemented by fundings through LMUexcellent and BMBF. Current research projects address key questions in reproductive biology, early mammalian embryogenesis and germ cell potential. Major collaborative projects comprise the analysis of phenotypic plasticity in the model organism Daphnia magna (C. Laforsch, Department of Biology, LMU), neurodegenerative diseases (H. Kretzschmar, ZNP, LMU), thrombozyte activation (C. Schulz & S. Massberg, Herzzentrum TUM) and archaeal ribosomes (D. Wilson, R. Beckmann, Gene Center, LMU).

ECKHARD WOLF
LAFUGA–ANIMAL MODELS

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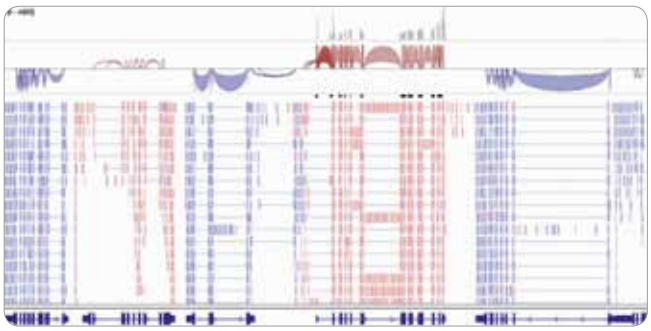
This unit is specialized in the generation and analysis of rodent and large animal models for biomedical research. Mouse models are generated by both gene-driven and phenotype-driven approaches. A broad spectrum of transgenic technologies is rou-



Splice pattern captured by next generation sequencing

tinely established for the functional analysis of specific genes. More than 100 novel mouse mutants, including highly interesting models for diabetes mellitus and kidney disease, were identified within a large-scale ENU mouse mutagenesis project. Biotechnologies of reproduction are used to produce genetically standardized large animals, such as monozygotic twins or clones, which are ideal models for systematic studies of complex traits, e.g. by holistic transcriptome and proteome approaches. Further, state-of-the-art techniques for the genetic modification of large animals, including lentiviral gene transfer and nuclear transfer from genetically modified donor cells are routinely established and applied for the genetic modification of pigs, e.g. for xenotransplantation or diabetes research.

RESEARCH HIGHLIGHTS 2009-2012

LAFUGA is part of international and national research consortia in the fields of early embryonic development and pluripotency of stem cells (e.g. EU "Plurisys") and biology of mammalian reproduction and fertility (e.g. EU "Fecund", DFG FOR 1041 "Germ cell potential").

Microarray-based analyses revealed that during the preimplantation period the response of the bovine endometrium differs significantly between embryos generated by in vitro fertilization or cloning. By next generation sequencing of transcriptomes we could discriminate gene expression from maternal or paternal alleles in bovine preimplantation embryos. We found that the expression of the parental alleles is highly dynamic and changes with respect to embryonic stages and tissues.

By proteomic approaches, we characterized protein networks in embryonic stages and corresponding stem cell lines during the transition from pluripotency to multipotency, and developed multiplexed SRM assays to determine stage-specific protein expression levels in single embryos.

We generated a panel of novel animal models, including transgenic pigs as large animal models for biomedical research and analyzed the effects of the genetic modification on molecular (transcriptome, proteome, metabolome), structural and functional levels (see E. Wolf).

FUTURE DIRECTIONS

The challenge for the next years will be to mantain the "OMICS" technologies of LAFUGA at the cutting edge level. We will use these techniques to study developmental processes and tailored disease models. LAFUGA is involved in national and international consortia addressing these questions, such as the ongoing BMBF-funded research network PHENOMICS and the EU project FECUND starting in 2013.

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- Schulz, C., Leuschen, N.V., Frohlich, T., Lorenz, M., Pfeiler, S., Gleissner, C.A., Kremmer, E., Kessler, M., Khandoga, A.G., Engelmann, B., Ley, K., Massberg, S. and **Arnold, G.J.** (2010). Identification of novel downstream targets of platelet glycoprotein VI activation by differential proteome analysis: implications for thrombus formation. Blood 115, 4102-4110.
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- Frohlich, T., and **Arnold, G.J.** (2011). Quantifying attomole amounts of proteins from complex samples by nano-LC and selected reaction monitoring. Methods in molecular biology (Clifton, NJ) 790, 141-164.
- **Arnold, G.J.**, and Frohlich, T. (2011). Dynamic proteome signatures in gametes, embryos and their maternal environment. Reproduction, fertility, and development 23, 81-93.

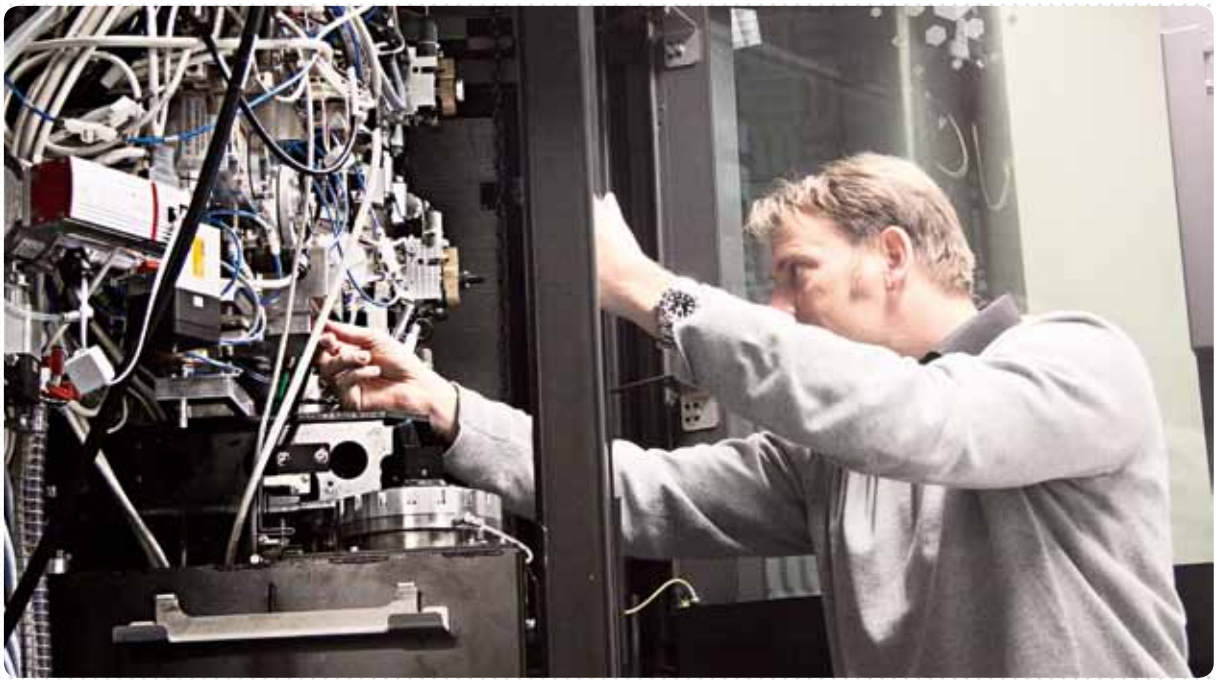
OTHER RESEARCH FACILITIES

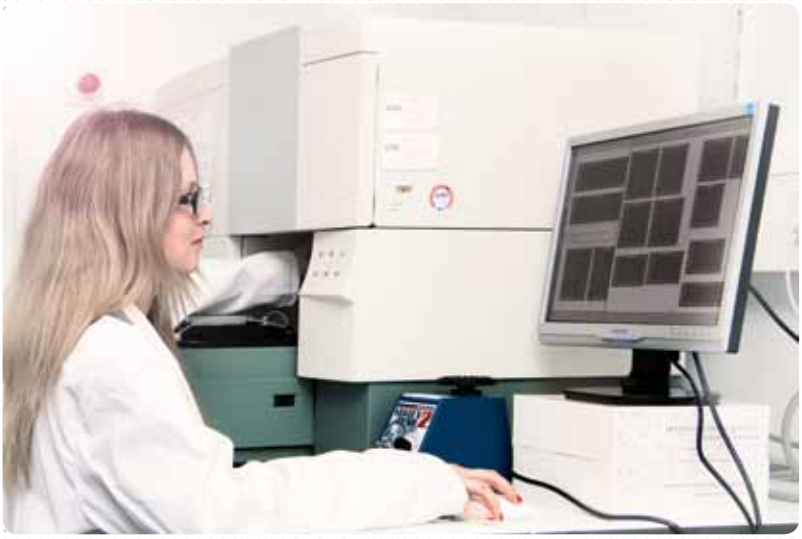
CUTTING-EDGE RESEARCH REQUIRES STATE-OF-THE-ART TECHNOLOGY PLATFORMS. OVER THE LAST FEW YEARS, RESEARCH FACILITIES HAVE BEEN EXTENDED AND NEW TECHNOLOGIES HAVE BEEN ESTABLISHED.

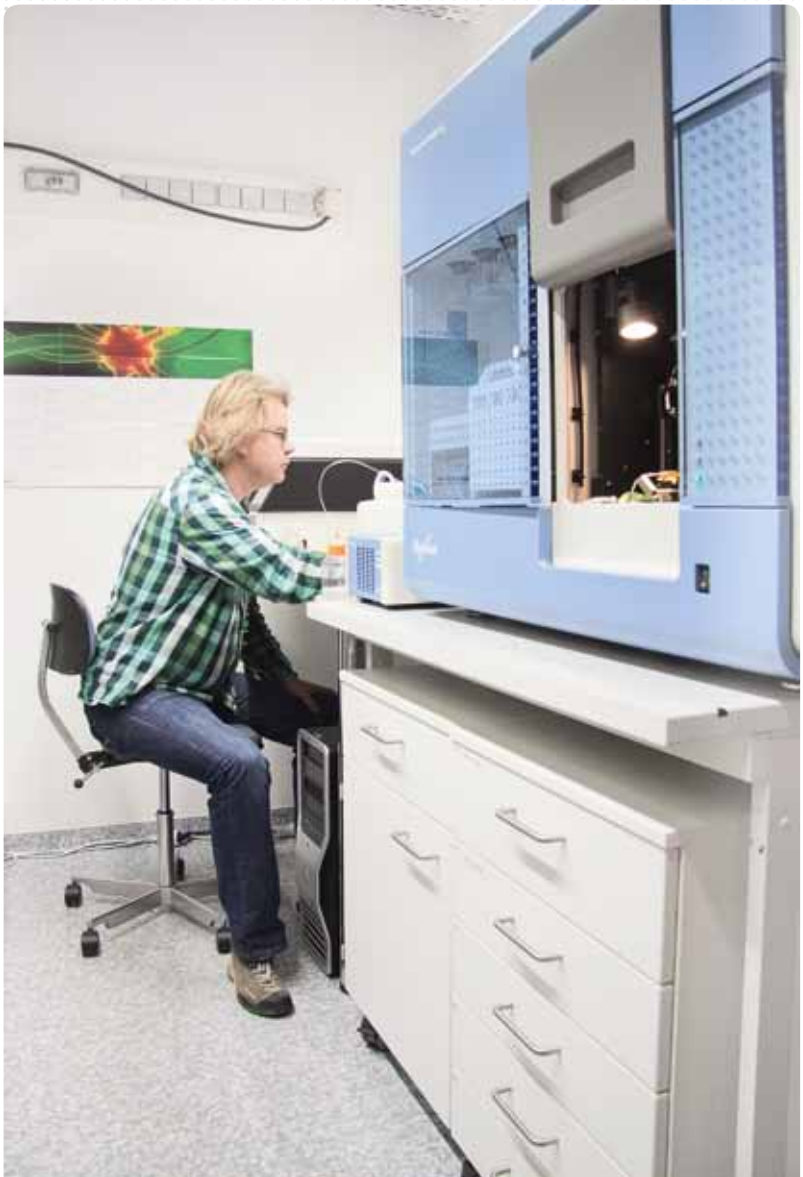
Our structural biology facilities have been expanded. A new **fermentation facility** contains one small (15 l) and one large (200 l) fermenter for the cultivation of yeast cells (*S. cerevisiae, S. pombe*). All fermentation parameters including temperature, pressure, stirring rate and oxygen level can be controlled externally, resulting in highly reproducible cultivation conditions.

A **crystallization facility** allows for semi-automated macromolecular crystallization using different approaches. State-of-the art liquid-handling systems enable fast and easy preparation of crystallization screens and setups. A free interface diffusion system is available for crystallization setups at the nanoliter scale. The results of crystallization experiments can be monitored using an automated crystallization-plate incubation and imaging system.

The **cryo-electron microscopy facility** has been further extended. It permits large-scale data collection for single particle reconstruction. A 100-kV Morgagni routine transmission electron microscope (EM) can be used for rapid sample screening. The 120-kV Spirit G12 EM with cryo-capabilities enables rapid data collection for medium-resolution analysis. For high-resolution cryo-EM we use a 300-kV Titan Krios EM, currently the most advanced microscope on the market.







New facilities for functional genomics are available. A **robotic high-throughput facility** is currently being established and will provide state-of-the-art instrumentation and expertise to advance industrial-type research in academia. The facility is equipped with flexible liquid handling workstations, into which additional instruments are integrated for sample management, handling and various types of assays. In addition, the facility houses detection and analysis systems, which permit assay read-out and quality control.

The **DNA microarray facility** provides instrumentation for gene expression analysis. It includes an Affymetrix microarray work station, comprising a GeneChip Hybridization Oven, a GeneChip Fluidics Station and a GeneChip Scanner. The platform can be used for transcriptomics and genome-wide protein-DNA interaction studies.

Our **DNA sequencing platform** includes an Illumina Genome Analyzer IIx and Miseq tabletop sequencer. A variety of protocols and data analysis pipelines are established, including exome sequencing, RNAseq, multiplex sequencing, ChIPseq, and targeted re-sequencing.

For **cell sorting** we have one analytical FACS machine available (Calibur), a modular bench top flow cytometer from Becton Dickinson. The Calibur is an automated, three-color system capable of analyzing a wide variety of reagents; it has been designed for applications that range from routine cell biology to high-throughput analysis.

Established in 2009, the **bio-imaging facility** provides access to high-end fluorescence microscopes, permitting the observation and analysis of fixed samples as well as living organisms. The facility holds a variety of microscopes, including a confocal microscope (inverted Zeiss LSM710), an epifluorescence microscope (inverted Leica DM6000), a stereomicroscope (LEICA M205).

We have also extended our **mass spectrometry facilities**. The LAFUGA proteomics platform provides instrumentation for protein identification using nano-chromatography and high-resolution FT mass spectrometers. Targeted proteomics to quantify protein sets down to the attomolar range is performed by nano-LC-QTRAP mass spectrometry and selected reaction monitoring approaches. A new orbitrap mass spectrometer is currently being set up that will allow for the identification of cross-linked peptides in macromolecular complexes.

The **scientific computing infrastructure** is constantly being extended as the need for data processing and storage increases rapidly. The computing resources available range from high-end 3D workstations and dedicated servers to multiple computing clusters.

ADMINISTRATION AND INFRASTRUCTURE AT THE GENE CENTER

The Gene Center's administration and infrastructure is run by a team whose philosophy is to support all of our scientists – from principal investigators to students – in the most efficient way. We enable our scientists to focus on their research by reducing the time they spend on administrational concerns to an unavoidable minimum. Thus, we contribute to the creation of a stimulating atmosphere for scientists, which is one of the keys to the Gene Center's success.

Since spring 2010, administration and infrastructure at the Gene Center have been headed by Dr. Katja Ketterle, who has worked as an administration manager for many years in natural sciences at both Munich universities. Her office is run by Adriane Krömer. As a translator for the English language Adriane also provides any information in English which might be helpful for an increasingly international team of scientists.

Due to the commitment of Dr. Friederike Itzen we have managed to increase our efforts in acquiring third-party funding, coordinating research grants and organizing scientific events. Friederike also coordinates public outreach activities such as the compilation of this report.

At the core of our administration team there are our secretaries Petra Fulde, Rike Menacher, Ingegerd Walz, and Stephanie Wolf. They are responsible for human resources in cooperation with LMU's central staff office, traveling and events, apart from many other things. They are supported part-time by Karin Hauck-Otte and Birgit Mewes.

Accounting and financial controlling of our regular budget and our extensive third-party funding is provided by Jutta Hohmann and Thomas Stein. We also host Ricarda Grünauer who runs the administration and finance of the collaborative research center SFB 646.

With an ever increasing impact of the computational infrastructure and its maintenance, particularly in structural and computational biology, and the newly established systems biology at the Gene Center, we are lucky to rely on the expertise of Reinhold Härtel and Andreas Hauser. They are of course supported by computational experts from different labs.

Michael Englschall, supported by Gabriela Bittner, is in charge of the Gene Center's general supply with chemicals, gases, consumables and basic lab equipment. Together with Michael Till, Dieter Zech and Manfred Schülein from the Gene Center's precision mechanics and electronic workshops they do a great job in running the labs smoothly, and in helping new groups getting their labs started within a short time.

Olga Fettscher supports the labs with the preparation of media. Sriwan Jandee, Homa Popal, Bozica Radojevic and Dorchanai Schams run the sculleries and take care of labware dishwashing.

Dr. Georg Arnold, Dr. Helmut Blum and Michael Englschall provide the Gene Center groups with expertise in biological, workplace, fire and radiation safety. LMU's company doctor, Dr. Winfried Kapfhammer, regularly offers in-house medical check-ups and advice, thus contributing largely to health prevention at the Gene Center.

TEACHING AND TRAINING

UNDERGRADUATE TEACHING

The education of students is a key part of our work. Gene Center scientists are actively involved in conducting undergraduate course. 200-250 students enroll each year in a Bachelor course in Chemistry and Biochemistry. For the advanced Master course in Biochemistry, 182 students have been selected over the last four years. This course optimally prepares young scientists for a future career in academia or industry. The course is taught in English, which improves students' language skills, enables international professors to contribute to teaching, and makes the program attractive for foreign students. Students are free to select their preferred subjects and are highly encouraged to obtain research experience in laboratories abroad. Over the last four years, 30% of the master thesis research projects have been carried out abroad, most of them in the US, and one out of seven students carried out a research internship abroad. The high standard of education and training at the Gene Center owes much to the commitment of our teaching coordinator Dr. Heidi Feldmann and to the continuous efforts of Dr. Birgitta Beatrix, Dr. Johanna Turck, Dr. Louiza Papatheodorou, and Timo Weiler. The quality of our teaching efforts is further underlined by the "Prize for Excellent Teaching at Bavarian Universities", which was granted to Klaus Förstemann in 2012. During the report period, we could set up new, larger and well-equipped teaching labs for conducting undergraduate practical courses outside the Gene Center building in Martinsried. This led to improved facilities for hands-on training and also freed up laboratory space on the ground floor of the Gene Center for the newly recruited research groups.

GRADUATE TRAINING

The training of young scientists continues with our support of PhD students at the Gene Center. PhD students are the heartblood of our institute. In 2009-2012, 122 PhD students graduated in Biochemistry at the LMU, 56% of whom were female. Graduate students participate in the Gene Center graduate program, which involves an annual retreat at Wildbad Kreuth in the Alps, a weekly international research seminar series, and a weekly institute seminar series where PhD students and postdoctoral researchers present their work. PhD students obtain advice from a thesis advisory committee. Many PhD students also participate in specialized graduate schools and programs. These include, amongst others, the International Max Planck Research School 'From Biology to Medicine' at the neighboring Max Planck Institute of Biochemistry. In 2012, two new graduate schools were funded by the German Research Council DFG and are now located at the Gene Center. The 'Graduiertenkolleg' on the 'Integrated Analysis of Macromolecular Complexes and Hybrid Methods in Genome Biology' is coordinated by Karl-Peter Hopfner and the Graduate School of Quantitative Biosciences Munich is coordinated by Ulrike Gaul. Investigators from LMU and the Technical University Munich, the Max Planck Institute for Biochemistry and the Helmholtz Center Munich participate in these programs. Gene Center PhD students also participate in eight different Collaborative Research Centers (Sonderforschungsbereiche), including SFB646, which is coordinated by Patrick Cramer, and SFB594, which is coordinated by Roland Beckmann.

MOLECULAR BIOSYSTEMS RESEARCH INITIATIVE OF THE BAVARIAN GOVERNMENT

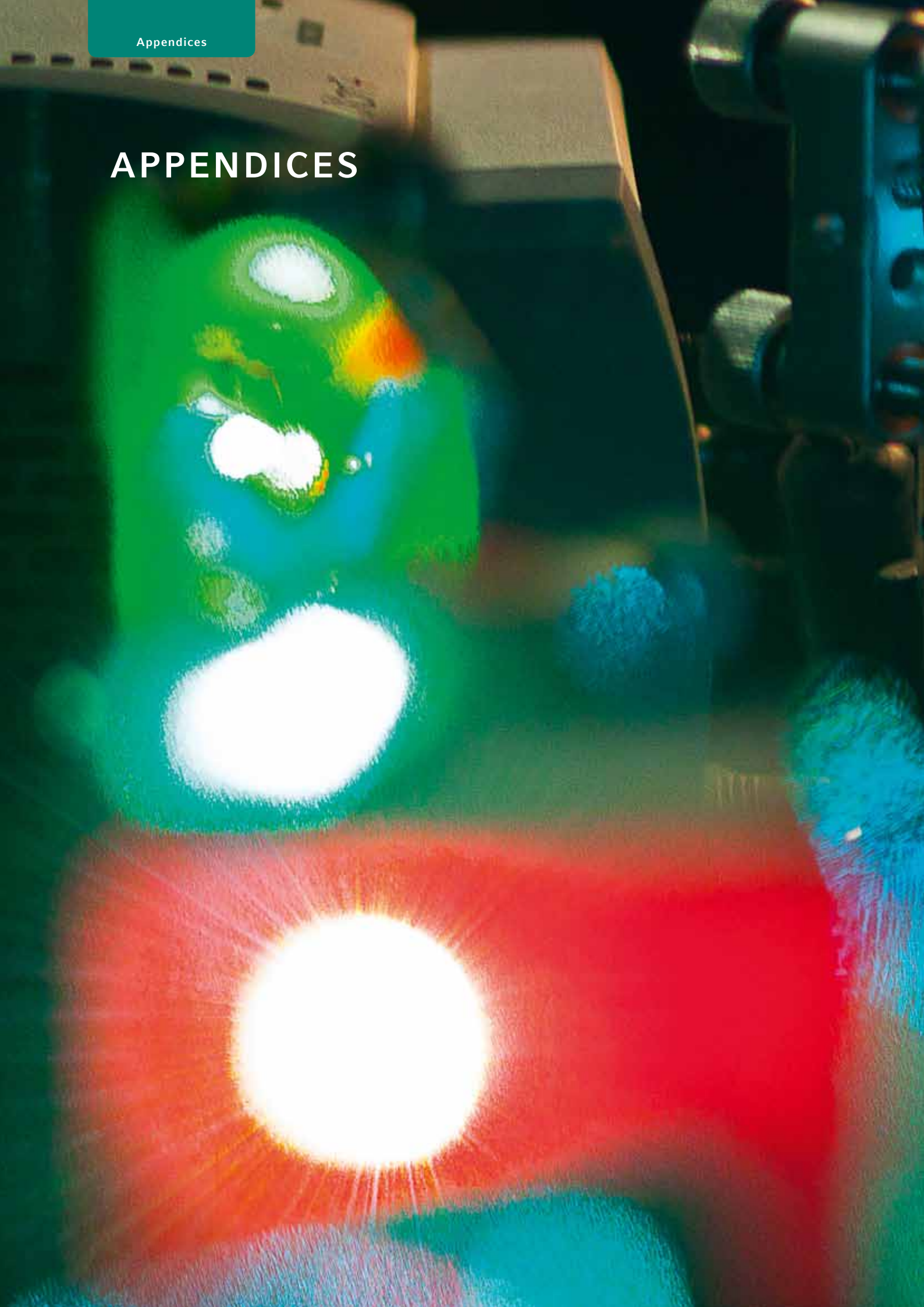
The life sciences are entering a new era. In the past, we successfully studied individual genes and gene products, leading to a detailed understanding of the mechanisms underlying the function of living cells in health and disease. Today, new systemic methods extend these classical approaches. We can now identify thousands of gene products in living cells, and can map interaction networks between components of living systems. A new discipline emerges that we refer to as molecular systems biology or molecular biosystems research. The long-standing question on how the information encoded in the genome is used is of particular interest. What are the mechanisms that ensure that the right sets of genes are activated at the right place at the right time? To answer this fundamental and complex question, we rely on new frameworks that foster interaction and scientific exchange. To achieve our goals, geneticists, molecular biologists, and structural biochemists must interact with computational biologists.

