LMU LUDWIG-MAXIMILIANS-UNIVERSITÄT MÜNCHEN

GENE CENTER MUNICH

RESEARCH AND EDUCATION FOR THE LIFE SCIENCES

GENE CENTER MUNICH REPORT 2004-2008

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Gene Center Munich
Ludwig-Maximilians-Universität (LMU) Munich
Feodor-Lynen-Strasse 25
81377 Munich
Germany

Phone: +49 89 2180 - 769 65
Fax: +49 89 2180 - 769 99

Email: genecenter@lmb.uni-muenchen.de
Internet: www.lmb.uni-muenchen.de

Planning, co-ordination, graphics, and editing:
Manuela Niessing, Gene Center Munich

Co-ordination LMU Munich:
Communications & Media Relations, LMU Munich

Contributions:
Responsible for the contents are Patrick Cramer and the other group leaders of the Gene Center Munich.

Layout and design:
Christine Meyer Design, Munich

Translations:
Alison Moffat, Translation Services, Munich

Print:
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Photography:
Gene Center Munich
Communications & Media Relations, LMU Munich
Jan Greune
Thorsten Naeser
Sebastian Vollmert
Tobias Koschubs
Otto Berninghausen
Elmar Czeko
Anselm Kusser
Heidi Feldmann
Manfred Schülein

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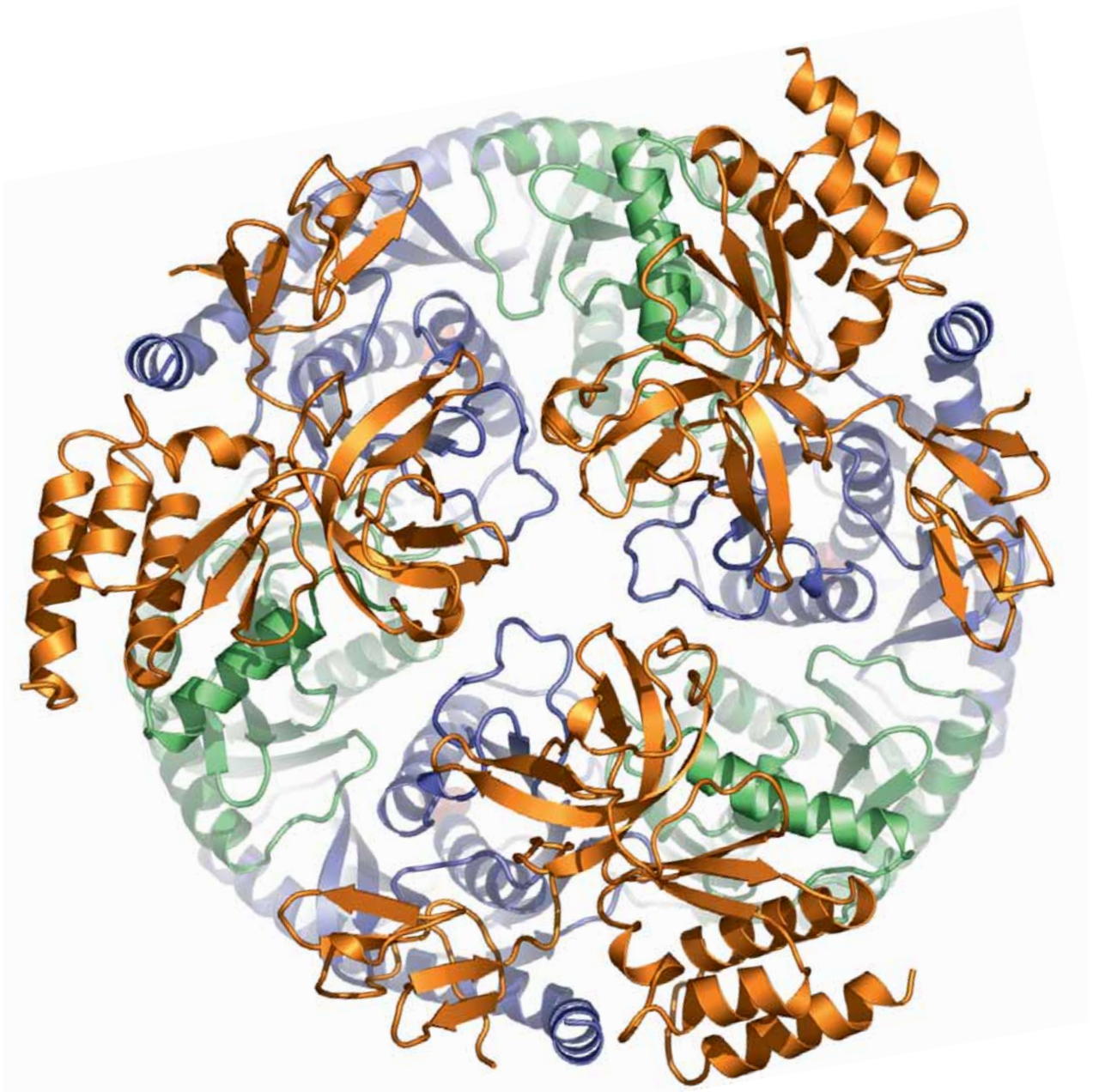