We have worked continually to promote molecular systems biology. A milestone was the establishment of a new Bavarian research network for molecular biosystems, BioSysNet. The network brings together 24 excellent junior and senior research groups at four locations in Bavaria, including four Gene Center groups. The research network is coordinated by Horst Domdey. The BioSysNet office is located at the Gene Center and run by Dr. Ulrike Kaltenhauser, Claudia Szeibert and Gabriele Jeske. The network forms part of an initiative coordinated by Patrick Cramer, Reinhard Lührmann (Göttingen) and Horst Domdey and aims at establishing a Bavarian Research Center for Molecular Biosystems. A new research building for Molecular Biosystems (BioSysM) that is currently being built on the campus Großhadern-Martinsried will contribute to this goal. We celebrated the laying of the foundation stone in November 2012 and look forward to completion of the building in 2015. Together these measures will foster technical advances, cutting-edge research and innovations, and will help us to train the next generation of life scientists. We are grateful for the strong support of the Bavarian government and the Ministry of Sciences, Research and the Arts.

BIOSYSNET RESEARCH GROUPS

- **Bosserhoff, Anja** – Universitätsklinikum Regensburg
- **Engelhardt, Stefan** – Technische Universität München
- **Eulalio, Ana** – Julius-Maximilians-Universität Würzburg
- **Gerland, Ulrich** – Ludwig-Maximilians-Universität München
- **Groß, Olaf** – Technische Universität München
- **Halic, Mario** – Ludwig-Maximilians-Universität München
- **Hopfner, Karl-Peter** – Ludwig-Maximilians-Universität München
- **Klein, Christoph** – Ludwig-Maximilians-Universität München
- **Korber, Philipp** – Ludwig-Maximilians-Universität München
- **Ladurner, Andreas** – Ludwig-Maximilians-Universität München
- **Madl, Tobias** – Technische Universität München
- **Medenbach, Jan** – Universität Regensburg
- **Meister, Gunter** – Universität Regensburg
- **Perocchi, Fabiana** – Ludwig-Maximilians-Universität München
- **Sharma, Cynthia** – Julius-Maximilians-Universität Würzburg
- **Slany, Robert** – Friedrich-Alexander-Universität Erlangen-Nürnberg
- **Spang, Rainer** – Universität Regensburg
- **Söding, Johannes** – Ludwig-Maximilians-Universität München
- **Theis, Fabian** – Technische Universität München
- **Vogel, Jörg** – Julius-Maximilians-Universität Würzburg
- **Westmeyer, Gil** – Technische Universität München
- **Winner, Beate** – Friedrich-Alexander-Universität Erlangen-Nürnberg
- **Wolf, Eckhard** – Ludwig-Maximilians-Universität München
- **Zimmer, Ralf** – Ludwig-Maximilians-Universität München

APPENDICES



PUBLICATIONS AND INVITED LECTURES

Roland Beckmann

PUBLICATIONS

2009

Becker, T., Bhushan, S., Jarasch, A., Armache, J.P., Funes, S., Jossinet, F., Gumbart, J., Mielke, T., Berninghausen, O., Schulten, K., et al. and **Beckmann, R.** (2009). Structure of monomeric yeast and mammalian Sec61 complexes interacting with the translating ribosome. Science 326, 1369-1373

Seidelt, B., Innis, C.A., **Wilson, D.N.**, Gartmann, M., Armache, J.P., Villa, E., Trabuco, L.G., Becker, T., Mielke, T., Schulten, K., et al. and **Beckmann, R.** (2009). Structural insight into nascent polypeptide chain-mediated translational stalling. Science 326, 1412-1415.

2010

Armache, J.P., Jarasch, A., Anger, A.M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., et al. and **Beckmann, R.** (2010a). Localization of eukaryote-specific ribosomal proteins in a 5.5-A cryo-EM map of the 80S eukaryotic ribosome. Proc Natl Acad Sci U S A 107, 19754-19759.

Armache, J.P., Jarasch, A., Anger, A.M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., et al. and **Beckmann, R.** (2010b). Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. Proc Natl Acad Sci U S A 107, 19748-19753.

Bhushan, S., Meyer, H., Starosta, A.L., Becker, T., Mielke, T., Berninghausen, O., Sattler, M., **Wilson, D.N.**, and **Beckmann, R.** (2010a). Structural basis for translational stalling by human cytomegalovirus and fungal arginine attenuator peptide. Mol Cell 40, 138-146.

Bhushan, S., Gartmann, M., **Halic, M.**, Armache, J.P., Jarasch, A., Mielke, T., Berninghausen, O., **Wilson, D.N.**, and **Beckmann, R.** (2010b). alpha-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. Nat Struct Mol Biol, 17, 313-317.

Pech, M., Spreter, T., **Beckmann, R.**, and Beatrix, B. (2010). Dual binding mode of the nascent polypeptide-associated complex reveals a novel universal adapter site on the ribosome. J Biol Chem 285, 19679-19687.

Liu, C., Young, A.L., Starling-Windhof, A., Bracher, A., Saschenbrecker, S., Rao, B.V., Rao, K.V., Berninghausen, O., Mielke, T., Hartl, F.U., **Beckmann, R.**, et al. (2010). Coupled chaperone action in folding and assembly of hexadecameric Rubisco. Nature 463, 197-202.

Gartmann, M., Blau, M., Armache, J.P., Mielke, T., Topf, M., and **Beckmann, R.** (2010). Mechanism of eIF6-mediated inhibition of ribosomal subunit joining. J Biol Chem 285, 14848-14851.

2011

Becker, T., Armache, J.P., Jarasch, A., Anger, A.M., Villa, E., Sieber, H., Motaal, B.A., Mielke, T., Berninghausen, O., and **Beckmann, R.** (2011). Structure of the no-go mRNA decay complex Dom34-Hbs1 bound to a stalled 80S ribosome. Nat Struct Mol Biol 18, 715-720.

Bhushan, S., Hoffmann, T., Seidelt, B., Frauenfeld, J., Mielke, T., Berninghausen, O., **Wilson, D.N.**, and **Beckmann, R.** (2011). SecM-stalled ribosomes adopt an altered geometry at the peptidyl transferase center. PLoS biology 9, e1000581.

Braig, D., Mircheva, M., Sachelaru, I., van der Sluis, E.O., Sturm, L., **Beckmann, R.**, and Koch, H.G. (2011). Signal sequence-independent SRP-SR complex formation at the membrane suggests an alternative targeting pathway within the SRP cycle. Mol Biol Cell 22, 2309-2323.

Frauenfeld, J., Gumbart, J., Sluis, E.O., Funes, S., Gartmann, M., Beatrix, B., Mielke, T., Berninghausen, O., Becker, T., Schulten, K., et al. and **Beckmann, R.** (2011). Cryo-EM structure of the ribosome-SecYE complex in the membrane environment. Nat Struct & Mol Biol, 18, 614-621.

Wilson, D.N., Bhushan, S., Becker, T. and **Beckmann, R.** (2011). Nascent polypeptide chains within the ribosomal tunnel analyzed by cryo-EM. In: Ribosomes: Structure, Function and Dynamics. eds. Rodnina, M, Wintermeyer, W, and Green, R (Springer-Verlag, Wein). pp. 393-404.

Marquez, V., Frohlich, T., Armache, J.P., Sohmen, D., Donhofer, A., Mikolajka, A., Berninghausen, O., Thomm, M., **Beckmann, R.**, **Arnold, G.J.**, et al. (2011). Proteomic characterization of archaeal ribosomes reveals the presence of novel archaeal-specific ribosomal proteins. J Mol Biol 405, 1215-1232.

Wilson, D.N., and **Beckmann, R.** (2011). The ribosomal tunnel as a functional environment for nascent polypeptide folding and translational stalling. Current Op Struct Biol 21, 274-282.

Wollmann, P., Cui, S., Viswanathan, R., Berninghausen, O., Wells, M.N., Moldt, M., Witte, G., Butryn, A., **Wendler, P.**, **Beckmann, R.**, et al. and **Hopfner, K.P.**H. (2011). Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. Nature 475, 403-407.

2012

Becker, T., Franckenberg, S., Wickles, S., Shoemaker, C.J., Anger, A.M., Armache, J.P., Sieber, H., Ungewickell, C., Berninghausen, O., Daberkow, I., et al. and **Beckmann, R.** (2012). Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. Nature 482, 501-506.

Jarasch, A., Dziuk, P., Becker, T., Armache, J.P., Hauser, A., **Wilson, D.N.**, and **Beckmann, R.** (2012). The DARC site: a database of aligned ribosomal complexes. Nuc Acids Res 40, D495-500.

Grela, P., Gajda, M.J., Armache, J.P., **Beckmann, R.**, Krokowski, D., Svergun, D.I., Grankowski, N., and Tchorzewski, M. (2012). Solution structure of the natively assembled yeast ribosomal stalk determined by small-angle X-ray scattering. Biochem J 444, 205-209.

Gumbart, J., Schreiner, E., **Wilson, D.N.**, **Beckmann, R.**, and Schulten, K. (2012). Mechanisms of SecM-mediated stalling in the ribosome. Biophys J 103, 331-341.

Donhofer, A., Franckenberg, S., Wickles, S., Berninghausen, O., **Beckmann, R.**, and **Wilson, D.N.** (2012). Structural basis for TetM-mediated tetracycline resistance. Proc Natl Acad Sci U S A 109, 16900-16905.

Franckenberg, S., Becker, T., and **Beckmann, R.** (2012). Structural view on recycling of archaeal and eukaryotic ribosomes after canonical termination and ribosome rescue. Current Op in Struct Biol, in press.

Bradatsch, B., Leidig, C., Granneman, S., Gnadig, M., Tollervey, D., Bottcher, B., **Beckmann, R.**, and Hurt, E. (2012). Structure of the pre-60S ribosomal subunit with nuclear export factor Arx1 bound at the exit tunnel. Nat Struct & Mol Biol 19, 1234-1241.

Leidig, L., Bange, G., Kopp, J., Amlacher, S., Aravind, A., Wickles,S., Witte,G., Hurt,E., **Beckmann, R.**, and Sinning, I. (2012). Structural characterization of a eukaryotic chaperone, the ribosome-associated complex (RAC). Nat Struct & Mol Biol 20: 23-28.

INVITED LECTURES

- Ringberg Meeting, Tegernsee, Germany, 2009
- SFB594 Meeting, Munich, Germany, 2009
- ASBMB Meeting, New Orleans, USA, 2009
- Rockefeller University, New York, USA, 2009
- Columbia University, New York, USA, 2009
- Membrane Meeting, Groningen, Netherlands, 2009
- ETH PhD Retreat, Zurich, Switzerland, 2009
- EMBL Cryo-EM course, London, UK, 2009
- ZMBH Meeting, Heidelberg, Germany, 2009
- International FOR967 Meeting, Homburg, Germany, 2009
- CPSM Meeting , Kloster Irsee, Germany, 2009
- SFB Membrane Meeting, Berlin, Germany, 2009
- Ringberg Meeting, Tegernsee, Germany, 2010
- FOR967 Meeting, Heidelberg, Germany, 2010
- UCL, London, UK, 2010
- GRC Meeting, Galveston, USA, 2010
- Nierhaus Meeting, Berlin, Germany, 2010
- Ribosome Conference, Orvieto, Italy, 2010
- SFB594 Meeting, Bad Staffelstein, Germany, 2010
- FASEB Conference, Saxton River, USA, 2010
- IMC17 Conference, Rio de Janeiro, Brasil, 2010
- Murnau Conference, Murnau, Germany, 2010
- SFB449 Meeting, Berlin, Germany, 2010
- FEI Titan Krios User Club Meeting, Eindhoven, NL, 2011
- EMBO Meeting, Grundlsee, Austria, 2011
- X-ray Meeting, Madrid, Spain, 2011
- Intl. Biophysical Society, Peking, China, 2011
- Mol. Biol. Soc. Japan, Tokio, Japan, 2011
- Kyoto University, Kyoto, Japan, 2011
- Protein Folding GRC, Ventura Beach, USA, 2012
- Protein Transport GRC, Galveston, USA, 2012
- MRC Cambridge, UK, 2012
- Rockefeller University, USA, 2012
- FASEB Protein Folding, Saxton River, USA, 2012
- SFBM Meeting, Tällberg, Sweden, 2012
- FOR 967 2nd Intl. Meeting, Homburg, Germany, 2012
- CSHL Translational Control, Cold Spring Harbor, USA, 2012
- Cryo-EM Meeting, Runcola, Italy, 2012

Karl-Klaus Conzelmann

PUBLICATIONS

2009

Marschalek, A., Finke, S., Schwemmle, M., Mayer, D., Heimrich, B., Stitz, L., **Conzelmann, K.K.** (2009) Attenuation of rabies virus replication and virulence by picornavirus IRES elements. J. Virol. 83(4):1911-9.

Brzózka, K., and **Conzelmann, K.K.** (2009) Rhabdoviruses and Mechanisms of Type I Interferon Antagonism. Pages 211-227 In: Cellular signaling and innate immune responses to RNA virus infections. ed. A. Brasier, A. Garcia-Sastre, S.M. Lemin. ASM Press, Washington, D.C. ISBN 978-1-55581-436-6

Conzelmann, K.K. (2009) Rhabdoviridae - Grundlagen. In: Medizinische Virologie. Grundlagen, Diagnostik und Therapie virologischer Krankheitsbilder. Herausg. H.W. Dörr und W. Gerlich. Georg Thieme Verlag, Stuttgart.

Rieder, M., and **Conzelmann, K.K.** (2009). Rhabdovirus evasion of the interferon system. J Interferon Cytokine Res. 2009 Sep;29(9):499-509.PMID: 19715459

2011

Schuhmann, K.M., Pfaller, CK., and **Conzelmann, K.K.** (2011) The measles virus V protein binds to p65 (RelA) to suppress NF-kappaB activity. J Virol. 85(7):3162-71.

Rieder, M., Brzózka, K., Pfaller, C.K., Cox, J.H., Stitz, L., and **Conzelmann, K.K.** Genetic Dissection of Interferon-Antagonistic Functions of Rabies Virus Phosphoprotein (2011): Inhibition of Interferon Regulatory Factor 3 Activation Is Important for Pathogenicity. J. Virol. 85(2):842-852.

Rieder, M., and **Conzelmann, K.K.** (2011). Interferon in rabies virus infection. Adv Virus Res. 2011;79:91-114.

2012

Ghanem, A., Kern, A., **Conzelmann, K.K.** (2012). Significantly improved rescue of rabies virus from cDNA plasmids. Eur J Cell Biol. 91(1):10-6.

Marschalek, A., Drechsel, L., **Conzelmann, K.K.** (2012) The importance of being short: the role of rabies virus phosphoprotein isoforms assessed by differential IRES translation initiation. Eur J Cell Biol. Jan;91(1):17-23.

Rieder, M., Drechsel, L., and **Conzelmann, K.K.** (2012). Rabies Virus Evasion of the Interferon System. In: Interferons: Characterization, Mechanism of Action and Clinical Applications (Ed. Joe H. Thomas and Adrian Roberts), Nova Science Publishers, Inc., Hauppauge, N.Y ISBN 978-1-62081-298-3.

Sparrer, K.M., Pfaller, C.K., **Conzelmann, K.K.** (2012). Measles virus C protein interferes with Beta interferon transcription in the nucleus. J Virol. 86(2):796-805.

Rieder M., Finke S., Conzelmann K.K. Interferon in lyssavirus infection (2012). Berl Munch Tierarztl Wochenschr. 125(5-6):209-18.

Vos, A., **Conzelmann, K.K.**, Finke, S., Müller, T., Teifke, J., Fooks, A.R., Neubert, A. (2011) Immunogenicity studies in carnivores using a rabies virus construct with a site-directed deletion in the phosphoprotein. Adv Prev Med 2011: 898171.

Kaltenborn, E., Kern, S., Frixel, S., Fragnet, L., **Conzelmann, K.K.**, Zarbock, R., Griese, M. (2012). Respiratory syncytial virus potentiates ABCA3 mutation-induced loss of lung epithelial cell differentiation. Hum Mol Genet 21(12):2793-806

Cappello, S., Böhringer, C.-R., Bergami, M., **Conzelmann, K.K.**, Ghanem, A., Tomassy, G.S., Arlotta, P., Mainardi, M., Allegra, M., Caleo, M., van Hengel, J., Brakebusch, C., Götz, M. (2012). A radial glia-specific role of RhoA in double cortex formation. Neuron 73(5):911-24.

Genz, B., Nolden, T., Negatsch, A., Teifke, J.P., **Conzelmann, K.K.**, Finke S. (2012) Chimeric rabies viruses for trans-species comparison of lyssavirus glycoprotein ectodomain functions in virus replication and pathogenesis. Berl Munch Tierarztl Wochenschr. 125(5-6):219-27.

Ghanem, A., **Conzelmann, K.K.** (2012) Reverse Genetics of Rhabdoviruses. In: Reverse Genetics of RNA Viruses: Applications and Perspectives., ed. Anne Bridgen, Wiley Blackwell ISBN: 978-0-470-97965-5, OI: 10.1002/9781118405338.ch5

Pollin, R., Granzow, H., Köllner, B., **Conzelmann, K.K.**, Finke, S. (2012) Membrane and Inclusion Body Targeting of Lyssavirus Matrix Proteins. Cell. Microbiol, doi: 10.1111/cmi.12037.

Willibald, J., Harder, J., Sparrer, K., **Conzelmann, K.K.**, Carell T. (2012) Click-modified anandamide siRNA enables delivery and gene silencing in neuronal and immune cells. J Am Chem Soc. Aug 1;134(30):12330-3.

Niedworok, C.; Schwarz, I., Ledderose, J.; Giese, G.; **Conzelmann, K.K.**; Schwarz M. (2012) Charting monosynaptic connectivity maps by two-color light-sheet fluorescence microscopy. Cell Reports, 2(5): 1375-86.

Ginger, M., Haberl, M., **Conzelmann, K.K.**, Schwarz, M.K., Frick, A. (2012) Revealing the secrets of neuronal circuits with recombinant rabies virus technology, Frontiers in Neural Circuits, accepted.

Motz, C., Schuhmann, K.M., Kirchhofer, A., Moldt, M., Witte, G., **Conzelmann, K.K.**, **Hopfner K.P.** Paramyxovirus V proteins disrupt the fold of the innate immune sensor MDA5 to inhibit antiviral interferon response. Science, in press.

Fehling, S.K., Noda, T., Maisner, A., Lamp, B., **Conzelmann, K.K.**, Kawaoka, Y., Klenk, H.D., Garten, W., Strecker, T. (2012) Intracellular trafficking of the Lassa virus matrix protein Z requires the microtubule motor protein KIF13A Cell. Microbiol, Dec 24. doi: 10.1111/cmi.12095. [Epub ahead of print]

INVITED LECTURES

- Friedrich Miescher Institute, Basel, CH, 2009
- Georg-Speyer-Haus Frankfurt, 2009
- 5th EMVZ, St. Raphael, F, 2009
- Universität St. Gallen, CH, 2009
- Universität Zürich, CH, 2010
- ECV Como, 2010
- ENS Lyon, France 2010
- Universität Freiburg, 2011
- 10th ICV, Sapporo, Japan, 2011
- FLI Tübingen, 2011
- Intl. Interferon Workshop, St. Andrews, UK, 2011
- HZI Braunschweig, Killer Day, 2011
- Ringberg Meeting, 2011
- Heinrich-Pette Institute Hamburg, 2011
- Awaji Forum on Immunology, Awaji, Japan, 2012
- HZI Braunschweig, Summer School Rügen, 2012
- Universität Erlangen 2012

Patrick Cramer

PUBLICATIONS

2009

Koschubs, T., Seizl, M., Lariviere, L., Kurth, F., Baumli, S., Martin, D.E., and **Cramer, P.** (2009). Identification, structure, and functional requirement of the Mediator submodule Med7N/31. EMBO J 28, 69-80.

Brueckner, F., Armache, K.J., Cheung, A., Damsma, G.E., Kettenberger, H., Lehmann, E., Sydow, J., and **Cramer, P.** (2009a). Structure-function studies of the RNA polymerase II elongation complex. Acta Crystallogr D Biol Crystallogr 65, 112-120.

Reich, C., Zeller, M., Milkereit, P., Hausner, W., **Cramer, P.**, Tschochner, H., and Thomm, M. (2009). The archaeal RNA polymerase subunit P and the eukaryotic polymerase subunit Rpb12 are interchangeable in vivo and in vitro. Mol Microbiol 71, 989-1002.

Dengl, S., Mayer, A., Sun, M., and **Cramer, P.** (2009). Structure and in vivo requirement of the yeast Spt6 SH2 domain. J Mol Biol 389, 211-225.

Brueckner, F., Ortiz, J., and **Cramer, P.** (2009b). A movie of the RNA polymerase nucleotide addition cycle. Curr Opin Struct Biol 19, 294-299.

Dengl, S., and **Cramer, P.** (2009). Torpedo nuclease Rat1 is insufficient to terminate RNA polymerase II in vitro. J Biol Chem 284, 21270-21279.

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Andrecka, J., Treutlein, B., Arcusa, M.A., Muschielok, A., Lewis, R., Cheung, A.C., **Cramer, P.**, and Michaelis, J. (2009). Nano positioning system reveals the course of upstream and nontemplate DNA within the RNA polymerase II elongation complex. Nucleic Acids Res 37, 5803-5809.

Damsma, G.E., and **Cramer, P.** (2009). Molecular basis of transcriptional mutagenesis at 8-oxoguanine. J Biol Chem 284, 31658-31663.

Kostrewa, D., Zeller, M.E., Armache, K.J., Seizl, M., Leike, K., Thomm, M., and **Cramer, P.** (2009). RNA polymerase II-TFIIB structure and mechanism of transcription initiation. Nature 462, 323-330.

Cramer, P., and Arnold, E. (2009). Proteins: how RNA polymerases work. Curr Opin Struct Biol 19, 680-682.

Sydow, J.F., and **Cramer, P.** (2009). RNA polymerase fidelity and transcriptional proofreading. Curr Opin Struct Biol 19, 732-739.

2010

Chen, Z.A., Jawhari, A., Fischer, L., Buchen, C., Tahir, S., Kamenski, T., Rasmussen, M., Lariviere, L., Bukowski-Wills, J.C., Nilges, M., **Cramer, P.** and Rappsilber, J. (2010). Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. EMBO J 29, 717-726.

Koschubs, T., Lorenzen, K., Baumli, S., Sandstrom, S., Heck, A.J., and **Cramer, P.** (2010). Preparation and topology of the Mediator middle module. Nucleic Acids Res 38, 3186-3195.

Hirtreiter, A., Damsma, G.E., Cheung, A.C., Klose, D., Grohmann, D., Vojnic, E., Martin, A.C., **Cramer, P.**, and Werner, F. (2010). Spt4/5 stimulates transcription elongation through the RNA polymerase clamp coiled-coil motif. Nucleic Acids Res 38, 4040-4051.

Cramer, P. (2010). Towards molecular systems biology of gene transcription and regulation. Biol Chem 391, 731-735.

Beck, K., Vannini, A., **Cramer, P.**, and Lipps, G. (2010). The archaeo-eukaryotic primase of plasmid pRN1 requires a helix bundle domain for faithful primer synthesis. Nucleic Acids Res 38, 6707-6718.

Geiger, S.R., Lorenzen, K., Schreieck, A., Hanecker, P., Kostrewa, D., Heck, A.J., and **Cramer, P.** (2010). RNA polymerase I contains a TFIIF-related DNA-binding subcomplex. Mol Cell 39, 583-594.

Mayer, A., Lidschreiber, M., Siebert, M., Leike, K., **Soding, J.**, and **Cramer, P.** (2010). Uniform transitions of the general RNA polymerase II transcription complex. Nat Struct Mol Biol 17, 1272-1278.

Vannini, A., Ringel, R., Kusser, A.G., Berninghausen, O., Kassavetis, G.A., and **Cramer, P.** (2010). Molecular basis of RNA polymerase III transcription repression by Maf1. Cell 143, 59-70.

Sun, M., Lariviere, L., Dengl, S., Mayer, A., and **Cramer, P.** (2010). A tandem SH2 domain in transcription elongation factor Spt6 binds the phosphorylated RNA polymerase II C-terminal repeat domain (CTD). J Biol Chem 285, 41597-41603.

Clausing, E., Mayer, A., Chanarat, S., Muller, B., Germann, S.M., **Cramer, P.**, Lisby, M., and **Strasser, K.** (2010). The transcription elongation factor Bur1-Bur2 interacts with replication protein A and maintains genome stability during replication stress. J Biol Chem 285, 41665-41674.

2011

Miller, C., Schwalb, B., Maier, K., Schulz, D., Dumcke, S., Zacher, B., Mayer, A., Sydow, J., Marcinowski, L., Dolken, L., et al. and **Cramer, P.**(2011). Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol 7, 458.

Cheung, A.C., and **Cramer, P.** (2011). Structural basis of RNA polymerase II backtracking, arrest and reactivation. Nature 471, 249-253.

Vojnic, E., Mourao, A., Seizl, M., Simon, B., Wenzeck, L., Lariviere, L., Baumli, S., Baumgart, K., Meisterernst, M., Sattler, M., and **Cramer, P.** (2011). Structure and VP16 binding of the Mediator Med25 activator interaction domain. Nat Struct Mol Biol 18, 404-409.

Martinez-Rucobo, F.W., Sainsbury, S., Cheung, A.C., and **Cramer, P.** (2011). Architecture of the RNA polymerase-Spt4/5 complex and basis of universal transcription processivity. EMBO J 30, 1302-1310.

Ruan, W., Lehmann, E., Thomm, M., Kostrewa, D., and **Cramer, P.** (2011). Evolution of two modes of intrinsic RNA polymerase transcript cleavage. J Biol Chem 286, 18701-18707.

Seizl, M., Lariviere, L., Pfaffeneder, T., Wenzeck, L., and **Cramer, P.** (2011b). Mediator head subcomplex Med11/22 contains a common helix bundle building block with a specific function in transcription initiation complex stabilization. Nucleic Acids Res 39, 6291-6304.

Czeko, E., Seizl, M., Augsberger, C., Mielke, T., and **Cramer, P.** (2011). Iwr1 directs RNA polymerase II nuclear import. Mol Cell 42, 261-266.

Muller, M., Heym, R.G., Mayer, A., Kramer, K., Schmid, M., **Cramer, P.**, Urlaub, H., Jansen, R.P., and **Niessing, D.** (2011). A cytoplasmic complex mediates specific mRNA recognition and localization in yeast. PLoS Biol 9, e1000611.

Geiger, S.R., Bottcher, T., Sieber, S.A., and **Cramer, P.** (2011). A conformational switch underlies ClpP protease function. Angew Chem Int Ed Engl 50, 5749-5752.

Blattner, C., Jennebach, S., **Herzog, F.**, Mayer, A., Cheung, A.C., Witte, G., Lorenzen, K., **Hopfner, K.P.**, Heck, A.J., Aebersold, R., and **Cramer, P.** (2011). Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. Genes Dev 25, 2093-2105.

Ringel, R., Sologub, M., Morozov, Y.I., Litonin, D., **Cramer, P.**, and Temiakov, D. (2011). Structure of human mitochondrial RNA polymerase. Nature 478, 269-273.

Cheung, A.C., Sainsbury, S., and **Cramer, P.** (2011). Structural basis of initial RNA polymerase II transcription. EMBO J 30, 4755-4763.

Cramer, P., and Wolberger, C. (2011). Proteins: histones and chromatin. Curr Opin Struct Biol 21, 695-697.

Seizl, M., Hartmann, H., Hoeg, F., Kurth, F., Martin, D.E., **Soding, J.**, and **Cramer, P.** (2011a). A conserved GA element in TATA-less RNA polymerase II promoters. PLoS One 6, e27595.

2012

Koschubs, T., Dengl, S., Durr, H., Kaluza, K., Georges, G., Hartl, C., Jennewein, S., Lanzendorfer, M., Auer, J., Stern, A., et al., **Cramer, P.**, and Mundigl, O. (2012). Allosteric antibody inhibition of human hepsin protease. Biochem J 442, 483-494.

Wild, T., and **Cramer, P.** (2012). Biogenesis of multisubunit RNA polymerases. Trends Biochem Sci 37, 99-105.

Schwalb, B., Schulz, D., Sun, M., Zacher, B., Dumcke, S., Martin, D.E., **Cramer, P.**, and **Tresch, A.** (2012). Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). Bioinformatics 28, 884-885.

Mayer, A., Schreieck, A., Lidschreiber, M., Leike, K., Martin, D.E., and **Cramer, P.** (2012b). The spt5 C-terminal region recruits yeast 3' RNA cleavage factor I. Mol Cell Biol 32, 1321-1331.

Lariviere, L., Seizl, M., and **Cramer, P.** (2012b). A structural perspective on Mediator function. Curr Opin Cell Biol 24, 305-313.

Vannini, A., and **Cramer, P.** (2012). Conservation between the RNA polymerase I, II, and III transcription initiation machineries. Mol Cell 45, 439-446.

Jennebach, S., **Herzog, F.**, Aebersold, R., and **Cramer, P.** (2012). Crosslinking-MS analysis reveals RNA polymerase I domain architecture and basis of rRNA cleavage. Nucleic Acids Res 40, 5591-5601.

Walmacq, C., Cheung, A.C., Kireeva, M.L., Lubkowska, L., Ye, C., Gotte, D., Strathern, J.N., Carell, T., **Cramer, P.**, and Kashlev, M. (2012). Mechanism of translesion transcription by RNA polymerase II and its role in cellular resistance to DNA damage. Mol Cell 46, 18-29.

Treutlein, B., Muschielok, A., Andrecka, J., Jawhari, A., Buchen, C., Kostrewa, D., Hog, F., **Cramer, P.**, and Michaelis, J. (2012). Dynamic architecture of a minimal RNA polymerase II open promoter complex. Mol Cell 46, 136-146.

Sun, M., Schwalb, B., Schulz, D., Pirkl, N., Etzold, S., Lariviere, L., Maier, K.C., Seizl, M., **Tresch, A.**, and **Cramer, P.** (2012). Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. Genome Res 22, 1350-1359.

Cheung, A.C., and **Cramer, P.** (2012). A movie of RNA polymerase II transcription. Cell 149, 1431-1437.

Niederberger, T., Etzold, S., Lidschreiber, M., Maier, K.C., Martin, D.E., Frohlich, H., **Cramer,**

P., and **Tresch, A.** (2012). MC EMiNEM maps the interaction landscape of the Mediator. PLoS Comput Biol 8, e1002568.

Mayer, A., Heidemann, M., Lidschreiber, M., Schreieck, A., Sun, M., Hintermair, C., Kremmer, E., Eick, D., and **Cramer, P.** (2012a). CTD tyrosine phosphorylation impairs termination factor recruitment to RNA polymerase II. Science 336, 1723-1725.

Dumcke, S., Seizl, M., Etzold, S., Pirkl, N., Martin, D.E., **Cramer, P.**, and **Tresch, A.** (2012). One Hand Clapping: detection of condition-specific transcription factor interactions from genome-wide gene activity data. Nucleic Acids Res 40, 8883-8892.

Martinez-Rucobo, F.W., and **Cramer, P.** (2012). Structural basis of transcription elongation. Biochim Biophys Acta, published online September 13.

Lariviere, L., Plaschka, C., Seizl, M., Wenzeck, L., Kurth, F., and **Cramer, P.** (2012a). Structure of the Mediator head module. Nature 492, 448-451.

Wu, C.C., **Herzog, F.**, Jennebach, S., Lin, Y.C., Pai, C.Y., Aebersold, R., **Cramer, P.**, and Chen, H.T. (2012). RNA polymerase III subunit architecture and implications for open promoter complex formation. Proc Natl Acad Sci USA 109, 19232-19237.

Miller, C., Matic, I., Maier, K., Schwalb, B., Roether, S., Straesser, K., **Tresch, A.**, Mann, M., and **Cramer, P.** (2012). Mediator phosphorylation prevents stress response transcription during non-stress conditions. J Biol Chem 287, 44017-44026.

Sainsbury, S., Niesser, J. and Cramer P. (2012). Structure and function of the initially transcribing RNA polymerase II-TFIIB complex. Nature, published online November 14.

INVITED LECTURES

- Institute de Biologie et Technologie Saclay, Paris, 2009
- Ringberg Meeting Academia meets Industry, Ringberg, 2009
- Familie-Hansen award ceremony, Berlin, 2009
- 12. Steinheimer Gespräche, Frankfurt, 2009
- Friedrich-Miescher-Institut, Basel, Switzerland, 2009
- Clare Hall Laboratories, Clare Hall, UK, 2009
- ISMB Retreat, Robinson College, Cambridge, UK, 2009
- Department of Biochemistry, Oxford, OK, 2009
- Bayreuther Strukturtage, Thurnau, 2009
- Ringvorlesung NanoBioTechnology, Munich, 2009
- Eukaryotic Transcription Meeting, Cold Spring Harbor, USA, 2009
- NIEHS, Raleigh, USA, 2009
- BSM Retreat ETH Zürich, Filzbach, Switzerland, 2009
- Heidelberg Forum for Young Life Scientists, Heidelberg, 2009
- First International Symposium on Structural Systems Biology, Hamburg, 2009
- CIPSM conference, Kloster Irsee, 2009
- MPI for Molecular Genetics, Berlin, 2009
- Welcome Trust Centre for Gene Regulation and Expression, Dundee, UK, 2009
- NanoDay Deutsches Museum, München, 2009
- Wissenschaftlich-technischer Beirat der Staatsregierung, St. Quirin, 2009
- International Symposium on Membranes and Modules, Berlin, 2009
- Ringberg Meeting Academia meets Industry, Ringberg, 2010
- Robert Koch Kolloquium, Berlin, 2010
- 3rd International Students' Meeting Crossroads in Biology, Köln, 2010
- HFSP Frontiers Meeting, Strasbourg, France, 2010
- SFB 646 workshop, Hohenkammer, 2010
- EMBL Conference on The Complex Life of mRNA, Heidelberg, 2010
- 42nd Erice Course on Macromolecular Crystallography, Erice, Italy, 2010
- EMBO Conference on Gene transcription in yeast, St. Feliu, Spain, 2010
- Center for Genomic Regulation, Barcelona, Spain, 2010
- Interfaculty Insitute of Biochemistry, Tübingen, 2010
- Harvard Gene Expression Meeting, Boston, USA, 2010
- MIT, Boston, USA, 2010
- University of Massachusetts, Worchester, USA, 2010
- LMU-Harvard Young Scientists Symposium, Boston, USA, 2010
- Gordon Research Conference on Chromatin, Smithfield, USA, 2010
- Albert Einstein College, New York, USA, 2010
- Sloan Kettering Cancer Research Center, New York, USA, 2010
- Rockefeller University, New York, USA, 2010
- CSH course on gene expression, Cold Spring Harbor, USA, 2010
- Genentech, South San Francisco, USA, 2010
- UC Berkeley, Berkeley, USA, 2010
- Meeting of P-TEFb and regulation of transcriptional elongation, Ringberg, 2010
- RNAP 2010 Symposium, Hinxton, UK, 2010
- CPE Closure Symposium, Cambridge, UK, 2010
- CIPSM Symposium, Wildbad-Kreuth, 2010
- Symposium TRR 80, Freising, 2010
- Murnau Conference on The modern RNA world, Murnau, 2010
- EU Workshop on Trends in the life sciences, Brüssel, Belgium, 2010
- Wacker Chemie, Munich, 2010
- EMBO New Members Workshop, Heidelberg, 2010
- 5th EMBL/EMBO Conference, Heidelberg, 2010
- Alexander von Humboldt Symposium, Munich, 2010
- Symposium SFB 860 Georg-August-Universität, Göttingen, 2010
- Ringberg Meeting Academia meets Industry, Ringberg, 2011
- Lausanne Genomics Days 2011, University of Lausanne, Lausanne, 2011
- 7th International Forum Life Science, Garching, 2011
- CEF Seminar, Goethe University Frankfurt, Frankfurt, 2011
- 62. Mosbacher Kolloquium on Mechanisms of RNA-mediated regulation, Mosbach, 2011
- Dialogforen der Münchner Rück Stiftung, München, 2011
- Peutinger Collegium Symposium, Munich, 2011
- Feldberg Prize Lecture, Birkbeck College, London, UK, 2011
- Wellcome Trust Centre for Cell Biology, Edinburgh, UK, 2011
- EMBO Conference on Modern Molecular Biology at Institute Pasteur, Paris, France, 2011
- Mikrobiologisches Kolloquium, Biozentrum der Universität Würzburg, Würzburg, 2011
- IMTB Westfälische Wilhelms-Universität Münster, Münster, 2011
- Max-Planck-Institut für Biochemie Faculty Retreat, Ohlstadt, 2011
- Bayreuth Structure Days, Bayreuth, 2011
- IUCR Congress, Madrid, 2011
- CSIC Spanish National Research Council, Madrid, 2011
- Eukaryotic Transcription Meeting, Cold Spring Harbor, 2011
- FASEB Summer Research Conference on Transcription Elongation, Lucca, Italien, 2011
- 104th Titisee Conference, Titisee, 2011
- Münchner Wissenschaftstage, München, 2011
- Forum Sozial-Diakonische Ethik, Nürnberg, 2011
- 13th International EMBL PHD Symposium, Heidelberg, 2011
- Ringberg Meeting Academia meets Industry, Ringberg, 2012
- Dialogreihe Gentechnik, Deutsches Museum München, München, 2012
- Tsinghua University, Department of Structural Biology, Beijing, China, 2012
- Academia Sinica Institute of Molecular Biology, Taipei, Taiwan, 2012
- Lorne Genome Conference, Lorne, Australia, 2012
- University of Queensland, Institute of Molecular Biology, Brisbane, Australia, 2012
- Yonsei University, Seoul, Korea, 2012
- Friedrich Miescher Institute, Basel, Switzerland, 2012
- Biozentrum, Universität Würzburg, Würzburg, 2012
- RNA: Synthesis & Regulation at Rockefeller University, New York, USA, 2012
- Odd Polymerases Meeting, Warrenton, USA, 2012
- National Institutes of Health, Bethesda, USA, 2012
- EMBO Conference on Gene transcription in yeast, St. Feliu, Spain, 2012
- RNA Annual Workshop, Bordeaux, France, 2012
- Department of Biochemistry, Oxford University, Oxford, UK, 2012
- Division of Structural Biology, Oxford, UK, 2012
- London Research Institute, London, UK, 2012
- Symposium of the Vallee Foundation, Reykjavik, Iceland, 2012
- Department of Biochemistry, Cambridge University, Cambridge, UK, 2012
- MRC Laboratory of Molecular Biology, Cambridge, UK, 2012
- EMBL Meeting on Transcription and Chromatin, Heidelberg, 2012
- 60th Birthday Symposium R. Großschedl, Freiburg, 2012
- Workshop on Gene Transcription and Regulation, Venice, Italy, 2012
- EMBO/EMBL Symposium on Quality Control, Heidelberg, 2012
- Bayer GEC Conference, Düsseldorf, 2012
- Chefarztklausur Diakoniewerk Martha-Maria, Nürnberg, 2012
- EMBO/EMBL Symposium on The Complex Life of mRNA, Heidelberg, 2012
- 106th Titisee Conference, Titisee, 2012
- Symposium 75th Birthday G. Huttner, Heidelberg, 2012
- Weizmann Institute of Science, Rehovot, Israel, 2012
- Hebrew University of Jerusalem, Jerusalem, Israel, 2012
- Max-Planck-Institut für Pflanzenzüchtung, Köln, 2012

Klaus Förstemann

PUBLICATIONS

2009

Esslinger, S., **Förstemann, K.** (2009): MicroRNAs repress mainly through mRNA decay. Angew Chem Int Ed Engl. 48, 853-855

Hartig, J.V., Esslinger, S., Böttcher, R., Saito, K., **Förstemann, K.** (2009): Endo-siRNAs depend on a new isoform of loquacious and target artificially introduced, high-copy sequences. EMBO J. 28, 2932-2944

2010

Förstemann, K. (2010): Transposon defense in Drosophila somatic cells: A model for distinction of self and non-self in the genome. RNA Biol. 7, 158-161

2011

Hartig, J.V., **Förstemann, K.** (2011): Loqs-PD and R2D2 define independent pathways for RISC generation in Drosophila. Nucleic Acids Res. 39, 3836-3851

2012

Helfer, S., Schott, J., Stoecklin, G. and **Förstemann, K.** (2012): AU-rich Element Mediated mRNA Decay can occur independently of the miRNA machinery in Mouse Embryonic Fibroblasts and Drosophila S2-cells. PLoS One 7, e28907

Dittmer, A., **Förstemann, K.** (2012): MCMV infection of cultured mouse cells induces expression of miR-7a. J Gen Virol. 93, 1537-1547

Aumiller, V.A., Graebsch, A., Kremmer, E., **Niessing, D.**, **Förstemann, K.** (2012): Drosophila Pur-α binds to trinucleotide-repeat containing cellular RNAs and translocates to the early oocyte. RNA Biol. 9, 633-643

Michalik, K., Böttcher, R., **Förstemann, K.** (2012): A small RNA response at DNA ends in Drosophila, Nucleic Acids Research 40, 9596-603

Schertel, C., Rutishauser, T., **Förstemann, K.**, Basler, K. (2012): Functional Characterization of Drosophila microRNAs by a Novel in vivo Library. Genetics 192,1543-1552.

INVITED LECTURES

- Ringberg-Meeting, Schloss Ringberg/Tegernsee, 2009
- Nikolaus-Fiebiger-Zentrum, Erlangen, 2009
- École Polytechnique Féderale, Lausanne / CH, 2009
- Ringberg-Meeting, Schloss Ringberg/Tegernsee, 2010
- Tagung der GBM Studiengruppe RNA, Hohenwart, 2010
- Ringberg-Meeting, Schloss Ringberg/Tegernsee, 2011
- Europäisches Patentamt, München, 2011
- BioMedS Meeting, Martinsried, 2011
- MicroSymposium, Vienna, 2011
- Martin-Luther-Universität Halle, 2011
- Ringberg-Meeting, Schloss Ringberg/Tegernsee, 2012
- University of Vancouver, Vancouver/CA, 2012
- Junior European Drosophila Investigator Meeting, Leysin/CH, 2012
- Conférence Jacques Monod, Roscoff/Fr, 2012

Julien Gagneur

PUBLICATIONS

2009

Zinzen, R.P., Girardot, C., **Gagneur, J.**, Braun, M., Furlong, E.E. (2009) Combinatorial binding predicts spatio-temporal cis-regulatory activity. Nature,. 462, p. 65-70.

Xu, Z., Wei, W., **Gagneur, J.**, **Perocchi, F.**, Clauder-Münster, S., Camblong, J., Guffanti, E., Stutz, F., Huber, W., and Steinmetz, L.M. (2009) Bidirectional promoters generate pervasive transcription in yeast. Nature, 457, 1033-7.

Gagneur J., Sinha .H, Perocchi F., Bourgon R., Huber W., and Steinmetz L.M. (2009) Genome-wide allele- and strand-specific expression profiling. Mol Syst Biol,. 5, 274.

Blandin, S.A., Wang-Sattler, R., Lamacchia, M., **Gagneur, J.**, Lycett, G., Ning, Y., Levashina, E.A., Steinmetz L.M. (2009) Dissecting the genetic basis of resistance to malaria parasites in Anopheles gambiae. Science, 326, 147-50.

2010

Bauer, S., **Gagneur, J.** and P.N. Robinson. (2010) GOing Bayesian: model-based gene set analysis of genome-scale data. Nucleic Acids Res, 38, 3523-32.

2011

Xu, Z., Wei, W., **Gagneur, J.**, Clauder-Münster, S., Smolik, M., Huber, W., and Steinmetz, L.M. (2011) Antisense expression increases gene expression variability and locus interdependency. Mol Syst Biol. 7, 468.

Couplan, E., Aiyar, R.S., Kucharczyk, R., Kabala, A., Ezkurdia, N., **Gagneur, J.**, St Onge, R.P., Salin, B., Soubigou, F., Le Cann, M., Steinmetz, L.M., di Rago, J.P., Blondel, M. (2011) A yeast-based assay identifies drugs active against human mitochondrial disorders. Proc Nat Acad Sci 108, 11989-94.

Bauer, S., P.N. Robinson, and J. Gagneur. (2011) Model-based gene set analysis for Bioconductor. Bioinformatics, 27, 1882-3.

Gagneur, J., M.C. Elze, and A. Tresch. (2011) Selective phenotyping, entropy reduction, and the mastermind game. BMC Bioinformatics. 12, 406.

2012

Izquierdo-Carrasco, F., **Gagneur, J.**, and Stamatakis, A. (2012) Trading Memory for Running Time in Phylogenetic Likelihood Computations. in Bioinformatics conference. Vilamoura, Portugal.

Bietenhader, M., Martos, A., Tetaud, E., Aiyar, R.S., Sellem, C.H., Kucharczyk, R., Clauder-Münster, S., Giraud, M.F., Godard, F., Salin, B., Sagot, I., **Gagneur, J.**, et al., (2012) Experimental relocation of the mitochondrial ATP9 gene to the nucleus reveals forces underlying mitochondrial genome evolution. PLoS genetics. 8, e1002876.

INVITED LECTURES

- Oberwolfach Workshop Statistical Issues in Prediction: what can be learned for individualized predictive medicine?, Oberwolfach, 2010
- Biotec institute, Dresden, 2011
- German Cancer Research Center (DKFZ), Heidelberg, 2011

Ulrike Gaul

PUBLICATIONS

2009

Sawyer, J. K., Harris, N. J., Slep, K. C., **Gaul, U.**, and Peifer, M. (2009). The Drosophila afadin homologue Canoe regulates linkage of the actin cytoskeleton to adherens junctions during apical constriction. J Cell Biol 186 (1), 57-73.

Iovino, N., Pane, A., and **Gaul, U.** (2009). miR-184 has multiple roles in Drosophila female germline development. Dev Cell 17, 123-133.

2010

Gaul, U., (2010). Decoding transcription and microRNA-mediated translation control in Drosophila development. Biol Chem 391, 767-770.

2011

Schroeder, M., Greer, C., and **Gaul, U.** (2011). How to make stripes - deciphering the transition from non-periodic to periodic patterns in Drosophila segmentation. Development 138, 3067-3078.

Gaul, U. (2011). Systembiologie – Herausforderungen und Perspektiven. Biotechnologie in Bayern 2011, 70-74.

INVITED LECTURES

- Bayer Schering AG, Berlin, Germany, 2009
- Symposium in Honor of Herbert Jäckle, Max Planck Society, Ringberg Castle, Germany, 2009
- Technical University, Department of Bioinformatics (Convocation speaker), Munich, Germany, 2009
- Workshop Data 2 Dynamics D2D, Helmholtz Center Munich, Freising, Germany, 2009
- 1st International Symposium on Structural Systems Biology, Hamburg, Germany, 2009
- CIPSM Conference, Kloster Irsee, Germany, 2009
- BayGene Network Conference "Durch Genomics und Systembiologie zu Innovationen in Industrie und Medizin", Munich, Germany, 2009
- Poppelsdorfer Schlossgespräche (Keynote address), Bonn, Germany, 2010
- Ringberg Symposium on Neurodegeneration in Zebrafish, Ringberg Castle, Germany (Keynote speaker), 2010
- TIPP (International PhD Program Tübingen) Retreat (Keynote speaker), Bad Ditzenbach, Germany, 2010
- Alexander-von-Humboldt Foundation (Keynote address), Munich, Germany, 2010
- IZB, Innovations- und Gründerzentrum Biotechnologie, Martinsried, Germany, 2010
- Elite Network of Bavaria, Graduate Program "Theoretical and Mathematical Physics", St. Ottilien, Germany, 2010
- GAIN (German Academic International Network) Conference, Boston, USA, 2010
- CeNS Workshop, "Nanosciences – Merging Disciplines", Venice, Italy, 2010
- CNC, 1st Cell Networks Conference, Heidelberg, Germany, 2010
- "Academia meets Industry", Ringberg Castle, Germany, 2011
- Roche Diagnostics GMBH, Penzberg, Germany, 2011
- "Miteinander reden: Frauen in den Life Sciences im Dialog", Munich, Germany, 2011
- Symposium in Honor of Detlef Weigel, Tübingen, Germany, 2011
- TR5 Seminar series, Munich, Germany, 2012
- "Systems Biology of Human Disease", Heidelberg, Germany, 2012
- Women in IP Forum, Munich, Germany, 2012
- Meeting TR5, "Chromatin Day", Munich, Germany, 2012
- "Regulatory Networks in Development", GfE Summer School, Günzburg, Germany 2012
- 50 Years of Biochemistry in Tübingen, Tübingen, Germany

Mario Halic

PUBLICATIONS

2009

Halic, M., Moazed, D. Transposon silencing by piRNAs. (2009) Cell. 138, 1058-60.

Halic, M., Moazed, D. (2009) 22G-RNAs in transposon silencing and centromere function. Mol Cell. 36, 170-1.

2010

Bhushan, S., Gartmann, M., **Halic, M.**, Armache, J.P., Jarasch, A., Mielke, T., Berninghausen, O., **Wilson, D.N.**, **Beckmann, R.** (2010) α-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. Nat Struct Mol Biol 17, 313-317.

Halic, M. and Moazed, D. (2010) Dicer-Independent priRNAs and Argonaute Trigger RNAi and Heterochromatin Formation. Cell. 140, 504-516

Gerace, E., **Halic, M.**, Moazed, D. (2010) The Methyltransferase Activity of Clr4Suv39h triggers RNAi Independently of Histone H3K9 Methylation. Mol Cell. 39, 360-72.

INVITED LECTURES

Small RNA conference, Vienna, Austria, 2010

104th ITC, Titisee, Germany, 2011

Franz Herzog

PUBLICATIONS

2009

Herzog, F., Primorac, I., Dube, P., Lenart, P., Sander, B., Mechtler, K., Stark, H., and Peters, J.M. (2009). Structure of the anaphase-promoting complex/cy-

closome interacting with a mitotic checkpoint complex. Science 323, 1477-1481.

2010

Leitner, A., Walzthoeni, T., Kahraman, A., **Herzog, F.**, Rinner, O., Beck, M., and Aebersold, R. (2010). Probing native protein structures by chemical cross-linking, mass spectrometry, and bioinformatics. Mol Cell Proteomics 9, 1634-1649.

2011

Buschhorn, B.A., Petzold, G., Galova, M., Dube, P., Kraft, C., **Herzog, F.**, Stark, H., and Peters, J.M. (2011). Substrate binding on the APC/C occurs between the coactivator Cdh1 and the processivity factor Doc1. Nat struct mol boil, 18, 6-13.

Blattner, C., Jennebach, S., **Herzog, F.**, Mayer, A., Cheung, A.C., Witte, G., Lorenzen, K., **Hopfner, K.P.**, Heck, A.J., Aebersold, R., et al. (2011). Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. Genes Dev 25, 2093-2105.

Beck, M., Schmidt, A., Malmstroem, J., Claassen, M., Ori, A., Szymborska, A., **Herzog, F.**, Rinner, O., Ellenberg, J., and Aebersold, R. (2011). The quantitative proteome of a human cell line. Mol Syst Biol 7, 549.

2012

Leitner, A., Reischl, R., Walzthoeni, T., **Herzog, F.**, Bohn, S., Foerster, F., and Aebersold, R. (2012). Expanding the chemical cross-linking toolbox by the use of multiple proteases and enrichment by size exclusion chromatography. Mol Cell Proteomics. Epub 2012 Jan 27.

Jennebach, S., **Herzog, F.**, Aebersold, R., and **Cramer, P.** (2012). Crosslinking-MS analysis reveals RNA polymerase I domain architecture and basis of rRNA cleavage. Nucleic Acids Res 40, 5591-5601.

Escher, C., Reiter, L., MacLean, B., Ossola, R., **Herzog, F.**, Chilton, J., MacCoss, M.J., and Rinner, O. (2012). Using iRT, a normalized retention time for more targeted measurement of peptides. Proteomics 12, 1111-1121.

Walzthoeni, T., Claassen, M., Leitner, A., **Herzog, F.**, Bohn, S., Forster, F., Beck, M., and Aebersold, R. (2012). False discovery rate estimation for cross-linked peptides identified by mass spectrometry. Nat Methods 9, 901-903.

Herzog, F., Kahraman, A., Boehringer, D., Mak, R., Bracher, A., Walzthoeni, T., Leitner, A., Beck, M., Hartl, F.U., Ban, N., et al. (2012). Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. Science 337, 1348-1352.

Ciferri, C., Lander, G.C., Maiolica, A., **Herzog, F.**, Aebersold, R., and Nogales, E. (2012). Molecular architecture of human polycomb repressive complex 2. eLife 1, e00005.

Wu, C.C., **Herzog, F.**, Jennebach, S., Lin, Y.C., Pai, C.Y., Aebersold, R., **Cramer, P.**, and Chen, H.T. (2012). RNA polymerase III subunit architecture and implications for open promoter complex formation. Proc Natl Acad Sci U S A 109, 19232-19237.

INVITED LECTURES

- Swiss Society of Mass Spectrometry Conference. Beatenberg, Switzerland, 2010
- American Society of Mass Spectrometry Conference. Salt Lake City, USA, 2010.
- High Throughput Structural Biology Keystone Symposium. Keystone, USA, 2012.

Karl-Peter Hopfner

PUBLICATIONS

2009

Kirchhofer, A., Helma, J., Schmidthals, K., Frauer, C., Cui, S., Karcher, A., Pellis, M., Muyldermans, S., Casas-Delucchi, C.S., Cardoso, M.C., Leonhardt, H., **Hopfner, K.P.**, Rothbauer, U. (2009) Modulation of protein properties in living cells using nanobodies. Nat Struct Mol Biol. 17(1):133-8.

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INVITED LECTURES

- 2009 Friedrich Miescher Institute
- 2009 Foundation des Treilles, France
- 2009 EU DNA Repair Conference, Kreta
- 2009 Seeberg Symposium on DNA Repair, Geiranger, Norway
- 2009 FASEB Helicases, Les Diablerets, Switzerland
- 2009 The EMBO Meeting 2009
- 2009 Universität Tromsoe, Norway
- 2009 CIPSM-Irsee-Konferenz
- 2009 IMVC Meeting, Washington DC
- 2009 Uni Bonn
- 2010 Biozentrum Wien
- 2010 Host Pathogen Insitute Beijing
- 2010 CEF Seminar Uni/MPI Frankfurt
- 2010 ASBMB Conference Experimental Biology 2010, Anaheim
- 2010 GRK1202 Retreat
- 2010 IMVC Meeting, Los Angeles
- 2010 CIPSM-Wildbad-Kreuth-Konferenz
- 2010 Universität/BioQuant Heidelberg
- 2010 University of Virgina, Charlottsville
- 2010 IMVC Meeting, Washington DC
- 2010 Cancer Research UK Claire Hall
- 2011 2nd International Meeting "Conformational Transitions " Halle
- 2011 The 4th EU-USA conference on DNA base damage and repair, Oslo
- 2011 m4 Award
- 2011 FASEB Conference Helicases and NTP-Driven Nucleic Acid Translocases
- 2011 Curr. Op. Struct. Biol. and DNA Repair Conference, Amsterdam, NL
- 2011 ATIP-Avenir Conference, Roscoff, France
- 2011 The EMBO Members Workshop, Heidelberg
- 2011 Institut für Strahlenbiologie, LMU
- 2011 IMCV Meeting, Los Angeles
- 2012 Wintermeeting of the Norwegian Biochemical Society, Sturefiell, Norway
- 2012 Alumni Meeting 75th Birthday Robert Huber
- 2012 DGK Jahrestagung, München
- 2012 Deutsche Biotechnologietage, Frankfurt
- 2012 Max-Planck-Symposion on The Future of Structural Biology, Hamburg
- 2012 3rd Erling Seeberg Meeting, Trondheim, Norway
- 2012 DGDR Meeting, Neuherberg
- 2012 IRB Barcelona
- 2012 IBS, Grenoble

Christoph Klein

PUBLICATIONS

2009

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Schober, T., Framke, T., Kreipe, H., Schulz, T.F., Großhennig, A., Hussein, K., Baumann, U., Pape, L., Schubert, S., Wingen, A.M., Jack, T., Koch, A., **Klein, C.**, Maecker-Kolhoff, B. (2012) Factors determining the development of early and late PTLD in pediatric solid organ transplant recipients. Transplantation (in press).

Jonigk, D., Laenger, F., Maegel, L., Izykowski, N., Rische, J., Tiede, C., **Klein, C.**, Maecker-Kolhoff, B., Kreipe, H., Hussein, K. (2012) Molecular and clinicopathological analysis of Epstein Barr Virus associated posttransplant smooth muscle tumors. Am J Transplant. 12, 1908-17.

Langemeier, J., Schrom, E.M., Rabner, A., Radtke, M., Zychlinski, D., Saborowski, A., Bohn, G., Mandel-Gutfreund, Y., Bodem, J., **Klein, C.**, Bohne, J. (2012) A complex immunodeficiency is based on U1 snRNP-mediated poly(A) site suppression. EMBO J 31, 4035-4.

Wilsdorf, N., Eiz-Vesper, B., Henke-Gendo, C., Diestelhorst, J., Hussein, K., Pape, L., Baumann, U., **Klein, C.**, Maecker-Kohlhoff, B. (2012) EBV-specific T cell immunity in pediatric solid organ grafts recipients with post-transplant lymphoproliferative disease. Transplantation (in press).

Mynarek, M., Tolar, J., Albert, M.H., Escolar, M.L., Boelens, J.J., Cowan, M.J., Finnegan, N., Glomstein, A., Jacobsohn, D.A., Kühl, J.S., Yabe, H., Kurtzberg, J., Malm, D., Orchard, P.J., **Klein, C.**, Lücke, T., Sykora, K.W. (2012) Allogeneic hematopoietic SCT for alpha-mannosidosis: an analysis of 17 patients. Bone Marr Transpl 47:352-359, 2012

Bégin, P., Patey, N., Mueller, P., **Klein, C.**, Haddad, E., Drouin, E., Le Deist, F. (2012) Inflammatory bowel disease and T cell lymphopenia in G6PC3 deficiency. J Clin Immunol (in press)

Wali, Y., Beshlawi, I., Fawaz, N., Alkhayat, A., Zalabany, M., Elshinawy, M., Al-Kindi, S., Al-Rawas, A.H., **Klein, C.** (2012) Co-existence of Sickle Cell Disease and Severe Congenital Neutropenia: First Impressions can be deceiving. Eur J Haematol. 89, 245-249.

Patiroglu, T., Eke Gungor, H., Sawalle-Belohradsky, J., Unal, E., **Klein, C.** (2012) Myeloperoxidase deficiency, the secret under the flag of unstained cell. Turk J Hematol 2012 (in press)

Klein, C. (2012) Congenital Neutropenia. In Ochs H (Ed) Primary Immunodeficiency Syndromes (scheduled 2012)

Klein, C. (2012) Störungen des angeborenen Immunsystems. In Peter HH (Ed) Klinische Immunologie (scheduled 2012)

Boztug, K., **Klein, C.** (2012) Gentherapie. In Reinhardt D (Ed) Therapie der Krankheiten im Kindesalter (2013) in press

Klein, C. (Hrs). (2012) Quantitative and Qualitative Diseases of Neutrophil Granulocytes. Elsevier NY (2013) in press

INVITED LECTURES (SELECTION)

- European Bone Marrow Transplant Meeting Venice, Italy, 2010
- University Medical Center Cairo, Dep. Pediatrics, Egypt, 2010
- University Medical Center Alexandria, Dep. Pediatrics, Egypt, 2010
- American Society of Gene Therapy, Washington D.C., USA, 2010
- Clinical Immunology Society, Philadelphia, USA, 2010
- European Society for Gene Therapy, Milano, Italy, 2010
- German Society of Immunology, Leipzig 2010
- Libanese Society of Hematology, Beirut, Lebanon, 2010
- American Society of Hematology, New Orleans, USA, 2010
- African Society of Immunodeficiency, Casablanca, Morocco, 2010
- Memorial Sloan Kettering Cancer Center, New York, USA, 2011
- University Ulm, 2011
- German and Italian Society of Immunology Meeting, Riccione, Italy 2011
- German Society of Rheumatology Meeting, Munich 2011
- Sheba Medical Center, Dep. Pediatrics, Tel Aviv, Israel, 2011
- Evangelische Akademie Stuttgart 2011
- Schneider Children's Hospital, Dep. Pediatrics Tel Aviv, Israel 2011

- JM Foundation International Meeting, New York, USA 2011
- University Erlangen Lecture Series, 2011
- European Hematology Association, London and Bangalore, 2011
- German Society of Pediatrics, Bielefeld 2011
- CIBERER, Barcelona, Spain, 2011
- American Society of Hematology, San Diego, USA, 2011
- International Society of Cell Therapy, Seattle, USA 2012
- German Society for Gene and Cell Therapy, Frankfurt 2012
- European Society of Gene Therapy, Geneva, Switzerland, 2012
- Sanford-Burnham-Institute, San Diego, USA, 2012
- Keynote speaker, Austrian Society of Pediatrics, Salzburg 2012
- Leibniz Lecture, German Research Foundation, NY, Bethesda, Memphis, USA 2012
- European Society of immunodeficiency, Florence, Italy, 2012
- European Hematology Association, Amsterdam, Netherlands, 2012
- Robert Good Lecture CIS, Chicago, USA 2012
- Center for Chronic Immunodeficiency, Freiburg 2012
- Children's Hospital, Harvard Medical School, Boston, USA 2012
- Middle Eastern Conference on Hematology, Beirut, Lebanon, 2012
- German Bundestag (National Parlament), Berlin, 2012
- Swiss Academy of National Sciences, Solothurn, Switzerland, 2012

Fabiana Perocchi

PUBLICATIONS

2009

Xu, Z.*, Wie, W.*, **Gagneur, J.**, **Perocchi, F.**, Clauder-Münster, S., Camblong, J., Guffanti, E., Stutz, F., Huber, W., Steinmetz, L.M. (2009). Bidirectional promoters generate pervasive transcription in yeast. Nature 457(7232), 1033-7.

Gagneur, J., Sinha, H., **Perocchi, F.**, Bourgon, R., Huber, W., Steinmetz, L.M. (2009). Genome-wide allele- and strand-specific expression profiling. Mol. Syst. Biol. 5, 274.

2010

Gohil, V.M.*, Sheth, S.A.*, Nilsson, R., Wojtovich, A.P., Lee, J.H., **Perocchi, F.**, Chen, W., Clish, C.B., Ayata, C., Brookes, P.S., Mootha, V.K. (2010). Nutrient-sensitized screening for drugs that shift energy metabolism from mitochondrial respiration to glycolysis. Nature Biotechnol. 28, 249-55.

Perocchi, F., Gohil, V.M., Girgis, H.S., Bao, X.R., McCombs, J.E., Palmer, A.E., Mootha, V.K. (2010). MICU1 encodes a mitochondrial EF hand protein required for Ca(2+) uptake. Nature 467(7313), 291-6.

2011

Baughman, J.M.*, **Perocchi, F.***, Girgis, H.S., Plovanich, M., Belcher-Timme, C.A., Sancak, Y., Bao, X.R., Strittmatter, L., Goldberger, O., Bogorad, R.L., Koteliansky, V., Mootha, V.K. (2011). Integrative genomics identifies MCU as an essential component of the mitochondrial calcium uniporter. Nature 476(7360), 341-5.

INVITED LECTURES

- Sonderforschungsbereich Collaborative Research Centre 593, Marburg, Germany, 2011
- Gordon Research Conference on Calcium Signaling, Maine, USA, 2011
- Gordon Research Seminar on Calcium Signaling, Maine, USA, 2011
- Helmholtz Zentrum Munich, Institute of Human Genetics, Munich, Germany, 2011
- Interdisciplinary Center for Neurosciences, Heidelberg University, Germany, 2011
- Institute of Biology and Molecular Genetics, Valladolid, Spain, 2011
- FEPS Congress 2012, Santiago de Compostela, Spain, 2012
- Targeting Mitochondria 2012 Conference/ISANH, Berlin, Germany, 2012

Johannes Söding

PUBLICATIONS

2009

Biegert, A. and **Söding, J.** (2009) A boost for sequence searching. BIOforum Europe 10, 26–27.

Hildebrand, A., Remmert, M., Biegert, A., and **Söding, J.** (2009) Fast and accurate automatic structure prediction with HHpred. Proteins 77 Suppl 9, 128–132.

Remmert, M., Linke, D., Lupas, A., and **Söding, J.** (2009) HHomp - Prediction and classification of outer membrane proteins. Nucleic Acids Res. 37, W446–451.

Biegert, A. and **Söding, J.** (2009) Sequence context-specific amino acid similarities for homology searching. Proc. Natl. Acad. Sci. USA 106, 3770–3775.

Bateman, A., Finn, R. D., Sims, P. J., Wiedmer, T., Biegert, A., and **Söding, J.** (2009) Phospholipid scramblases and Tubby like proteins belong to a new superfamily of membrane tethered transcription factors. Bioinformatics 25, 159–162.

2010

Armache, J. P., Jarasch, A., Anger, A. M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., Marquez, V., Mielke, T., Thomm, M., Berninghausen, O., Beatrix, B., **Söding, J.**, Westhof, E., **Wilson, D. N.**, and **Beckmann, R.** (2010) Localization of eukaryote-specific ribosomal proteins in a 5.5 cryo-EM map of the 80S eukaryotic ribosome. Proc. Natl. Acad. Sci. U S A 107, 19754–19759.

Armache, J. P., Jarasch, A., Anger, A. M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., Marquez, V., Mielke, T., Thomm, M., Berninghausen, O., Beatrix, B., **Söding, J.**, Westhof, E., **Wilson, D. N.**, and **Beckmann, R.** (2010) Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. Proc. Natl. Acad. Sci. U S A 107, 19748–19753.

Graebsch, A., Roche, S., Kostrewa, D., **Söding, J.**, and **Niessing, D.** (2010) Of bits and bugs - on the use of bioinformatics and a bacterial crystal structure to solve a eukaryotic repeat-protein structure. PLoS ONE 5, e13402.

Mayer, A., Lidschreiber, M., Siebert, M., Leike, K., **Söding, J.**, and **Cramer, P.** (2010) Uniform transitions of the general RNA polymerase II transcription complex. Nat. Struct. Mol. Biol. 17, 1272–1278.

Lasi, M., Pauly, B., Schmidt, N., Cikala, M., Stiening, B., Ksbauer, T., Zenner, G., Popp, T., Wagner, A., Knapp, R., Huber, A., Grunert, M., **Söding, J.**, David, C., and Bttger, A. (2010) The molecular cell death machinery in the simple cnidarian hydra includes an extended caspase family, APAF-1 and pro- and antiapoptotic Bcl-2 proteins. Cell Res. 20, 812–825.

Remmert, M., Biegert, A., Linke, D., Lupas, A., and **Söding, J.** (2010) Evolution of outer membrane beta-barrels from an ancestral beta beta hairpin. Mol. Biol. Evol. 27, 1348–1358

Alva, V., Remmert, M., Biegert, A., Lupas, A., and **Söding, J.** (2010) A galaxy of folds. Protein Sci. 19, 124–130.

2011

Remmert, M., Biegert, A., Hauser, A., and **Söding, J.** (2011) HHblits: Lightning-fast iterative protein sequence searching by HMM-HMM alignment. Nat. Methods 9, 173–175.

Seizl, M., Hartmann, H., Hoeg, F., Kurth, F., Martin, D., **Söding, J.**, and **Cramer, P.** (2011) A functional GA element in TATA-less RNA polymerase II promoters. PLoS ONE 6, e27595.

Feller, C., Prestel, M., Hartmann, H., Straub, T., **Söding, J.**, and Becker, P. (2011) The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. Nucleic Acids Res. 40, 1509–1522.

Sievers, F., Wilm, A., Dineen, D., Gibson, T., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., **Söding, J.**, Thompson, J., and Higgins, D. (2011) Fast, scalable generation of high quality protein multiple sequence alignments using Clustal Omega. Mol. Syst. Biol. 7, 539.

Söding, J. and Remmert, M. (2011) Protein sequence comparison and fold recognition: progress and good- practice benchmarking. Curr. Opin. Struct. Biol. 21, 404–411.

Lammens, K., Bemeleit, D. J., Möckel, C., Clausing, E., Schele, A., Hartung, S., Schiller, C. B., Lucas, M., Angermüller, C., **Söding, J.**, Strer, K., and Hopfner, K.-P. (2011) X-ray structure of a bacterial Mre11:Rad50 complex reveals an ATP dependent molecular clamp in DNA double-strand break repair. Cell 145, 54–66.

Frauer, C., Rottach, A., Meilinger, D., Bultmann, S., Fellinger, K., Hasenoeder, S., **Söding, J.**, Spada, F., and Leonhardt, H. (2011) Different binding properties and function of CXXC zinc finger domains in Dnmt1 and Tet1. PLoS ONE 6, e16627.

2012

Angermüller, C., Biegert, A., and **Söding, J.** (2012) Discriminative modeling of context-specific amino acid substitution probabilities. Bioinformatics 28, 3240-3247.

Hartmann, H., Guthhrlein, E. W., Siebert, M., Luehr, S., and **Söding, J.** (2012) P-value based regulatory motif discovery using positional weight matrices. Genome Res. 23, 181-194.

Luehr, S., Hartmann, H., and **Söding, J.** (2012) The XXmotif web server for eXhaustive, weight matriX- based motif discovery in nucleotide sequences. Nucleic Acids Res., W104–109.

Close, P., East, P., Dirac-Svejstrup, A. B., Hartmann, H., Heron, M., Maslen, S., Chariot, A., **Söding, J.**, Skehel, M., and Svejstrup, J. Q. (2012) DBIRD integrates alternative mRNA splicing with RNA polymerase transcript elongation. Nature 484, 386–389.

INVITED LECTURES

- Symposium Future of Computational Biology der Max-Planck-Gesellschaft, Potsdam, Germany, 2009
- ISMB 2009, Stockholm, Sweden, 2009
- Gene Center Retreat, Wildbad Kreuth, 2009
- Universita di Padua, Italien, 2009
- Ringberg Meeting of BioM, Schloss Ringberg, 2009
- Critical Assessment of Techniques for Protein Structure Prediction (CASP9), Asilomar, USA, 2010
- SMBE2010, Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, France, 2010
- Lunch seminar at the LMU department for physics of soft matter, LMU Munich, 2010

- International Institute of Molecular and Cell Biology, Warsaw, Poland, 2010
- BIT10 Bioinformatics in Torun 2010, Poland, 2010
- Sanger Center, Hinxton, UK, 2010
- Gene Center Retreat, Wildbad Kreuth, 2010
- Institute of Biotechnology, Vilnius University, Lithuania, 2010
- 104'th International Titisee conference by Boehringer Ingelheim Fonds, Germany, 2011
- ISMB 2011 / 3DSIG, Vienna, 2011
- Annual Meeting of the Society for Bioinformatics of the Nordic Countries (SocBin 2011), Helsinki, Finland 2011
- Conti lab retreat (MPI Biochemistry), Schloss Ringberg, 2011
- Gene Center Retreat, Wildbad Kreuth, 2011
- Munich Bioinformatics Retreat 2011, Garching, 2011
- BioMed-S Workshop Martinsried, 2011
- Ringberg-Meeting of BioM, Schloss Ringberg, 2011
- Institute of Molecular Biology, University of Mainz, 2012
- Sektion Informatik, Universtity of Lübeck, 2012
- ISMB 2012, Long Beach, USA, 2012
- Munich Bioinformatics Retreat 2012, Garching, 2012
- CECAM workshop: Integrated Software for Integrative Structural Biology, Abington, UK, 2012
- European Bioinformatics Institute (EBI-EMBL), Hinxton, UK, 2012

Katja Sträßer

PUBLICATIONS

2009

Röther, S. and **Sträßer, K.** (2009) mRNA Export – an integrative component of gene expression. In: Nuclear Transport, edited by Ralph Kehlenbach, Austin: Landes Bioscience, (invited review).

2010

Röther, S., Burkert, C., Brünger, K.M., Mayer, A., Kieser, A., and **Sträßer, K.** (2010) Nucleocytoplasmic shuttling of the La motif-containing protein Sro9 might link its nuclear and cytoplasmic functions, RNA 16, 1393-1401.

Clausing, E., Mayer, A., Chanarat, S., Müller, B., Germann, S.M., **Cramer, P.**, Lisby, M., and **Sträßer, K.** (2010) The transcription elongation factor Bur1-Bur2 interacts with Replication Protein A to maintain genome stability, J. Biol. Chem. 285, 41665-41674.

2011

Lammens, K., Bemeleit, D.J., Möckel, C., Clausing, E., Schele, A., Hartung, S., Schiller, C.B., Lucas, M., Angermüller, C., **Söding, J.**, **Sträßer, K.**, and **Hopfner, K.-P.** (2011) X-ray structure of a bacterial Mre11:Rad50 complex reveals an ATP dependent molecular clamp in DNA double-strand break repair, Cell 145, 54-66.

Chanarat, S., Seizl, M., and **Sträßer, K.** (2011) The Prp19 Complex is a Novel Transcription Elongation Factor Required for TREX Occupancy at Transcribed Genes, Genes Dev. 25, 1147-1158.

2012

Schenk, L., Meinel D.M., **Sträßer, K.**, and Gerber A.P. (2012) La-motif dependent mRNA binding of La-related proteins mediates copper detoxification in yeast, RNA 18, 449-461

Chanarat, S., Burkert-Kautzsch, C., Meinel, D.M., and **Sträßer, K.** (2012) Prp19C and TREX: Interacting to promote transcription elongation and mRNA export, Transcription 3, 8-12 (invited review).

Schiller, C., Lammes, K., Guerini, I., Coordes, B., Schlauderer, F., Möckel, C., Schele, A., **Sträßer, K.**, Jackson, S.P., **Hopfner, K.-P.** (2012) Structural Biology of the Mre11:Nbs1 complex reveals insights into ataxia telangiectasia like disease mutations and DNA damage signaling, Nat Struct Mol Biol 19, 693-700.

INVITED LECTURES

- "Academia meets Industry", Ringberg, 2009
- EU-Büro des BMBF, Munich, 2009
- "Academia meets Industry", Ringberg, 2010
- Annual Meeting of the German Society for Cell Biology (DGZ), Regensburg, 2010
- Cancer Research UK, Clare Hall, London, UK, 2010
- 4th LMB Graduate Student Symposium 2010 "Changing Biology", Cambridge, UK, 2010
- EMBO Young Scientist Forum, Prague, Czech Republic, 2010
- University of Geneva, Switzerland, 2010
- EU-Büro des BMBF, Munich, 2010
- "Academia meets Industry", Ringberg, 2011
- IMRS-LS lecture, Martinsried, 2011
- Graduate School Life Science Munich (LSM), Martinsried, 2011
- Fakultät für Chemie und Biochemie, Ruhr-Unversität Bochum, 2011
- Institut für Biologie, Humboldt-Universität zu Berlin, 2012
- Institut für Biochemie und Molekularbiologie, Universität Hamburg, 2012
- EMBO-YIP meeting, Lisboa, Portugal, 2012
- EMBO Conference „Transcription and Chromatin", Heidelberg, 2012
- AMGEN Scholars Programme, Martinsried, 2012
- Institute of Chemistry and Biochemistry, Berlin, 2012

Petra Wendler

PUBLICATIONS

2009

Wendler, P., Shorter, J., Snead, D., Plisson, C., Clare, D.K., Lindquist, S., and Saibil, H.R. (2009). Motor mechanism for protein threading through Hsp104. Mol Cell 34, 81-92.

2010

Wendler, P., and Saibil, H.R. (2010). Cryo electron microscopy structures of Hsp100 proteins: crowbars in or out? Biochem Cell Biol 88, 89-96.

Wendler, P. (2010). Hsp104- ein eiskaltes Hitzeschockprotein. BIOspektrum 6:648-650.

2011

Stotz, M., Mueller-Cajar, O., Ciniawsky, S., **Wendler, P.**, Hartl, F.U., Bracher, A., and Hayer-Hartl, M. (2011). Structure of green-type Rubisco activase from tobacco. Nat Struct Mol Biol 18, 1366-1370.

Mueller-Cajar, O., Stotz, M., **Wendler, P.**, Hartl, F.U., Bracher, A., and Hayer-Hartl, M. (2011). Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. Nature 479, 194-199.

Wollmann, P., Cui, S., Viswanathan, R., Berninghausen, O., Wells, M.N., Moldt, M., Witte, G., Butryn, A., **Wendler, P.**, **Beckmann, R.**, et al. (2011). Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. Nature 475, 403-407.

2012

Wendler, P., Ciniawsky, S., Kock, M., and Kube, S. (2012). Structure and function of the AAA+ nucleotide binding pocket. Biochim Biophys Acta 1823, 2-14.

INVITED LECTURES

- ZMBH, Heidelberg, 2009
- EMBO conference, Dubrovnik, 2009
- MPI für Biochemie, Martinsried, 2010
- Institut für Chemie, TU München, 2012
- Institut für Genetik, Köln, 2012
- Biologie LMU, München, 2012

Daniel Wilson

PUBLICATIONS

2009

Petropoulos, A.D., Kouvela, E.C., Starosta, A.L., **Wilson, D.N.**, Dinos, G.P., Kalpaxis, D.L. (2009) Time-resolved binding of azithromycin to Escherichia coli ribosomes. J Mol Biol 385: 1179-1192.

Kouvela, E.C., Kalpaxis, D.L., **Wilson, D.N.**, Dinos, G.P. (2009) Distinct mode of interaction of a novel ketolide antibiotic that displays enhanced antimicrobial activity. Antimicrob Agents Chemother 53: 1411-1419.

Wilson, D.N.* (2009) Less is more for leaderless mRNA translation. Mol Cell 33: 141-142.

Moroder, H., Steger, J., Graber, D., Fauster, K., Trappl, K., Marquez, V., Polacek, N., **Wilson, D.N.**, Micura, R. (2009) Non-hydrolyzable RNA-peptide conjugates: a powerful advance in the synthesis of mimics for 3'-peptidyl tRNA termini. Angew Chem Int Ed Engl 48: 4056-4060.

Sohmen, D., Harms, J.M., Schlunzen, F., **Wilson, D.N.*** (2009) SnapShot: Antibiotic inhibition of protein synthesis I. Cell 138: 1248 e1241.

Dhote, V., Starosta, A.L., **Wilson, D.N.**, Reynolds, K.A. (2009) The final step of hygromycin A biosynthesis, oxidation of C-5''-dihydrohygromycin A, is linked to a putative proton gradient-dependent efflux. Antimicrob Agents Chemother 53: 5163-5172.

Sohmen, D., Harms, J.M., Schlunzen, F., **Wilson, D.N.*** (2009) Enhanced SnapShot: Antibiotic inhibition of protein synthesis II. Cell 139: 212-212 e211.

Starosta, A.L., Qin, H., Mikolajka, A., Leung, G.Y., Schwinghammer, K., Nicolaou, K.C., Chen, D.Y., Cooperman, B.S.*, **Wilson, D.N.*** (2009) Identification of distinct thiopeptide-antibiotic precursor lead compounds using translation machinery assays. Chem Biol 16: 1087-1096.

Wilson, D.N.* (2009) The A-Z of bacterial translation inhibitors. Crit Rev Biochem Mol Biol 44: 393-433.

Seidelt, B., Innis, C.A., **Wilson, D.N.**, Gartmann, M., Armache, J.P., Villa, E., Trabuco, L.G., Becker, T., Mielke, T., Schulten, K., Steitz, T.A., **Beckmann, R.** (2009) Structural insight into nascent polypeptide chain-mediated translational stalling. Science 326: 1412-1415.

Palaniappan, N., Dhote, V., Ayers, S., Starosta, A.L., **Wilson, D.N.**, Reynolds, K.A. (2009) Biosynthesis of the aminocyclitol subunit of hygromycin A in Streptomyces hygroscopicus NRRL 2388. Chem Biol 16: 1180-1189.

2010

Sharma, M.R., Donhofer, A., Barat, C., Marquez, V., Datta, P.P., Fucini, P., **Wilson, D.N.***, Agrawal, R.K.* (2010) PSRP1 is not a ribosomal protein, but a ribosome-binding factor that is recycled by the ribosome-recycling factor (RRF) and elongation factor G (EF-G). J Biol Chem 285: 4006-4014.

Bhushan, S., Gartmann, M.,

Halic, M., Armache, J.P., Jarasch, A., Mielke, T., Berninghausen, O., **Wilson, D.N.**, **Beckmann, R.** (2010) alpha-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. Nat Struct Mol Biol 17: 313-317.

Starosta, A.L., Karpenko, V., Shishkina, A., Mikolajka, A., Sumbatyan, N., Schluenzen, F., Korshunova, G., Bogdanov, A.*, **Wilson, D.N.*** (2010) Interplay between the ribosomal tunnel, nascent chain, and macrolides influences drug inhibition. Chem Biol 17: 504-14.

Blanchard, S.C., Cooperman, B.S., **Wilson, D.N.*** (2010) Probing translation with small molecule inhibitors. Chem. Biol. 17:633-45.

Bhushan, S., Meyer, H., Starosta, A.L., Becker, T., Mielke, T., Berninghausen, O., Sattler, M., **Wilson, D.N.***, **Beckmann, R.*** (2010) Structural basis for translational stalling by human cytomegalovirus and fungal arginine attenuator peptide. Molecular Cell, 40:138-46.

Armache, J.P., Jarasch, A., Anger, A.M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., Marquez, V., Mielke, T., Thomm, M., Berninghausen, O., Beatrix, B., **Soeding, J.**, Westhof, E., **Wilson, D.N.*** and **Beckmann, R.*** (2010) Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5 Å resolution, Proc. Natl. Acad. Sci. USA, 107:19748-53.

Armache, J.P., Jarasch, A., Anger, A.M., Villa, E., Becker, T., Bhushan, S., Jossinet, F., Habeck, M., Dindar, G., Franckenberg, S., Marquez, V., Mielke, T., Thomm, M., Berninghausen, O., Beatrix, B., **Soeding, J.**, Westhof, E., **Wilson, D.N.*** and **Beckmann, R.*** (2010) Localization of eukaryote-specific ribosomal proteins in a 5.5 Å cryo-EM map of the 80S eukaryotic ribosome. Proc. Natl. Acad. Sci. USA, 107:19754-9.

Ratje, A.H., Loerke, J., Mikolajka, A., Brünner, M., Hildebrand, P.W., Starosta, A.L., Dönhöfer, A., Connell, S.R., Fucini, P., Mielke, T., Whitford, P.C., Onuchic, J.N., Yu, Y., Sanbonmatsu, K.Y., Hartmann, R.K., Penczek, P.A., **Wilson, D.N.***, and Spahn, C.M.T.* (2010) Head swivel on the ribosome facilitates translocation via intra-subunit tRNA hybrid sites. Nature, 468:713-6.

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INVITED LECTURES

- Institute of Organic Chemistry, Leopold Franzens University, Innsbruck, 2009
- Department of Chemistry, University of Pennsylvania, Philadelphia, USA, 2009
- 25th Anniversary of the Gene Center, University of Munich, Germany, 2009
- Jefferson Medical College, Thomas Jefferson University, Philadelphia, USA, 2009
- Weill Cornell Medical College, Cornell University, New York, USA, 2009
- Center for Pharmaceutical Biotechnology, University of Illinois, Chicago, USA, 2009
- 29th Interscience Conference on Antimicrobial Agents and Chemotherapy (ICAAC), San Francisco, USA, 2009
- Department of Molecular Biology, Tartu University, Estonia, 2009
- Ribosome symposium, Max-Planck-Institute for Molecular Genetics, Berlin, Germany, 2010
- Department of Chemistry, Moscow Lomonosov State University, Russia, 2010
- Ribosome conference, Orvieto, Italy, 2009
- Department of Cell and Molecular Biology, Uppsala University, Sweden, 2010
- Medical Department, University of Patras, Greece, 2010
- Paul-Ehrlich Foundation, Frankfurt, Germany, 2010
- Ringberg Meeting, Schloss Ringberg, Tegernsee, Germany, 2011
- Fraunhofer Institut für Biomedizinische Technik IBMT, Potsdam Berlin, Germany, 2011
- Department of Chemistry, Technical University, Munich Germany, 2011
- University of Kassel Bioscience, Kassel, Germany, 2011
- EMBO Young investigators meeting, Heidelberg, Germany, 2011
- Vienna Biocenter, University of Vienna, Austria, 2011
- Antibiotics and ribosomes meeting, Tartu, Estonia, 2011
- EMBO Young Scientists Forum, Warsaw, Poland, 2011
- IGBMC, Université de Strasbourg, Strasbourg, France, 2012
- Institute of Organic Chemistry, Leopold Franzens University, Innsbruck, 2012
- EMBO Young investigators meeting, Lisbon, Portugal, 2012
- Jacque Monod Conference, Roscoff, France, 2012
- John Hopkins Medical College, Baltimore, USA, 2012
- CSH Translational Control Meeting, New York, USA, 2012
- Birkbeck, University College London, London, UK, 2012

Eckhard Wolf

PUBLICATIONS

2009

Aigner, B., Rathkolb, B., Klaften, M., Sedlmeier, R., Klempt, M., Wagner, S., Michel, D., Mayer, U., Klopstock, T., de Angelis, M.H., and **Wolf, E.** (2009). Generation of N-ethyl-N-nitrosourea-induced mouse mutants with deviations in plasma enzyme activities as novel organ-specific disease models. Experimental physiology 94, 412-421.

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Fuchs, H., Sabrautzki, S., Seedorf, H., Rathkolb, B., Rozman, J., Hans, W., Schneider, R., Klaften, M., Holter, S.M., Becker, L., et al. (2012). Does enamelin have pleiotropic effects on organs other than the teeth? Lessons from a phenotyping screen of two enamelin-mutant mouse lines. European journal of oral sciences 120, 269-277.

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Schneider, M.R., Dahlhoff, M., Andrukhova, O., Grill, J., Glosmann, M., Schuler, C., Weber, K., **Wolf, E.**, and Erben, R.G. (2012). Normal epidermal growth factor receptor signaling is dispensable for bone anabolic effects of parathyroid hormone. Bone 50, 237-244.

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INVITED LECTURES

- 35th Conference of the International Embryo Transfer Society, San Diego, USA, 2009
- 52. Symposium der Deutschen Gesellschaft für Endokrinologie, Giessen, 2009
- International Symposium Xenotransplantation, Robert-Koch-Institut, Berlin, 2009
- Institute «Lymphocyte et Immunité des Muqueuses», INRA, Nouzilly, France, 2009
- UC Davis Transgenic Animal Research Conference, Lake Tahoe, USA, 2009
- Roche and Pembroke College Cambridge Workshop "Stem Cell Research – Business Mission or Medical Vision", Basel, 2009
- Wageningen UR, Lelystad, The Netherlands, 2010
- Leopoldina-Symposium „Das gläserne Tier: Ein- und Ausblicke in Genome und Gene von Haustieren", Wien, 2010
- 6th Pfizer Bovine Reproduction Consortium, Swansea, UK, 2010
- 8th International Ruminant Reproduction Symposium, Anchorage, AK, USA, 2010
- Workshop "Pluripotent Stem Cells in Animals and Humans", Eger, Hungary, 2010
- 2nd International Workshop "Large Animal Models for Biomedicine", Fundación BBVA, Madrid, 2010
- 5th World Congress on Preventive & Regenerative Medicine, Hannover, 2010
- Cardiac Stem Cell and Tissue Engineering Conference, Venice, Italy, 2011
- BIOANIREP-Workshop, Wierzba, Poland, 2011
- ILAF, ESLAV and ECLAM Joint Scientific Meeting, Jerusalem, Israel, 2011
- Jahresversammlung der Leopoldina – Nationale Akademie der Wissenschaften, Halle (Saale), 2011
- 4th International Symposium on Animal Functional Genomics, Dublin, Ireland, 2011
- Fondation Mérieux Symposium "Animal Models and Relevance/ Predictivity", Veyrier-du-Lac, France, 2011
- 10th Transgenic Technology Meeting, St. Pete Beach, Florida, USA, 2011
- HTF Platform "Pigs & Health", Copenhagen, Denmark, 2011
- Novo Nordisk, Copenhagen, Denmark, 2011
- EFOR workshop "Transgenesis of Farm Animals – Methods and Objectives", Paris, France, 2012
- F. Hoffmann-La Roche AG, Basel, Switzerland, 2012
- COST Action FA0902 "Understanding and Combating PRRS in Europe", Lodi, Italy, 2012
- Wageningen UR, Wageningen, The Netherlands, 2012
- RE(ACT)® 2012 – International Congress on Research of Rare and Orphan Diseases, Basel, Switzerland, 2012
- Roche Diagnostics, Penzberg, 2012
- Sanofi Deutschland GmbH, Frankfurt, 2012
- Paul Langerhans Institut, Dresden, 2012
- Institut für Humangenetik der Universität Göttingen, 2012
- Lund University Diabetes Centre, Malmö, Sweden, 2012
- DZD Workshop and Satellite Symposium, Dresden, 2012
- 17th International Congress on Animal Reproduction, Vancouver, Canada, 2012
- Universitäts-Kinderspital Zürich, Switzerland, 2012

Dierk Niessing

PUBLICATIONS

2009

Graebsch, A., Roche, S., **Niessing, D.** (2009). X-ray structure of Pur-alpha reveals a Whirly-like fold and an unusual nucleic-acid binding surface. Proc Natl Acad Sci USA (Direct submission) 106, 18521-18526.

Müller, M., Richter, K., Heuck, A., Kremmer, E., Buchner, J., Jansen, R.-P., **Niessing, D.** (2009). Formation of She2p Tetramers is Required for mRNA Bindung, mRNP Assembly, and Localization. RNA 15, 2002-2012.

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Heuck, A., Fekta, I., Brewer, D.N., Hüls, D., Munson, M., Jansen, R.-P., **Niessing, D.** (2010). The structure of the Myo4p globular tail and its function in ASH1 mRNA localization. J Cell Biol 189, 497-510.

Graebsch, A., Roche, S., Kostrewa, D., **Söding, J.**, **Niessing, D.** (2010). Of Bits and Bugs - on the use of bioinformatics and a bacterial crystal structure to solve a eukaryotic repeat-protein structure. PLoS ONE 5(10): e13402.

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Müller, M.*, Heym, R.*, Mayer, A., Kramer, K., Schmid, M., **Cramer, P.**, Urlaub, H., Jansen, R.P., and **Niessing, D.** (2011). A Cytoplasmic Complex Mediates Specific mRNA Recognition and Localization in Yeast. PLoS Biol 9, e1000611 . *equal contribution

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Hüls, D., Storchova, Z. and **Niessing, D.** (2012). Posttranslational modifications regulate assembly of the early spindle-orientation complex in yeast. J Biol Chem 287(20), 16238-16245.

Hüls, D. and Niessing D. (2012). Purification, crystallization and preliminary crystallographic analysis of Kar9p from Saccharomyces cerevisiae. Acta Cryst Section F 68, 1251-1254.

Jansen, R.-P. and **Niessing, D.** (2012). Assembly of mRNA-protein complexes for directional mRNA transport in eukaryotes - an overview. (Review; Special Issue on "Proteins involved in post-transcriptional control of gene expression") (2012) Curr Prot Pept Sci 13(4), 284-293.

Aumiller V., Graebsch A., Kremmer E., **Niessing, D.**, and Förstemann K. (2012). Drosophila Pur-alpha binds to trinucleotide-repeat containing cellular RNAs and translocate to the early oocyte. (2012) RNA Biol 9(5), 633-643.

INVITED LECTURES

- ESF, Sant Feliu de Guixols, Spain, 2009
- EMBO, Heidelberg, Germany, 2009
- EMBL, Heidelberg, Germany, 2010
- EMBO-ESF, Vienna, Austria, 2010
- EURASNET, Poznan, Poland, 2010
- Cold Spring Harbor Conference, USA, 2010
- EMBO-ESF, Sant Feliu de Guixols, Spain, 2010
- EMBO, Barga, Italy, 2011
- EMBO, Heidelberg, Germany, 2011
- CIBIO, Lago di Garda, Italy, 2012
- EMBO, Heidelberg, Germany, 2012
- CNRS/Jaques Monod conference, Roscoff, France, 2012
- DFG Graduate School 1591, Halle, Germany, 2012

Ulrich Koszinowski

PUBLICATIONS

2009

Arapovic, J., Lenac, T., Antulov, R., Polic, B., Ruzsics, Z., Carayannopoulos, L.N., **Koszinowski, U.H.**, Krmpotic, A., and Jonjic, S. (2009). Differential susceptibility of RAE-1 isoforms to mouse cytomegalovirus. J. Virol. 83, 8198-8207.

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Kielczewska, A., Pyzik, M., Sun, T., Krmpotic, A., Lodoen, M.B., Munks, M.W., Babic, M., Hill, A.B., **Koszinowski, U.H.**, Jonjic, S., Lanier, L.L., and Vidal, S.M. (2009). Ly49P recognition of cytomegalovirus-infected cells expressing H2-Dk and CMV-encoded m04 correlates with the NK cell antiviral response. J. Exp. Med. 206, 515-523.

Muhlbach, H., Mohr, C.A., Ruzsics, Z., and **Koszinowski, U.H.** (2009). Dominant-negative proteins in herpesviruses - from assigning gene function to intracellular immunization. Viruses. 1, 420-440.

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Champsaur, M., Beilke, J.N., Ogasawara, K., **Koszinowski, U.H.**, Jonjic, S., and Lanier, L.L. (2010). Intact NKG2D-independent function of NK cells chronically stimulated with the NKG2D ligand Rae-1. J. Immunol. 185, 157-165.

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Dolken, L., Malterer, G., Erhard, F., Kothe, S., Friedel, C.C., Suffert, G., Marcinowski, L., Motsch, N., Barth, S., Beitzinger, M., Lieber, D., Bailer, S.M., Hoffmann, R., Ruzsics, Z., Kremmer, E., Pfeffer, S., Zimmer, R., **Koszinowski, U.H.**, Grasser, F., Meister, G., and Haas, J. (2010). Systematic analysis of viral and cellular microRNA targets in cells latently infected with human gamma-herpesviruses by RISC immunoprecipitation assay. Cell Host. Microbe 7, 324-334.

Hengel ,H. and **Koszinowski, U.H.** (2010). Virology. A vaccine monkey wrench? Science 328, 51-52.

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Popa, M., Ruzsics, Z., Lotzerich, M., Dolken, L., Buser, C., Walther, P., and **Koszinowski, U.H.** (2010). Dominant negative mutants of the murine cytomegalovirus M53 gene block nuclear egress and inhibit capsid maturation. J. Virol. 84, 9035-9046.

Scrivano, L., Esterlechner, J., Muhlbach, H., Ettischer, N., Hagen, C., Grunewald, K., Mohr, C.A., Ruzsics, Z., Koszinowski, U., and Adler, B. (2010). The m74 gene product of murine cytomegalovirus (MCMV) is a functional homolog of human CMV gO and determines the entry pathway of MCMV. J. Virol. 84, 4469-4480.

Slavuljica, I., Busche, A., Babic, M., Mitrovic, M., Gasparovic, I., Cekinovic, D., Markova, C.E., Pernjak, P.E., Cikovic, A., Lisnic, V.J., Britt, W.J., Koszinowski, U., Messerle, M., Krmpotic, A., and Jonjic, S. (2010). Recombinant mouse cytomegalovirus expressing a ligand for the NKG2D receptor is attenuated and has improved vaccine properties. J. Clin. Invest 120, 4532-4545.

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Lemnitzer, F., Raschbichler, V., Kolodziejczak, D., Israel, L., Imhof, A., Bailer, S.M., Koszinowski, U., and Ruzsics, Z. (2012). Mouse cytomegalovirus egress protein pM50 interacts with cellular endophilin-A2. Cell Microbiol. published online Nov 29.

Nopora, K., Bernhard, C.A., Ried, C., Castello, A.A., Murphy, K.M., Marconi, P., Koszinowski, U., and Brocker, T. (2012). MHC class I cross-presentation by dendritic cells counteracts viral immune evasion. Front Immunol. 3, 348.

Pogoda, M., Bosse, J.B., Wagner, F.M., Schauflinger, M., Walther, P., **Koszinowski, U.H.**, and Ruzsics, Z. (2012). Characterization of Conserved Region 2-Deficient Mutants of the Cytomegalovirus Egress Protein pM53. J. Virol. 86, 12512-12524.

Motamedi, N., Mairhofer, H., Nitschko, H., Jager, G., and **Koszinowski, U.H.** (2012). The polyomaviruses WUPyV and KIPyV: a retrospective quantitative analysis in patients undergoing hematopoietic stem cell transplantation. Virol. J. 9, 209.

Chiossone, L., Audonnet, S., Chetaille, B., Chasson, L., Farnarier, C., Berda-Haddad, Y., Jordan, S., **Koszinowski, U.H.**, Dalod, M., Mazodier, K., Novick, D., Dinarello, C.A., Vivier, E., and Kaplanski, G. (2012). Protection from inflammatory organ damage in a murine model of hemophagocytic lymphohistiocytosis using treatment with IL-18 binding protein. Front Immunol. 3, 239.

Bosse, J.B., Bauerfeind, R., Popilka, L., Marcinowski, L., Taeglich, M., Jung, C., Striebinger, H., von Einem, .J., **Gaul, U.**, Walther, P., **Koszinowski, U.H.**, and Ruzsics, Z. (2012). A beta-herpesvirus with fluorescent capsids to study transport in living cells. PLoS. One. 7, e40585.

Mohr, H., Mohr, C.A., Schneider, M.R., Scrivano, L., Adler, B., Kraner-Schreiber, S., Schnieke, A., Dahlhoff, M., **Wolf, E.**, **Koszinowski, U.H.**, and Ruzsics, Z. (2012). Cytomegalovirus replicon-based regulation of gene expression in vitro and in vivo. PLoS. Pathog. 8, e1002728.

Schnee, M., Wagner, F.M., **Koszinowski, U.H.**, and Ruzsics,

Z. (2012). A cell free protein fragment complementation assay for monitoring the core interaction of the human cytomegalovirus nuclear egress complex. Antiviral Res. 95, 12-18.

Marcinowski, L., Tanguy, M., Krmpotic, A., Radle, B., Lisnic, V.J., Tuddenham, L., Chane-Woon-Ming, B., Ruzsics, Z., Erhard, F., Benkartek, C., Babic, M., Zimmer, R., Trgovcich, J., **Koszinowski, U.H.**, Jonjic, S., Pfeffer, S., and Dolken, L. (2012). Degradation of cellular mir-27 by a novel, highly abundant viral transcript is important for efficient virus replication in vivo. PLoS. Pathog. 8, e1002510.

Koszinowski, U. (2012). Viral functions and immune modulation. Eur. J. Cell Biol. 91, 1.

Sacher, T., Mohr, C.A., Weyn, A., Schlichting, C., **Koszinowski, U.H.**, and Ruzsics, Z. (2012). The role of cell types in cytomegalovirus infection in vivo. Eur. J. Cell Biol. 91, 70-77.

INVITED LECTURES

- 14th International Conference on human Herpesviruses, Kobe, Japan, 2009
- 12th International CMV / Betaherpesvirus Workshop, Boston, USA, 2009
- 4th European Congress of Virology, Cernobbio, Italy, 2010
- Talk at the University of Birmingham Birmingham, England,
- 15th International Conference on Herpesvirus Infections, San Servolo, Italy, 2011
- Fritz-Hartmann-Lecture, Hannover, Germany, 2011
- SFB 796, Opening Lecture, Bamberg, Germany, 2011
- Summer School, Potsdam, Germany, 2011
- Seminar at the University of Bordeaux, Bordeaux, France, 2011
- International CMV / Betaherpesvirus Workshop, San Francisco, USA, 2012
- 7th Virus Assembly Meeting, Menorca, Spain, 2012
- Talk at Cambridge University, Cambridge, England, 2012

Achim Tresch

PUBLICATIONS

2009

Buness, A., Ruschhaupt, M., Kuner, R., **Tresch, A.** Classification across gene expression microarray studies. BMC Bioinformatics. 10:453.

Klein, K., Glaser, M., Reisch, R., **Tresch, A.**, Werner, C., Engelhard, K. Intraoperative Monitoring of Cerebral Microcirculation and Oxygenation - A Feasibility Study using a novel Photo-Spectrometric Laser Doppler Flowmetry. J Neurosurgical Anesthesiology. 22(1):38-45.

Hoffman, A., Basting, N., Goetz, M., **Tresch, A.**, Mudter, J., Biesterfeld, S., Galle, P., Neurath, M., Kiesslich, R. High-definition endoscopy with i-Scan and Lugol's solution for more precise detection of mucosal breaks in patients with reflux symptoms. Endoscopy.

Haaf, T., **Tresch, A.**, Lambrecht, A., Grossmann, B., Schwaab, E., Khanaga, O., Hahn, T., Schorsch, M. Outcome of intracytoplasmatic sperm injection with and without polar body diagnosis of oocytes. Fertil. Steril. 93(2):405-15.

Anchang, B., Sadeh, M., Jacob, J., **Tresch, A.**, Vlad, M., Oefner, P., Spang, R. Modelling the temporal interplay of molecular signalling and gene expression using dynamic nested effects models. PNAS. 106(16):6447-52.

Klein, K., Glaser, M., Reisch, R., **Tresch, A.**, Werner, C., Engelhard, K. Effects of PaCO2 and Sevoflurane on Simultaneous Measurements of Cortical Blood Flow and Oxygen Saturation during Craniotomy. Anesth Analg. 109(1):199-204.

Fröhlich, H., **Tresch, A.**, Beissbarth, T. Nested Effects Models for Learning Signalling Networks from Perturbation Data. Biometrical Journal. 51(2):304-23.

Zeller, C., Fröhlich, H., **Tresch, A.** A Bayesian network view on nested effects models. EURASIP J Bioinform Syst Biol. 2009:195272.

2010

Fröhlich, H., Praveen, P., **Tresch, A.** Fast and efficient dynamic Nested Effects Models. Bioinformatics. (2):238-44.

Joecker, A., Sonntag, J., Henjes, F., Goetschel, F., **Tresch, A.**, Beissbarth, T., Wiemann, S., Korf, U. QuantProReloaded: Quantitative analysis of Microspot Immunoassays. Bioinformatics (2010). (19):2480-1.

Stritzker, J., Weibel, S., Seubert, C., Götz, A., **Tresch, A.**, van Rooijen, N., Oelschlaeger, T., Hill, P., Gentschevl, I., Szalayl, A. Enterobacterial tumor colonization in mice depends on bacterial metabolism and macrophages but is independent of chemotaxis and motility. Int J Med Microbiol. (7):449-56.

Hoffman, A., Kagel, C., Goetz, M., **Tresch, A.**, Mudter, J., Biesterfeld, S., Galle, P., Neurath, M., Kiesslich, R. Recognition and characterization of small colonic neoplasia with high-definition colonoscopy using i-Scan is as precise as chromoendoscopy. Dig Liver Dis. 4:53.

Schneider, E., Pliushch, G., El Hajj, N., Galetzka, D., Puhl, A., Schorsch, M., Frauenknecht, K., Riepert, T., **Tresch, A.**, Müller, A., Coerdt, W., Zechner, U., Haaf, T. Spatial, temporal and interindividual epigenetic variation of functionally important DNA methylation patterns. Nucleic Acids Research. 38(12):3880-90.

Hartung, S., Niederberger, T., Hartung, M., **Tresch, A.**, **Hopfner, K.P.** Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. Nucleic Acids Research. (15):5166-76.

Zacher, B., Kuan, P.F., **Tresch, A.** Starr: Simple Tiling ARRay analysis of Affymetrix ChIP-chip data. BMC Bioinformatics. 11:194.

Zechner, U., Pliushch, G., Schneider, E., El Hajj, N., **Tresch, A.**, Shufaro, Y., Seidmann, L., Müller, A., Coerdt, W., Haaf, T. Quantitative methylation analysis of developmentally important genes in human pregnancy losses after ART and spontaneous conception. Molecular Human Reproduction. 16(9):704-13.

Pliusch, G., Schneider, E., Weise, D., El Hajj, N., **Tresch, A.**, Seidmann, L., Coerdt, W., Müller, A., Zechner, U., Haaf, T. Extreme Methylation Values of Imprinted Genes in Human Abortions and Stillbirths. The American Journal of Pathology. 176(3):1084-90.

2011

Gagneur, J., Elze, M., **Tresch, A.** Selective phenotyping, Entropy Reduction and the Mastermind Game. BMC Bioinformatics. 12:406.

Zacher, B., Torkler, P., **Tresch, A.** Analysis of Affymetrix ChIP-chip data using Starr and Bioconductor. Cold Spring Harbor Protocols. 1;2011(5)

Miller, C., Schwalb, B., Maier, K., Schulz, D., Dümcke, S., Zacher, B., Mayer, A., Sydow, J., Marcinowski, L., Dölken, L., Martin, D., **Tresch, A.**, **Cramer, P.** Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Molecular Systems Biology. 7:458.

Beerenwinkel, N., Knupfer, P., **Tresch, A.** Learning monotonic genotype-phenotype maps. Statistical Applications in Genetics and Molecular Biology. 10(1)

Niederberger, T., Hartung, S., **Hopfner, K.P.**, **Tresch, A.** Processive RNA decay by the Exosome: Merits of a quantitative Bayesian Sampling approach. RNA Biology. (1):55-60.

Krupp, M., Maass, T., Staib, F., Bauer, T., Biesterfeld, S., Galle, P., **Tresch, A.**, Teufel, A. The functional cancer map: A systems-level synopsis of dysregulation in cancer. BMC Medical Genomics. 4:53.

Siggelkow, W., Schmidt, M., Skala, C., Boehm, D., von Forstner, S., Koelbl, H., **Tresch, A.** A new algorithm for improving fetal weight estimation from ultrasound data at term. Archives of Gynecology and Obstetrics. 283:469–474.

2012

Niederberger, T., Etzold, S., Lidschreiber, M., Maier, K.C., Martin, D.E., Frohlich, H., **Cramer, P.**, and **Tresch, A.** (2012). MC EMiNEM maps the interaction landscape of the Mediator. PLoS Comput Biol 8, e1002568.

Dumcke, S., Seizl, M., Etzold, S., Pirkl, N., Martin, D.E., **Cramer, P.**, and **Tresch, A.** (2012). OneHandClapping: Detection of condition-specific transcription factor interactions from genome-wide gene activity data. Nucleic Acids Res 40, 8883-8892.

Zacher, B., Abnaof, K., Gade, S., Younesi, E., **Tresch, A.**, Fröhlich, H. Joint Bayesian Inference of Condition Specific miRNA and Transcription Factor Activities from Combined Gene and microRNA Expression Data, Bioinformatics, 28(13):1714-20.

Schwalb, B., Schulz, D., Sun, M., Zacher, B., Dumcke, S., Martin, D.E., **Cramer, P.**, and **Tresch, A.** (2012). Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). Bioinformatics 28, 884-885.

Sun, M., Schwalb, B., Schulz, D., Pirkl, N., Etzold, S., Lariviere, L., Maier, K.C., Seizl, M., **Tresch, A.**, and **Cramer, P.** (2012). Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. Genome Res 22, 1350-1359.

Miller, C., Matic, I., Maier, K., Schwalb, B., Roether, S., Straesser, K., **Tresch, A.**, Mann, M., and **Cramer, P.** (2012). Mediator phosphorylation prevents stress response transcription during non-stress conditions. J Biol Chem, Nov 7. [Epub ahead of print]

INVITED LECTURES

- ESF workshop, Paris, 2009
- University of Oslo, 2009
- Dept. of Genome Control, UMC Utrecht, 2010
- IMB Dresden, 2010
- ETH Zurich, Basel, 2010
- Dept. of Computational Systems Biology, University of Wien, 2011
- Boehringer Ingelheim, Titisee, 2011
- Cancer Research UK, Cambridge, 2012

LAFUGA

PUBLICATIONS

2009

Baehs, S., Herbst, A., Thieme, S.E., Perschl, C., Behrens, A., Scheel, S., Jung, A., Brabletz, T., Goke, B., **Blum, H.**, Kolligs, F.T. (2009). Dickkopf-4 is frequently down-regulated and inhibits growth of colorectal cancer cells. Cancer Lett 276, 152-159.

Bauersachs, S., Ulbrich, S.E., Zakhartchenko, V., Minten, M., Reichenbach, M., Reichenbach, H.D., **Blum, H.**, Spencer, T.E., and **Wolf, E.** (2009). The endometrium responds differently to cloned versus fertilized embryos. Proc Natl Acad Sci U S A 106, 5681-5686.

Krebs, S., Fischaleck, M., and **Blum, H.** (2009). A simple and loss-free method to remove TRIzol contaminations from minute RNA samples. Anal Biochem 387, 136-138.

Seeliger, H., Camaj, P., Ischenko, I., Kleespies, A., De Toni, E.N., Thieme, S.E., **Blum, H.**, Assmann, G., Jauch, K.W., and Bruns, C.J. (2009). EFEMP1 expression promotes in vivo tumor growth in human pancreatic adenocarcinoma. Mol Cancer Res 7, 189-198.

Frohlich, T., and **Arnold, G.J.** (2009). A newcomer's guide to nano-liquid-chromatography of peptides. Methods in molecular biology (Clifton, NJ) 564, 123-141.

Frohlich, T., **Arnold, G.J.**, Fritsch, R., Mayr, T., and Laforsch, C. (2009). LC-MS/MS-based proteome profiling in Daphnia pulex and Daphnia longicephala: the Daphnia pulex genome database as a key for high throughput proteomics in Daphnia. BMC genomics 10, 171.

Ulbrich, S.E., Frohlich, T., Schulke, K., Englberger, E., Waldschmitt, N., **Arnold, G.J.**, Reichenbach, H.D., Reichenbach, M., **Wolf, E.**, Meyer, H.H., et al. (2009). Evidence for estrogen-dependent uterine serpin (SERPINA14) expression during estrus in the bovine endometrial glandular epithelium and lumen. Biology of reproduction 81, 795-805.

Berendt, F.J., Frohlich, T., Bolbrinker, P., Boelhauve, M., Gungor, T., Habermann, F.A., **Wolf, E.**, and **Arnold, G.J.** (2009). Highly sensitive saturation labeling reveals changes in abundance of cell cycle-associated proteins and redox enzyme variants during oocyte maturation in vitro. Proteomics 9, 550-564.

2010

Bauersachs, S., **Blum, H.**, Krebs, S., Frohlich, T., **Arnold, G.J.**, and **Wolf, E.** (2010). Creating new knowledge for ruminant reproduction from rapidly expanding and evolving scientific databases. Society of Reproduction and Fertility supplement 67, 29-40.

Mitterhuemer, S., Petzl, W., Krebs, S., Mehne, D., Klanner, A., **Wolf, E.**, Zerbe, H., and **Blum, H.** (2010). Escherichia coli infection induces distinct local and systemic transcriptome responses in the mammary gland. BMC Genomics 11, 138.

Ostrup, E., Bauersachs, S., **Blum, H.**, **Wolf, E.**, and Hyttel, P. (2010). Differential endometrial gene expression in pregnant and nonpregnant sows. Biol Reprod 83, 277-285.

Shimizu, T., Krebs, S., Bauersachs, S., **Blum, H.**, **Wolf, E.**, and Miyamoto, A. (2010). Actions and interactions of progesterone and estrogen on transcriptome profiles of the bovine endometrium. Physiol Genomics 42A, 290-300.

Schulz, C., Leuschen, N.V., Frohlich, T., Lorenz, M., Pfeiler, S., Gleissner, C.A., Kremmer, E., Kessler, M., Khandoga, A.G., Engelmann, B., et al. and **Arnold, G.J.** (2010). Identification of novel downstream targets of platelet glycoprotein VI activation by differential proteome analysis: implications for thrombus formation. Blood 115, 4102-4110.

2011

Greif, P.A., Yaghmaie, M., Konstandin, N.P., Ksienzyk, B., Alimoghaddam, K., Ghavamzadeh, A., Hauser, A., Graf, A., Krebs, S., **Blum, H.**, and Bohlander, S.K. (2011). Somatic mutations in acute promyelocytic leukemia (APL) identified by exome sequencing. Leukemia : official journal of the Leukemia Society of America, Leukemia Research Fund, UK 25, 1519-1522.

Gunther, J., Esch, K., Poschadel, N., Petzl, W., Zerbe, H., Mitterhuemer, S., **Blum, H.**, and Seyfert, H.M. (2011). Comparative kinetics of Escherichia coli- and Staphylococcus aureus-specific activation of key immune pathways in mammary epithelial cells demonstrates that S. aureus elicits a delayed response dominated by interleukin-6 (IL-6) but not by IL-1A or tumor necrosis factor alpha. Infection and immunity 79, 695-707.

Arnold, G.J., and Frohlich, T. (2011). Dynamic proteome signatures in gametes, embryos and their maternal environment. Reproduction, fertility, and development 23, 81-93.

Blutke, A., Block, C., Berendt, F., Herbach, N., Kemter, E., Amann, K., Frohlich, T., **Arnold, G.J.**, and Wanke, R. (2011). Differential glomerular proteome analysis of two murine nephropathy models at onset of albuminuria. Proteomics Clinical applications 5, 375-381

Colbourne, J.K., Pfrender, M.E., Gilbert, D., Thomas, W.K., Tucker, A., Oakley, T.H., Tokishita, S., Aerts, A., **Arnold, G.J.**, Basu, M.K., et al. (2011). The ecoresponsive genome of Daphnia pulex. Science (New York, NY) 331, 555-561.

Frohlich, T., and **Arnold, G.J.** (2011). Quantifying attomole amounts of proteins from complex samples by nano-LC and selected reaction monitoring. Methods in molecular biology (Clifton, NJ) 790, 141-164.

Marquez, V., Frohlich, T., Armache, J.P., Sohmen, D., Donhofer, A., Mikolajka, A., Berninghausen, O., Thomm, M., **Beckmann, R.**, **Arnold, G.J.**, and **Wilson, D.N.** (2011). Proteomic characterization of archaeal ribosomes reveals the presence of novel archaeal-specific ribosomal proteins. Journal of molecular biology 405, 1215-1232.

Spinnler, K., Frohlich, T., **Arnold, G.J.**, Kunz, L., and Mayerhofer, A. (2011). Human tryptase cleaves pro-nerve growth factor (pro-NGF): hints of local, mast cell-dependent regulation of NGF/pro-NGF action. The Journal of biological chemistry 286, 31707-31713.

Ulbrich, S.E., Meyer, S.U., Zitta, K., Hiendleder, S., Sinowatz, F., Bauersachs, S., Buttner, M., Frohlich, T., **Arnold, G.J.**, Reichenbach, H.D., **Wolf, E.**, Meyer, H.H. (2011). Bovine endometrial metallopeptidases MMP14 and MMP2 and the metallopeptidase inhibitor TIMP2 participate in maternal preparation of pregnancy. Molecular and cellular endocrinology 332, 48-57.

2012

Greif, P.A., Dufour, A., Konstandin, N.P., Ksienzyk, B., Zellmeier, E., Tizazu, B., Sturm, J., Benthaus, T., Herold, T., Yaghmaie, M., Dörge, P., **Hopfner, K.P.**, Hauser, A., Graf, A., Krebs, S., **Blum, H.**, et al. (2012). GATA2 zinc finger 1 mutations associated with biallelic CEBPA mutations define a unique genetic entity of acute myeloid leukemia. Blood. 120(2):395-403.

Medugorac, I., Seichter, D., Graf, A., Russ, I., **Blum, H.**, Gopel, K.H., Rothammer, S., Forster, M., and Krebs, S. (2012). Bovine polledness--an autosomal dominant trait with allelic heterogeneity. PloS one 7, e39477.

Renner, S., Romisch-Margl, W., Prehn, C., Krebs, S., Adamski, J., Goke, B., **Blum, H.**, Suhre, K., Roscher, A.A., and **Wolf, E.** (2012). Changing metabolic signatures of amino acids and lipids during the prediabetic period in a pig model with impaired incretin function and reduced beta-cell mass. Diabetes 61, 2166-2175.

Streyl, D., Kenngott, R., Herbach, N., Wanke, R., **Blum, H.**, Sinowatz, F., **Wolf, E.**, Zerbe, H., and Bauersachs, S. (2012). Gene expression profiling of bovine peripartal placentomes: detection of molecular pathways potentially involved in the release of foetal membranes. Reproduction 143, 85-105.

Demant, M., Trapphoff, T., Frohlich, T., **Arnold, G.J.**, and Eichenlaub-Ritter, U. (2012). Vitrification at the pre-antral stage transiently alters inner mitochondrial membrane potential but proteome of in vitro grown and matured mouse oocytes appears unaffected. Human reproduction (Oxford, England) 27, 1096-1111.

Klymiuk, N., Bocker, W., Schonitzer, V., Bahr, A., Radic, T., Frohlich, T., Wunsch, A., Kessler, B., Kurome, M., Schilling, E., et al. **Arnold, G.J.**, Schwinzer, R., Schieker, M., **Wolf, E.** (2012). First inducible transgene expression in porcine large animal models. FASEB journal : official publication of the Federation of American Societies for Experimental Biology 26, 1086-1099.

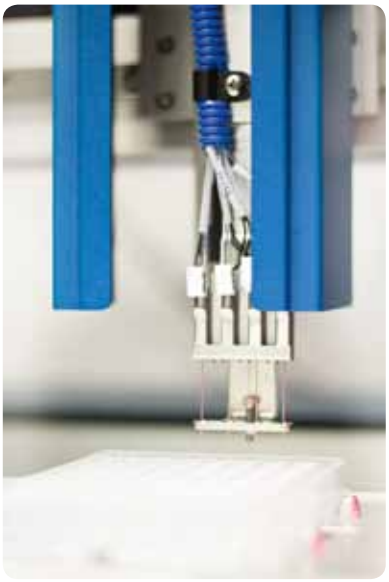
Armache, J.P., Anger, A.M., Marquez, V., Franckenberg, S., Fröhlich, T., Villa, E., Berninghausen, O., Thomm, M.; **Arnold, G.J.**, **Beckmann, R.**, and **Wilson, D.N.** (2012). Promiscuous behaviour of archaeal ribosomal proteins: Implications for eukaryotic ribosome evolution. Nucleic Acids Res. published online Dec 6.

Korte, J., Frohlich, T., Kohn, M., Kaspers, B., **Arnold, G.J.**, and Hartle, S. (2012). 2-D DIGE analysis of the bursa of Fabricius reveals characteristic proteome profiles for different stages of chicken B-cell development. Proteomics, published online Nov 8..

Arnold, G.J., and Frohlich, T. (2012). 2D DIGE saturation labeling for minute sample amounts. Methods in molecular biology (Clifton, NJ) 854, 89-112.

INVITED LECTURES

- 2009 European Society of Human Reproduction and Embryology, ESHRE CAMPUS, Potsdam, Germany (**G. Arnold**)
- 2010 European Society of Human Reproduction and Embryology, ESHRE,Potsdam, Brussels, Belgium (**G. Arnold**)
- 2011 International Embryo Transfer Society IETS, Annual conference, Orlando, USA (**G. Arnold**)
- 2011 International Conference on the Physiology and Genomics of Mastitis, Tutzing, Germany (**H. Blum**)



FUNDING, SERVICES AND TECHNOLOGY TRANSFER

Roland Beckmann

FUNDING

- 2009, Deutsche Forschungsgemeinschaft, SFB646 project A9, 2009-2012, 440 T€
- 2010, Deutsche Forschungsgemeinschaft, FOR967, project 1, 2010-2013, 225 T€
- 2010, Deutsche Forschungsgemeinschaft, FOR967, project 3, 2010-2013, 135 T€
- 2011, EMBO, Postdoctoral fellowship B. Beckert, 2011-2013, 120 T€
- 2012, Deutsche Forschungsgemeinschaft, FOR1805, project 3, 2012-2015, 360 T€
- 2012, Deutsche Forschungsgemeinschaft, GRK1721, 2012-2015, 135 T€
- 2012, ERC, Advanced Grant, 'Cryotranslation', 2012-2017, 2,999 T€

PROFESSIONAL SERVICES

- Dean of studies, Master of Biochemistry curriculum LMU, 2007-present
- Speaker of the SFB594, 2008-2012
- Member of DFG study section Biochemistry and Biophysics
- Reviewer for major international journals
- Conference organizer, Third International Symposium of the SFB594, Munich, 2012
- 'Molecular Machines in Protein Folding and Translocation'

Karl-Klaus Conzelmann

FUNDING

- 2009, DFG, SPP 1175, project RABV M, 2009-2011, 105 T€
- 2010, DFG, SFB 870, project Z1, 2010-2013, 578 T€
- 2010, DFG, Graduiertenkolleg 1202, project D2, 2010-2013, 131 T€
- 2011, BMBF, Lyssavirus Network, TP2, 2011-2012, 326 T€
- 2011, CSC, PhD student fellowship, 2011-2014, 60 T€

PROFESSIONAL SERVICES

- Member, editorial board of Journal of Virology, 2005-present
- Member, editorial board of Virus Research, 2001-present
- Reviewer for various scientific journals
- Proposal reviewer for various funding agencies

Patrick Cramer

FUNDING

- 2009, Roche Diagnostics GmbH, Postdoctoral research project 2009-2011, 200 T€
- 2009, Alexander von Humboldt Stiftung, Postdoctoral fellowship, 54 T€
- 2009, Deutsche Forschungsgemeinschaft, Transregio5 project M3, 2009-2012, 545 T€
- 2009, Deutsche Forschungsgemeinschaft, SFB646 project A1, 2009-2012, 537 T€
- 2009, Deutsche Forschungsgemeinschaft, SFB646 project Z2, 2009-2012, 977 T€
- 2010, Alexander von Humboldt Stiftung, Postdoctoral fellowship, 2010-2012, 54 T€
- 2010, IDK NanoBioTech, PhD student fellowship, 2010, 21 T€
- 2011, BFG Gleichstellungsförderung, Postdoctoral fellowship, 2011-2012, 24 T€
- 2011, European Research Council, Advanced Investigator Grant, 2011-2016, 2.226 T€
- 2011, Deutsche Forschungsgemeinschaft, Sonderforschungsbereich 960 project A2, 2011-2015, 403 T€
- 2011, Boehringer Ingelheim Fonds, PhD student fellowship, 2011-2013, 45 T€
- 2011, Boehringer Ingelheim Fonds, PhD student fellowship, 2011-2012, 40 T€
- 2011, Roche Diagnostics GmbH, Postdoctoral research project, 2011-2013, 200 T€
- 2012, Humboldt Foundation, Postdoctoral fellowship, 2012-2013, 54 T€
- 2012, Human Frontier Science Program Organization, Postdoctoral fellowship, 2012-2015, ~60 T€
- 2012, Schweizerischer Nationalfonds zur Förderung der Wissenschaftlichen Forschung, Postdoctoral fellowship, 2012-2014, 80 T€
- 2012, Deutsche Forschungsgemeinschaft, Cluster of excellence NIM2, 2012-2017, 210T€
- 2012, Deutsche Forschungsgemeinschaft, Cluster of excellence CIPSM2, 2012-2017, 600 T€
- 2012, Deutsche Forschungsgemeinschaft, Graduiertenkolleg GRK1721, 2012-2018, 164 T€

PROFESSIONAL SERVICES

- Executive board member, National Cluster of Excellence Center for Integrated Protein Science Munich, since 2006
- Member, Research Board of the LMU, since 2007
- Dean, Faculty of Chemistry and Pharmacy of the LMU, 2007-2009
- Coordinator, Research grant network Sonderforschungsbereich SFB646, since 2008
- Member, selection committee for the Heinz-Maier-Leibniz-Prize, since 2008
- Member of the Scientific Advisory Board, Max-Planck-Institute for Developmental Biology, Tübingen, since 2009
- Representative of the LMU for construction of the Research Center for Molecular Biosystems, Munich, since 2009
- Member, editorial board of The EMBO Journal, since 2009
- Member, editorial board of Transcription, since 2010
- Postdoctoral research projects, Roche Diagnostics GmbH, since 2009
- Director, Department of Biochemistry, LMU Munich, since 2010
- Organizer, EMBO conference on gene transcription in yeast, St. Feliu, Spain, 2010
- Member, Council of the Bavarian State Government (Wissenschaftlich-technischer Beirat und Zukunftsrat der Bayerischen Staatsregierung), 2009-2011
- Member, Scientific Advisory Board, Biochemie Zentrum Heidelberg BZH, since 2011
- Member, Council of the European Molecular Biology Laboratory EMBL, since 2011
- Member, Center for Nanoscience CeNS Munich, since 2002
- Member, Cluster of excellence Nanosystems Initiative Munich NIM, since 2006
- Member, Graduiertenkolleg Structural Biology Hybrid Methods, 2012
- Member, Graduate school Quantitative Biosciences Munich QBM, 2012

Klaus Förstemann

FUNDING

- 2009, Deutsche Forschungsgemeinschaft, SFB646 project A13, 2009-2012, 256 T€
- 2009, Fonds der Chemischen Industrie, PhD-Fellowship Milijana Mirkovic-Hösle, 2009-2011 65 T€
- 2010, BMBF, NGFN-Plus Teilprojekt, 2011-2013, 184 T€
- 2012, Deutsche Forschungsgemeinschaft, SFB646 project A13, 2013-20116, 204 T€

PROFESSIONAL SERVICES
- Mentoring of students for international exchange
- Review of scientific manuscripts for specific journals (e.g. Nucleic Acids Research, Current Biology, RNA, PLoS One, Journal of Biological Chemistry, FEBS letters etc.)
- Member of the Steering Board (Leitungskollegium), Dept. of Biochemistry, LMU München
- Member of the Exam board (Prüfungskommission), Bachelor of Science in Chemistry and Biochemistry, LMU München

Julien Gagneur

PROFESSIONAL SERVICES
- Reviewer for Molecular Systems Biology, PLoS Genetics, Nucleic Acids Research, Bioinformatics, BMC Bioinformatics
- Organizer, "Systems genetics: from statistical genetics to mechanistic models in systems biology", Heidelberg, workshop of the conference ICSB 2011
- Organizer, "Statistical and dynamical models in biology and medicine" in Heidelberg, 2010, Goettingen, 2011 and Stuttgart, 2012
- Contributor of free and open source scientific software, especially to the R/Bioconductor project.

PATENTS, INDUSTRY COLLABORATIONS AND START-UPS
- PhD student, Lion Bioscience, Heidelberg, 2001-2002
- PhD student and scientist, Cellzome GmbH, Heidelberg, 2002-2005
- Statistical consultant for febit GmbH, Heidelberg, 2006
- Gagneur J., V. Pelechano, L. Steinmetz, and C. Mertens (2012). " Methods and systems for tracking samples and sample combinations" Int. Patent Application Nr. WO 2012/019765

Ulrike Gaul

FUNDING
- 2009, Alexander von Humboldt-Foundation, Alexander von Humboldt-Professorship, 2009-2013, 5000 T€
- 2009, Deutsche Forschungsgemeinschaft, Excellence Initiative, Center for Integrated Protein Science Munich (CIPSM), 2009-2017, 1400 T€
- 2011, Wissenschaftsrat/GWK, Forschungsbau "Forschungszentrum für Molekulare Biosysteme (BioSysM)", 2012-15, 14300 T€ (jointly with P. Cramer)
- 2012, Deutsche Forschungsgemeinschaft, Grossgeräteantrag nach Art. 91b GG, "Automationsanlage für pro- und eukaryontisches Arbeiten inklusive Analytik", 2012-2013, 692 T€
- 2012, Deutsche Forschungsgemeinschaft, Graduate School of Quantitative Biosciences Munich (QBM), 2012-17, 7379 T€ (scientific coordinator/speaker)
- 2012, Bundesministerium für Bildung und Forschung, e:Bio – Innovationswettbewerb Systembiologie, "Systembiologie der Genexpression: Analyse des Basalpromotors (SysCore)", 2013-15, 1709 T€ (project coordinator)
- 2012, Deutsche Forschungsgemeinschaft, SFB646 project A16, 2013-16, 631 T€

PROFESSIONAL SERVICES
- Organizer, Symposium "From Genes to Networks – Systems Approaches in Developmental Biology", LMU Munich, 2010
- Member, Scientific Advisory Board, Care for Rare Foundation, 2011-present
- Co-Organizer, 3rd International Gene Center/SFB646 Symposium „Regulatory networks in genome expression and maintenance", LMU Munich, 2011
- Manuscript reviews for numerous journals, such as Nature, Cell, Genes & Development, PLoS Biology, PLoS Genetics
- Grant and promotion reviews for institutions such as Boehringer Ingelheim Foundation, DFG, Max-Planck-Society, Karolinska Institute
- Design and implementation of advanced high throughput robotics facility in collaboration with Beckman Coulter GmbH, 2010-13

Mario Halic

FUNDING
- 2012, ERC starting grant, 2012-2017, 1.5 M€
- 2012, BioSys, 2012-2017, 250 T€

Franz Herzog

FUNDING
- 2009, EMBO Longterm Fellowship, 2009, 57 k€
- 2009, Marie Curie Fellowship, 2010-2011, 190 k€

Karl-Peter Hopfner

FUNDING
- 2009, Deutsche Forschungsgemeinschaft SFB 646, 2009-2012, 460 K€
- 2009, National Institutes of Health USA, U19 Host-pathogen competition, 1.2 M$
- 2009, Deutsche Forschungsgemeinschaft SF/TR5, 2009-2012, 350 K€
- 2010, Deutsche Forschungsgemeinschaft SFB 684, 2010-2013, 350 K€
- 2011, Deutsche Forschungsgemeinschaft GRK 1202, 2011-2015, 175 T€
- 2012, Bavarian Government, BioSysNet, 2012-2017, 250 T€
- 2012, Bavarian Government, m4 Award, 2012-2014, 560 T€
- 2012, German Excellence Initiative, CIPSM, 2012-2017, 600 T€
- 2012, German Excellence Initiative, QBM, 2012-2017, 250 T€
- 2012, Deutsche Forschungsgemeinschaft GRK 1721, 2012-2016, 450 T€
- 2012, European Commission FP7, ERC Advanced Grant (2013-2017), 2.4 M€

PROFESSIONAL SERVICES
- Speaker, Graduate Research Training Program 1721 "Integrated Structural Analysis and Hybrid Methods in Genome Biology"
- Chair, ATIP-Avenir Biochemistry Panel (French Junior Excellence Research Group Grants)
- Member, editorial board of Biophysical Chemistry
- Member, editorial board of Open Biology
- Member, board of the CIPSM Excellence Cluster
- Session organizer, The EMBO Meeting, 2009
- Session organizer, FASEB conference on Helicases and Nucleic Acid Translocases 2010 (Les Diablerets), 2010
- Session organizer, DGK Jahrestagung, München, 2012
- Co-Organizer, GBM Jahrestagung, Frankfurt, 2013
- Reviewer for Nature, Science, Cell, Nature Structural & Molecular Biology, Nature Cell Biology, Molecular Cell, EMBO J, EMBO Reports, Current Biology, Journal of Molecular Biology, J. Clinical Investigation, Oncogene and others.
- Reviewer for DFG, EMBO, Welcome Trust, Cancer Research UK, European Research Council, Medical Research Council (UK), National Science Foundation (USA), Austrian Science Fund, German-Israeli Research Foundation and others.

INDUSTRY COLLABORATIONS AND START-UPS
- Collaborative research projects on therapeutic antibodies, Roche Pharma, 2009-2012
- Co-founder, SpectraMab GmbH, 2010

Christoph Klein

FUNDING
- 2010, German Research Foundation, KFO250, 2011-2013, 375 T€
- 2010, BMBF, ERARE, 2011-14 223 T€
- 2011, ERC Advanced Grant EXPLORE 2011-15 2.500 T€
- 2011, German Research Foundation, SFB914, Project A8, 2011-15 600.000 T€
- 2012, German Research Foundation, SFB1054, Project A5, 2013-16 300.00T€
- 2012, BioSysNet 2012-17 250.000 T€
- 2012, Bavarian Research Foundation, Fellowship Yanshan Liu 2012-13 40.000 T€

PROFESSIONAL SERVICES
- Reviewer for NEJM, Nat Immunol, Nat Med, J Exp Med, Blood, Gastroenterology and others
- Board, German Research Foundation 2012-
- Conference organizer, "The translational science of rare diseases: from rare to care", Vienna 2012
- Foundation of the Care-for-Rare Foundation for children with rare diseases, 2009

Fabiana Perocchi

FUNDING
- 2011, FEBS, Return-to-Europe Postdoctoral fellowship, 2011-2013, 72 T€
- 2012, Bavarian State Ministry of Science, Research, and the Arts, BioSysNet Junior Group Leader Grant, 2012-2017, 1.5 M€
- 2012, Deutsche Forschungsgemeinschaft, Emmy Noether Research Grant, 2012-2017, 1.9 M€

Johannes Söding

FUNDING
- 2009, Deutsche Forschungsgemeinschaft, SFB646 project A12, 2009-2012, 384 T€
- 2010, Deutsche Telekom-Stiftung, Fellowship M. Hauser, 2011-2013, ~62 T€
- 2012, Federal Ministry of Education and Research (BMBF), eBIO-M1-115, 2013-2015, 234 T€
- 2012, Bavarian Research Network for Moleculuar Biosystems (BioSysNet), 2012-2016, 228 T€
- 2012, Deutsche Forschungsgemeinschaft, Graduiertenkolleg GRK1721 project B2, 2012-2016, 228 T€

PROFESSIONAL SERVICES
- Member of the Management Committee of the Graduate School of Quantitative Biosciences Munich (QBM) (since 2012)
- Member of the Gene Center Steering Committee (since 2009)
- Member of four faculty search committees (Berufungskommissionen) for junior group leader positions at the Gene Center (since 2008)
- Member of the Berufungskommission for a Full Professorship for Molecular Biosystems at the Gene Center (2012)
- Member of the search committee for a bioinformatics core facility leader at the MPI forBiochemistry, Martinsried (2012)
- Reviewer for Bioinformatics, NAR, PNAS, Genome Biology, Genome Research, the German-Israeli Foundation (GIF), among others
- Program committee member at conferences ISMB 2012, and ECCB 2012
- Board member of the Society for Bioinformatics in Northern Europe (SocBiN) (since 2011)

Katja Sträßer

FUNDING
- 2009, Fonds der Chemischen Industrie, Predoctoral fellowship K. Brünger, 2009-2012, 63 T€
- 2009, Deutsche Forschungsgemeinschaft, SFB646 project A3, 2009-2012, 396 T€

PROFESSIONAL SERVICES
- Board Member of SFB646 "Networks in Genome Expression and Maintenance", 2009-2012
- Board Member of the Gender Equality Program of the Cluster of Excellence "Munich Center for Integrated Protein Science (CIPSM)", 2006-present
- Review of manuscripts for Genes and Development, EMBO J, MCB, JBC, RNA, FEBS Letters, Biological Chemistry, FASEB, BBA
- Review of EMBO long-term and short-term postdoctoral fellowship applications

› Review of Grant Proposals to the Boehringer Ingelheim Foundation (BIF), the German Research Foundation (DFG), the Swiss National Science Foundation (SNF), the American National Science Foundation (NSF), and the Biotechnology and Biological Sciences Research Council (BBSRC)

Petra Wendler

FUNDING

› 2009, Deutsche Forschungsgemeinschaft, Emmy Noether Fellowship, WE4628/1-1, 2009-2012, 791 T€
› 2012, Deutsche Forschungsgemeinschaft, GRK1721 project A6, 2012-2016, 134T€

PROFESSIONAL SERVICES

› Member of IMPRS
› Referee for scientific journals: JBC, Chemistry& Biology, BBA
› Co-Organizer, Gene Center Retreat 2010 and 2011

Daniel Wilson

FUNDING

› 2010, Deutscher Akademischer Austausch Dienst, 2010-2011, €19K/year.
› 2011, European Molecular Biology Organization, 2011-2013, €15K/year.
› 2012, National Institute of Health (NIH), 2012-2015, €50K/year.
› 2012, Deutsche Forschungsgemeinschaft FOR1805, 2012-2014, €50K/year.

PROFESSIONAL SERVICES

› Associate member of the Faculty › of 1000 (F1000), 2010-present
› Member of the RNA Society, 2008-present
› Associate member of the Center for integrated Protein Science, Munich (CiPSM)
› Reviewer for Nature, Science, Cell, etc

Eckhard Wolf

FUNDING

› 2009, Deutsche Forschungsgemeinschaft, WO 685/16-1, 274 T€, 2009-2012
› 2009, Deutsche Forschungsgemeinschaft, SCHN 1081/3-1, 241 T€, 2010-2013*
› 2010, Deutsche Forschungsgemeinschaft, FOR535 project III, 194 T€, 2010-2012
› 2010, Deutsche Forschungsgemeinschaft, FOR793 project II, 208 T€, 2010-2013
› 2010, Deutsche Forschungsgemeinschaft, ZA 425/1-3, 183 T€, 2010-2012
› 2010, Deutsche Forschungsgemeinschaft, KE 1673/1-1, 262 T€, 2011-2013*
› 2010, BMBF, Leading-Edge Cluster m4, PK1, 333 T€, 2010-2013
› 2010, Else-Kröner-Stiftung, Pankreatitis, 2010_A76, 203 T€, 2010-2012*
› 2010, Roche Pharma, R&D project, 100 T€, 2010-2012
› 2010, Bayern Genetik GmbH, R&D project, 220 T€, 2010-2015
› 2011, Deutsche Forschungsgemeinschaft, FOR1041 project 10, 160 T€, 2011-2014
› 2011, Deutsche Forschungsgemeinschaft, SCHN 1081/4-1, 298 T€, 2011-2014*
› 2011, BMBF, German Mouse Clinic, Clinical chemical lab, 422 T€, 2011-2013
› 2011, Else-Kröner-Stiftung, HST002, 2011_A54, 281 T€, 2011-2014*
› 2011, Mukoviszidose Institut gGmbH, Christiane Herzog Stiftung, 50 T€, 2011-2012
› 2012, Deutsche Forschungsgemeinschaft, TR-SFB127 project B3, 650 T€, 2012-2016
› 2012, Deutsche Forschungsgemeinschaft, TR-SFB127 project Z3,170 T€, 2012-2016
› 2012, Sanofi-Aventis Deutschland GmbH, Postdoctoral research project, 525 T€, 2012-2014
› 2012, BioSysNet, 250 T€, 2012-2017
› 2012, MWM Biomodels GmbH, R&D project, 50 T€, 2012-2013
› A 5 M€ grant was received from the Bavarian State Ministry of Science, Research and Arts to set up a new facility for biomedical pig models at the Moorversuchsgut Badersfeld. The facility will be opened in spring 2013.

*grants raised independently by members of the group

PROFESSIONAL SERVICES

› Dean of Research, Faculty of Veterinary Medicine of the LMU, 2009-present
› Member, DFG-Fachkollegium 207, 2009-2012
› Member, DFG-Senatskommission "Tierexperimentelle Forschung", 2009-2011
› Member, DFG-Senatskommission "Grundsatzfragen der Gentechnik", 2009-2011
› Member, DFG-Senatskommission "Stoffe und Ressourcen in der Landwirtschaft", 2009-2011
› Head, Scientific Advisory Board of the BMBF program FUGATO, 2009-2011
› Co-Founder and Scientific Director of MWM Biomodels GmbH, 2009-present
› Program Co-chairman 37th Annual Conference of the International Embryo Transfer Society "Reproductive Biotechnology at the Interface between Animal Agriculture and Biomedical Research", Orlando, FL, USA, January 8-12, 2011

PATENTS, INDUSTRY COLLABORATIONS AND START-UPS

› US 7,919,673 "Transgenic pig with altered incretin function" (issued on Apr 4, 2011)
› US 13/659,523 "Pancreatic islets of transgenic LEA29Y animals for treating diabetes" (filed Oct 24, 2012)
› Postdoctoral research project, Sanofi-Aventis Deutschland GmbH, 2012-2014
› R&D project, Roche Pharma, 2011-2012
› R&D project, MWM Biomodels GmbH, 2011-2013

Dierk Niessing

FUNDING

› 2011, Deutsche Forschungsgemeinschaft, Sachbeihilfe, 2011-2014, 132 T€
› 2011, Bayerisch-Französisches Hochschulzentrum (BFHZ), 2011-2013, 5 T€
› 2012, Wilhelm-Sander Stiftung, 2012-2014, 75 T€
›

› PROFESSIONAL SERVICES

› Reviewer for international, peer-reviewed journals
› Reviewer for funding agencies (e.g. Deutsche Forschungsgemeinschaft, Medical Research Council UK, Polish Academy of Sciences)

Ulrich Koszinowski

EXTRAMURAL FUNDING

› 2009, DFG, CMV, 2009-2011, 306 T€
› 2009, Bayer. Forschungsstiftung, FORPROTECT , 2009-2012, 266 T€
› 2011, DZIF, Antivirale Therapie, 2011-2012, 82 T€

PROFESSIONAL SERVICES

› 1998 – 2010, Committee member of "Somatische Gentherapie der Bundesärztekammer"
› 2004 – 2010, Board member of the Society of Virology (GfV)
› Organizer, International Symposium of the SFB 455 in Munich, Germany

INDUSTRY COLLABORATIONS

› Intervet Internationa BV, MSD Animal Health (Research cooperation on BAC technology) 2000-2012
› Hyglos GmbH (Research cooperation on bacteriophages lysis mechanisms) 2009-2012

Achim Tresch

FUNDING

› 2009, Deutsche Forschungsgemeinschaft, SFB646 project A1, 2009-2012, 200 T€

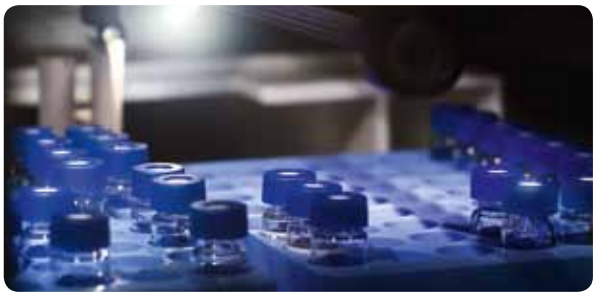
PROFESSIONAL SERVICES

› Member of the GMDS, 2009-present
› Organizer, IBS/GMDS conference "Statistical Methods in Bioinformatics", Munich 2009

LAFUGA

FUNDING

› 2009, BMBF, Competence Cluster Phänomics, VP3, TP3.1, 2009-2014, 955 T€
› 2009, European Union, PLURISYS, 2009-2012, 390 T€
› 2009, European Research Foundation ESF "EUROCORES: "Ecological and Evolutionary Functional Genomics", 2010-2013, 130 TE
› 2011, Deutsche Forschungsgemeinschaft, FOR1041 „Germ Cell Potential" project 04, 2011-2014, 148 TE
› 2011, Deutsche Forschungsgemeinschaft, FOR1041 „Germ Cell Potential" project 08, 2011-2014, 110 TE
› 2011, Deutsche Forschungsgemeinschaft, FOR1041 „Germ Cell Potential" project 10, 2011-2014, 205 TE
› 2012, European Union, FECUND, 2013-2016, 320 T€,



SEMINARS

2009

SPEAKER	INSTITUTION	TITLE	DATE
Anne Spang	University of Basel	The role of small GTPases in intracellular traffic and mRNA metabolism	01/19/09
Anne-Claude Gavin	EMBL Heidelberg	Dynamic macromolecular networks	02/02/09
Shura Mankin	University of Illinois	The Nascent Peptide´s Adventures in the Wonderland of the Ribosome Tunnel: Chapter I. Down the Rabbit Hole	02/09/09
Marc Timmers	University Medical Center Utrecht	Dynamic regulation of the eukaryotic transcription machinery	02/16/09
Takashi Fujita	University of Kyoto	Sensing Non-self RNA and Activation of Antiviral Responses	03/02/09
Geir Slupphaug	Norwegian University of Science and Technology	Regulation of genomic uracil processing by UNG2	03/09/09
Francoise Stutz	Université de Genève	Role of antisense transcripts in cis- and trans-gene silencing in the yeast S. cerevisiae	03/16/09
Joachim Lingner	ISREC Fondation	Telomeres and telomerase: RNA-dependent machines at chromosome ends	03/23/09
Karen Adelmann	National Institute of Environmental Health Sciences, USA	RNA polymerase is poised for gene activation	03/30/09
Ingrid Grummt	DKFZ, German Cancer Research Center, Heidelberg	Noncoding RNA and chromatin remodelling: Epigenetic control of rRNA genes	04/06/09
Simon Bullock	MRC Laboratory of Molecular Biology, Cambridge	Recognition and transport of mRNAs and vesicles by microtubule-based molecular motors	04/20/09
Gunnar von Heijne	Stockholm University	Insertion of membrane proteins into the endoplasmic reticulum	04/27/09
Knud H. Nierhaus	MPI für Molekulare Genetik, Berlin	Principles of Protein synthesis The importance of the third tRNA binding site for the accuracy of protein synthesis	05/04/09
Niko Beerenwinkel	ETH Zürich	Deep sequencing of a mixed sample	05/11/09

SPEAKER	INSTITUTION	TITLE	DATE
Dave Gilbert	Florida State University	Chromosome Replication and Nuclear Re-Programming During Stem Cell Differentiation	05/18/09
Steve Buratowski	Harvard University, USA	Pre- and Post-transcriptional mechanisms for suppressing promiscuous transcription	06/22/09
Michael Kiebler	Medical University of Vienna	First insight into how RNAs might be transported to the synapse	06/29/09
Ellen Fanning	Vanderbilt University, USA	DNA helicas B: a new player at the interface of vertebrate DNA replication and damage repair	07/06/09
Henri Tiedge	The Robert F. Furchgott Center for Neural and Behavioral Science, New York	RNA control in neurons	09/07/09
Jane Mellor	University of Oxford	Signalling to Chromatin	10/12/09
Tom A. Rapoport	Harvard University	Mechanism of protein transport across membranes	10/15/09
Jennifer Doudna	University of Berkeley	Dicer and Beyond: Regulatory RNA Processing and Function	10/19/09
Anindya Dutta	University of Virginia, School of Medicine	Genomic instability in cancer cells from disorders in replication	11/02/09
Marina Rodnina	MPI für biophysikalische Chemie, Uni Göttingen	The structure of the universal translator, the ribosome	11/30/09
2010			
Joachim Rädler	LMU München, Department Physik	Stochastic gene expression and phenotype heterogeneity in isogenic bacterial populations	01/18/10
Ruedi Aebersold	ETH Zürich		02/08/10
Elisa Izaurralde	MPI Tübingen	A role for PABPC1 in miRNA-mediated gene silencing	02/15/10
Niels Gehring	EMBL, Heidelberg	How pre-mRNA processing tunes the efficiency and accuracy of gene expression	03/01/10
Yuh Min Chook	University of Texas, Southwestern Medical Center	Structural biology of NLS and NES recognition	03/15/10
Jussi Taipale	University of Helsinki	Transcriptional control of growth	03/22/10
Scott Blanchard	Weill Medical College, Cornell University, USA	Single-molecule studies of ribosome activities and drug action	03/29/10
Dieter A. Wolf	Burnham Institute for Medical Research, USA	Function of PCI domain complexes in protein synthesis and degradation	04/12/10
Peter Sarnow	Stanford University School of Medicine	Subversion of liver-specific microRNA miR-122 by hepatitis C virus	04/19/10
Frank Uhlmann	London Research Institute	The irreversibility of cell cycle transitions: why the clock never turns back	05/31/10
Torben Heick Jensen	Aarhus University	Quality control of eukaryotic transcription	06/14/10
Veit Hornung	University of Bonn	Intracellular DNA regocnition by the innate immune system	07/19/10
Aseem Ansari	University of Wisconsin	Engineering Synthetic Transcription Factors	09/20/10
Thomas Lahaye	LMU Munich, Institute of Genetics	Tal-type bacterial transcription factors - a new alternative to designer zinc-fingers?	10/11/10
Jesper Q. Svejstrup	Cancer Research UK	Transcript elongation by RNA polymerase II: contending with obstacles	10/18/10
Yukihide Tomari	The University of Tokyo	How to make RISC (RNA Induced Silencing Complex)	10/25/10
John Diffley	London Research Institute	Mechanism and Regulation of DNA replication	11/15/10
Alain Jacquier	Institut Pasteur	Hidden transcription in yeast and regulation	11/22/10
Julius Brennecke	IMBA Vienna	The piRNA Pathway in the Drosophila Germline - Guardian of the Genome	11/29/10
Ben Luisi	University of Cambridge	Bacterial RNA processing and degration machinery and its contribution to the regulation of gene exprssion	12/06/10
Jamie Cate	Department of Chemistry and MCB, Berkeley	The structure of the universal translator, the ribosome	12/13/10

SPEAKER	INSTITUTION	TITLE	DATE
2011			
Jörg Vogel	Universität Würzburg	Molecular principles of small RNA regulators	01/10/11
Wolfgang Huber	EMBL Heidelberg	Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi	01/24/11
Carol Robinson	University of Oxford	Mass Spectrometry and its Role in Structural Biology	03/07/11
Wendy Gilbert	MIT Cambridge	Adapting to altered translatomes through functional specialization of ribosomes	03/14/11
Graham Pavitt	The University of Manchester	Translational control, recycling eIF2 in health, stress and disease	03/28/11
Irmgard Sinning	Biochemie-Zentrum der Universität Heidelberg (BZH)	Molecular machines in protein targeting	05/09/11
Anita Corbett	Emory University, USA	Mutations in a Polyadenosine RNA Binding Protein that Controls Poly (A) Tail Length Lead to Intellectual Disability in Humans and Neuronal Dysfunction in Flies: Size Matters	05/30/11
Camilla Sjörgren	Karolinska Institute, Stockholm	Replication-induced topological stress more than a substrate for topoisomerases	06/06/11
Tom Kodadek	Scripps Research Institute, USA	Chemical tools to monitor and manipulate the proteome	06/20/11
Ed. C. Hurt	Biochemie-Zentrum der Universität Heidelberg (BZH)	The Nuclear Pore Complex of a Eukaryotic Thermophile	06/27/11
Axel Behrens	London Research Institute	Transcriptional control in stem cells and cancer	07/04/11
Rachel Green	Molecular Biology & Genetics, Baltimore, USA	Quality control on the ribosome in bacteria and eukaryotes	09/12/11
Peter Wright	The Scripps Research Institute, USA	Promiscuous liaisons: functional interactions of intrinsically disordered proteins in signaling networks	10/17/11
Jens Timmer	University of Freiburg, Freiburg Institute for Advanced Studies	Systems Biology of the Erythropoietin Receptor	10/24/11
Lukas Pelkmans	Institute of Molecular Life Sciences, Zürich	Origins of regulated cell-to-cell variability	11/14/11
Stephen Michnik	Université de Montréal	Structure, dynamics, noise and contingency in signal transduction networks	11/28/11
2012			
Naama Barkai	Weizmann Institute of Science, Rehovot, Israel	Scaling in multicellular development: how tissue pattern adjusts with tissue size	01/23/12
Giacomo Cavalli	Institute of Human Genetics, Montpellier, France	Functional three-dimensional organization of the fly genome	01/30/12
Nir Friedman	The Hebrew University of Jerusalem, Israel	Systematic Dissection of Roles for Chromatin Regulators in a Yeast Stress Response	02/06/12
Alfred Pingoud	Justus-Liebig-Universität, Giessen, Germany	Approaches to engineering and controlling meganucleases for gene targeting	02/13/12
Jonathan Weissman	University of California, San Franscisco, US	Globally monitoring translation one codon at a time with ribosome profiling	02/27/12
Gabriel Waksman	Birkbeck College and University College London, London, UK	Structural and Molecular Biology of Bacterial Secretion Systems	03/05/12
Jürg Bahler	University College London, London, UK	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells	03/19/12
Roland Eils	Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany	To Die or Not To Die: Systems Biology of Cell Death Mechanisms	04/16/12
Javier Martinez	IMBA, Institute of Molecular Biotechnology, Vienna	Keep digging.... and you will find: New enzymes to splice RNA	04/23/12
Sjors Scheres	MRC Laboratory of Molecular Biology, Cambridge, UK	A Bayesian view on cryo-EM structure determination	05/14/12
Ivan Dikic	Frankfurt Institute for Molecular Life Sciences, Germany	Ubiquitin and autophagy networks	05/21/12

SPEAKER	INSTITUTION	TITLE	DATE
Thomas Dever	Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes for Health, Bethesda, USA	Protein Synthesis Factors eIF2 and eIF5A: Unexpected Links between Translation Initiation and Elongation	06/18/12
Marina Rodnina	Max Planck Institute for Biophysical Chemistry, Göttingen, Germany	The Assembly Landscape of Bacterial Translation Initiation Complexes	06/25/12
Nevan Krogan	University of California, San Francisco	Functional Insights from Genetic and Physical Interaction Maps	07/02/12
Seth Darst	The Rockefeller University, New York, USA.	Structural studies of bacterial transcription	09/17/12
Alexander Hoffmann	University of California San Diego	Post-genomic Immunology: models for experimentation and data analysis	09/24/12
Angela Krämer	Department of Cell Biology, University of Geneva, Switzerland	Splicing factor 1: Search for RNA targets and an unusual nuclear localization	10/01/12
Hans Krokan	Norwegian University of Science and Technology, Trondheim, Norway.	Genomic uracil - friend and foe?	10/29/12
Jan Lohmann	Centre for Organismal Studies, Heidelberg, Germany.	Hormonal control of a stem cell niche: Lessons from plants	11/12/12
Helen Saibil	Birkbeck College, University of London, London, UK.	Cryo-electron microscopy of molecular machines	11/19/12
Jonathan Howard	Institute for Genetics, University of Cologne, Germany	From Motors to Morphology	11/26/12
Elisa Izaurralde	MPI for Developmental Biology, Tübingen	Post-transcriptional mRNA regulation by miRNAs and RNA-binding proteins	12/03/12
Martin Eilers	Biozentrum at the University of Würzburg, Würzburg, Germany	Understanding and Targeting Myc Proteins	12/10/12

GENE CENTER IN THE MEDIA

DATE	TITLE	INVESTIGATOR	MEDIA
2009			
01/01/09	Vier Fragen an Ulrike Gaul	Ulrike Gaul	Forschung & Lehre
01/07/09	Die Tricks des Virensensors – Wie ein zelluläres Enzym die Erreger aufspürt	Karl-Peter Hopfner	LMU press release
01/08/09	Patrick Cramer erhält Ernst Jung-Forschungspreis	Patrick Cramer	LMU press release
01/21/09	Schweine als Organspender	Eckhard Wolf	LMU press release
01/27/09	Saubere Spender – Forscher machen Ersatzorgane von Tieren verträglicher	Eckhard Wolf	Deutschlandfunk
01/31/09	Pro und Contra: Klon-Fleisch aus der Kühltheke	Eckhard Wolf	Wiwo.de
02/19/09	Fliegen im Gespräch	Ulrike Gaul	Die Zeit
02/23/09	Mit der Verwandtschaft in Reih und Glied – Bessere Sequenzanalysen bei Genen und Proteinen	Johannes Söding	LMU press release
03/26/09	Bayer-Stiftung: Bildung stärken, Talente fördern	Patrick Cramer	Die Zeit
04/01/09	The Gene Center Munich at 25 – Interview mit Prof. Winnacker und Prof. Cramer	Patrick Cramer	Insight LMU
04/07/09	Dollys erfolgreiche Erben	Ekchard Wolf	Zeit Online
04/14/09	Genetisch gedoppelt hält nicht besser – Warum geklonte Tierembryonen oft abgestoßen werden	Eckhard Wolf	LMU press release
04/16/09	Spaß am Forschen – Brain Gain: Ulrike Gaul von New York nach München	Ulrike Gaul	Laborjournal
04/27/09	Im Profil Eckhard Wolf: Ersatzorgane vom Spenderschwein	Eckhard Wolf	Biotechnologie.de
05/02/09	Cells – Just big building sites	Karl-Peter Hopfner Daniel Wilson	Insight LMU Researach
06/06/09	Ein molekulares Kuckucksei enttarnen – Zwei virale Merkmale lösen Immunantwort aus	Karl-Peter Hopfner	LMU press release

DATE	TITLE	INVESTIGATOR	MEDIA
06/31/09	Parasiten auf dem Sprung - Wie die Zelle mobile genetische Elemente unterdrückt	Klaus Förstemann	LMU press release
06/31/09	Hüpfende Gene. Forscher finden Zellabwehr gegen Gar-Parasiten	Klaus Förstemann	Spiegel online
10/09/09	Start von der Pole-Position – Wie die Abschrift eines Gens beginnt	Patrick Cramer	LMU press release
10/19/09	EMBO welcomes 66 leading life scientists as members	Patrick Cramer	Press release EMBO
10/23/09	Zitternde Hände und ein molekularer Handschlag – Neue Proteinstruktur beteiligt an erblicher Neurodegeneration	Dierk Niessing	LMU press release
10/30/09	Licht am Ende des molekularen Tunnels – Wie der Membrantransport von Proteinen durchgezogen wird	Roland Beckmann, Daniel Wilson	LMU press release
11/01/09	Molekulare Kopiermaschinen – Familie-Hansen-Preis 2009 für Prof. Dr. Patrick Cramer	Patrick Cramer	Bayer Forschungsmagazin
11/04/09	Maschinerie des Lebens – Genzentrum in Großhadern with 25	Patrick Cramer	Die Süddeutsche Zeitung
11/23/09	Der Zelle auf der Spur – 25 Jahre Münchener Genzentrum	Patrick Cramer	Münchener Merkur
12/14/09	Neue Anwendungen in lebenden Zellen: Nanobodies verändern die Form und Funktion von Proteinen	Karl-Peter Hopfner	LMU press release
2010			
01/01/10	25 Jahre Genzentrum an der LMU – Raum für neue Ideen	Patrick Cramer	Münchner Uni Magazin
01/18/10	Im Kampf gegen Multiresistente Bakterien	Daniel Wilson	BRalpha Forschung aktuell
02/26/10	Wenn Diabetesforscher Schwein haben	Eckhard Wolf	LMU press release
04/23/10	Wasserflöhe im Stress	Georg Arnold	LMU press release
05/25/10	Molekularer Grenzverkehr – Protein verknüpft wichtigste Schritte der Genexpression	Katja Sträßer	LMU press release
07/24/10	Den Widerstand von Bakterien brechen Neue Einblicke in die Wirkung von Antibiotika	Daniel Wilson	LMU press release
06/05/10	Laserforschung und Biosystemforschung: Zwei neue Bauprojekte für die Spitzenforschung an der LMU	Patrick Cramer	LMU press release
06/15/10	Wirkungsweise der Makrolide als Weg zu neuen Antibiotika	Daniel Wilson	DAZ
08/08/10	Cracking Open a Cell Biology Mystery	Fabiana Perocchi	The Broad Institute | Research News
09/29/10	Rückkehrer	Ulrike Gaul	Deutschlandfunk
10/08/10	Sand im Getriebe erwünscht – Wie die Proteinsynthese gezielt blockiert wird	Roland Beckmann, Daniel Wilson	LMU press release
10/18/10	Klonen bald überflüssig? Es gibt effektivere Alternativen	Eckhard Wolf	n-tv
11/23/10	LMU-Forscher erhält „Young Investigator Award“ – Daniel Wilson möchte neue Antibiotika entwickeln	Daniel Wilson	LMU press release
11/23/10	Twenty-one group leaders join network of EMBO young investigators	Daniel Wilson	EMBO
12/08/10	Angriff auf das Getriebe	Daniel Wilson	Süddeutsche Zeitung
12/14/10	Drei millionenschwere ERC-Grants für LMU-Wissenschaftler	Patrick Cramer	LMU press release
12/14/10	Drei millionenschwere ERC-Grants für LMU-Wissenschaftler	Patrick Cramer	Süddeutsche Zeitung
12/28/10	Der Tanz der Gene	Ulrike Gaul	Süddeutsche Zeitung

2011

DATE	TITLE	INVESTIGATOR	MEDIA
02/04/11	Wandelbare Wasserflöhe	Georg Arnold	LMU press release
02/24/11	„Stop and go" – Wie die Zelle Blockaden der Genabschrift auflöst	Patrick Cramer	LMU press release
03/02/11	LMU nimmt wichtige Hürde in der zweiten Phase des Exzellenzwettbewerbs: Drei neue Graduiertenschulen und ein Exzellenzcluster in der Endrunde	LMU	LMU press release
04/01/11	Sensor mit Klettverschluss - Struktur eines Schlüsselmoleküls der DNA-Reparatur aufgeklärt	Karl-Peter Hopfner	LMU press release
04/14/11	Wenn Wissen wandert – Brain Drain oder Chance?	Patrick Cramer	Dialogforum der Munich Re Foundation
04/18/11	Forschung mit Tunnelblick – 3D-Bilder zeigen Integration von Proteinen in die Zellmembran	Roland Beckmann	LMU press release
04/20/11	Wie Moleküle zur rechten Zeit den rechten Ort finden – Essenzielle Transportmaschine der Zelle entschlüsselt	Dierk Niessing	LMU press release
05/18/11	Ein Molekularer Wegweiser - Proteinkomplex übernimmt Doppelrolle bei Gen-Expression	Katja Sträßer	LMU press release
05/23/11	Globalisierung und große Moleküle – Zwei neue DFG-Graduiertenkollegs an der LMU	Karl-Peter Hopfner	LMU press release
07/09/11	Wenn Ribosomen steckenbleiben - Entsorgung defekter RNA sichtbar gemacht	Roland Beckmann	LMU press release
07/17/11	Mitochondrial mystery demystified	Fabiana Perocchi	The Broad Institute | News and Publications
07/19/11	Cell's linchpin protein found: Discovery ends 50-year search for calcium channel	Fabiana Perocchi	Harvard University | The Harvard Gazette
07/22/11	Mystery of the mitochondria	Fabiana Perocchi	The Broad Institute | News and Publications
06/07/11	Molekularer Korkenzieher hat den Dreh raus. Strukturanalyse enthüllt Mechanismen der Genexpression	Karl-Peter Hopfner	LMU press release
06/19/11	m4 Award an Forscherteam von LMU und FAU: Förderung der Leukämieforschung	Karl-Peter Hopfner	LMU press release
09/26/11	Spickzettel für zelluläre Kraftwerke – Wie Gene in den Mitochondrien abgeschrieben werden	Patrick Cramer	LMU press release
10/13/11	Reproduktionsbiologen im "Laborjournal" - Zwei LMU-Forscher unter den "meistzitierten Köpfen"	Eckhard Wolf	LMU press release
11/06/11	Wissenschaft ist weiblich	Ulrike Gaul	Welt am Sonntag
11/13/11	Wenn Antibiotika nicht mehr helfen: Die Angst vor den Killerkeimen	Daniel Wilson	Bayerisches Fernsehen: Faszination Wissen
11/16/11	ERC-Advanced Grant für Roland Beckmann	Roland Beckmann	LMU press release
12/27/11	Schneller, genauer, empfindlicher: Neue Methode verbessert Sequenzanalysen entscheidend	Johannes Söding	LMU press release

DATE	TITLE	INVESTIGATOR	MEDIA
2012			
01/04/12	Kompositionen des Lebens	Ulrike Gaul	Systembiologie.de
01/05/12	BioSysNet: Start mit vier neuen Nachwuchsgruppen	LMU, Horst Domdey	LMU press release
02/23/12	Nachhaltig wirtschaften in der Zelle - Recycling nach evolutionärem Erfolgsrezept	Roland Beckmann	LMU press release
04/17/12	Bundesverdienstkreuz an vier LMU-Professoren	Patrick Cramer	LMU press release
04/23/12	Xenotransplantation bei Diabetes: Schweinezellen bewähren sich im Tiermodell	Eckhard Wolf	LMU press release
05/09/12	Ulrike Gaul elected new EMBO Member 2012	Ulrike Gaul	LMU press release
05/14/12	Auftaktveranstaltung von BioSysNet am Genzentrum der LMU	LMU, Horst Domdey	LMU press release
07/01/12	Diabetes - Alarmsignale aus dem Blut	Eckhard Wolf	LMU press release
07/15/12	LMU siegt auf ganzer Linie	LMU	LMU press release
07/19/12	Struktur von Reparaturfaktor identifiziert	Karl-Peter Hopfner	LMU press release
07/22/12	Molekularer Scharfmacher identifiziert	Daniel Wilson	LMU press release
06/31/12	Gefährliche DNA-Schäden signalisieren	Klaus Förstemann	LMU press release
08/28/12	Millionenförderung für LMU-Forscher	Mario Halic	LMU press release
09/18/12	Zusammenarbeit von Proteinen neu erforscht	Franz Herzog	ETH Life
09/27/12	Genetische Schaltzentralen leichter erkennen	Johannes Söding	LMU press release
10/08/12	Molekularer Rausschmeißer macht resistent	Daniel Wilson	LMU press release
11/02/12	Ein Krokodilskopf für die Genabschrift	Patrick Cramer	LMU press release
11/12/12	Forschungszentrum für Molekulare Biosysteme wird gebaut	Patrick Cramer	LMU press release
11/15/12	Genabschrift mit integrierter Starthilfe	Patrick Cramer	LMU press release
12/06/12	Vorbildlicher Unterricht und intensive Betreuung	Klaus Förstemann	LMU press release
12/11/12	Karl-Peter Hopfner erhält ERC Advanced Gran	Karl-Peter Hopfner	LMU press release
12/14/12	Kontrollstopp für die Proteinsynthese	Daniel Wilson	LMU press release

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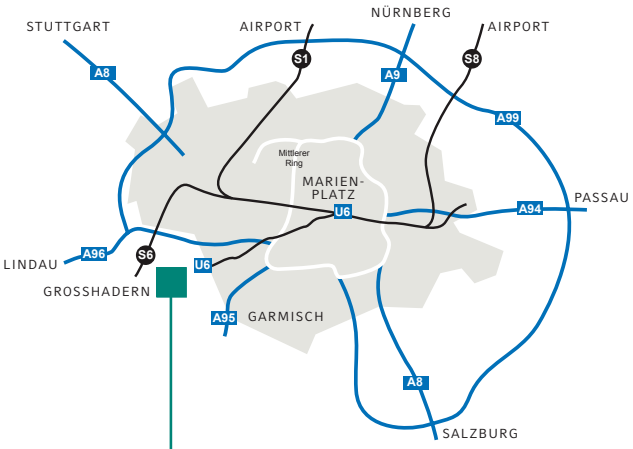
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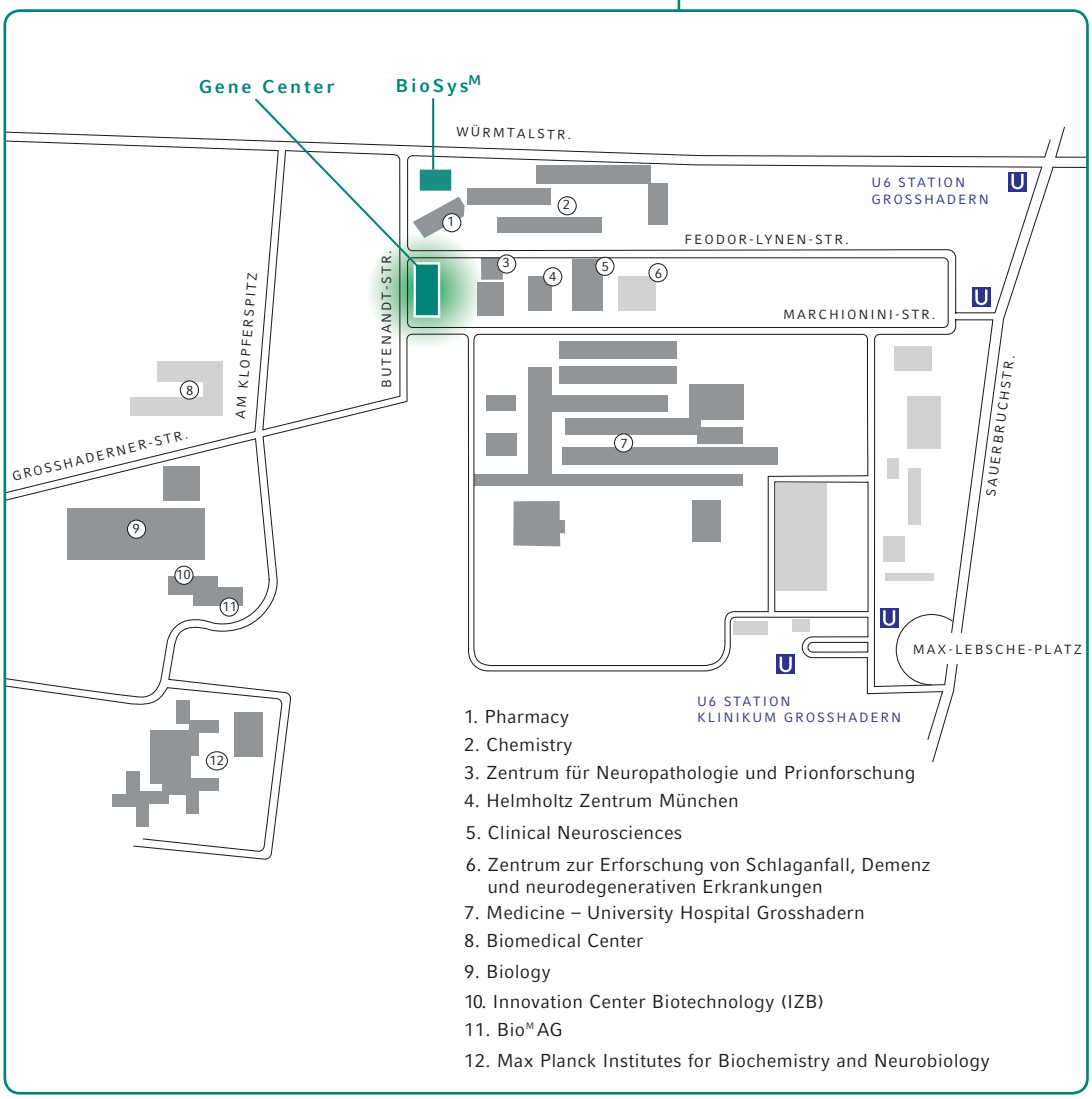
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10. Innovation Center Biotechnology (IZB)
11. BioM AG
12. Max Planck Institutes for Biochemistry and Neurobiology