Discovering new frontiers in the life sciences

Ludwig-Maximilians-Universität (LMU) Munich is among the leading universities in Europe where a wide-ranging array of research topics is pursued. This status was significantly enhanced in the fall of 2006 when the university achieved major success in the Germany-wide Excellence Initiative, aimed at strengthening top-level university research. A keystone of this success which focuses on the field of life sciences is the Gene Center, many of the researchers at which are also actively engaged as Principle or Associate Investigators in our Clusters of Excellence.

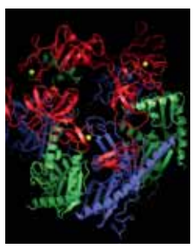
Established by Professor Ernst-Ludwig Winnacker in 1984, the Gene Center features a revolutionary organizational structure which has founded its outstanding reputation as a leading scientific institution. From the outset, the Gene Center has provided young academics with the opportunity to pursue independent research in self-contained research groups. The introduction of tenure-track professorships further increased the institution's attraction, enabling it to compete for the best young researchers at an international level. In addition, interdisciplinary contacts to the biomedical and biotech sectors were established as the foundation for the HighTechCampus[MU] at Grosshadern/Martinsried near Munich. The HighTechCampus[MU] network is a hub for the fields of natural science and medicine which is unique throughout Europe.

The Gene Center sets new standards in both research and teaching by launching innovative courses such as the inter-faculty “Master of Science Biochemistry” and focusing on graduate programs.

Occupying dedicated premises in Grosshadern since 1994, the Gene Center has continued to consolidate its outstanding reputation as an innovative research institute and think tank. Such wide-ranging networks among academic institutions are a critical element in furthering top-level interdisciplinary research. The appeal of the Gene Center is demonstrated by its successful appointment policy, which has attracted outstanding academics and scientists in recent years. The latest such is Professor Ulrike Gaul; an Alexander von Humboldt Professor from Rockefeller University New York, Professor Gaul will head a research group at the Gene Center and establish molecular systems biology as a research focus. As the policy demonstrates, the correct action can transform the oft-bemoaned “brain drain” in Germany as a research location into a “brain gain”.

This report presents the people involved in research at the Gene Center and provides an overview of their wide-ranging areas of specialization. It contains information on current and completed research projects and outlines prospects for future challenges and goals. The report is an impressive document of the performance and potential of the Gene Center in a central area of research and innovation in the 21st century.

Prof. Dr. Bernd Huber
President, Ludwig-Maximilians-Universität Munich



Thank you for your interest in the Gene Center Munich!

The years 2004-2008 have been very exciting for us. We successfully extended our efforts in research and teaching and have obtained an internationally leading position in several areas of the life sciences. We were able to attract outstanding new faculty, secure extensive extramural funding, and establish a highly visible and biomedically relevant research focus in genome expression and maintenance. We made our teaching portfolio more interdisciplinary and interactive, to optimize the education of the best young scientists and prepare them for their future work in academia or industry. Over the next few years, we will make full use of our strengths to stay competitive and highly productive in our existing research efforts. We will also extend into complementary future research fields, in particular molecular systems biology.

Our successes in research are reflected in many excellent publications, prestigious awards, and new extramural funding projects. Between 2004 and 2008, scientists at the Gene Center published 394 scientific papers and reviews, including 24 in the leading journals Nature, Science, and Cell. Among the 14 current principal investigators, three have received the EMBO Young Investigator award, one a Humboldt Professorship, one a grant from the European Research Council, and one the Leibniz Award from the German Research Council. The total amount of extramural funding received per year has tripled in the last five years, rising from 3.4 million euros in 2004 to 10.8 million euros in 2008 **(Figure 1)**. Accordingly, our scientific personnel has grown very rapidly. While 158 people were working at the Gene Center in 2004, this figure has risen to 224 in 2008 **(Figure 2)**.

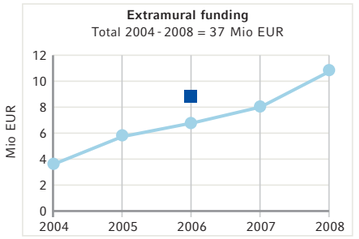


FIGURE 1: Development of extramural funding available per year

FIGURE 2: Development of total personnel at the Gene Center

The key to this success has been the recruitment of outstanding, scientifically independent group leaders and professors with complementary research interests and technical expertise. An international scientific advisory board monitors the recruitment process. Members of the board are currently Steve Cohen, director of the Temasek Life Sciences Laboratory in Singapore, Angus Lamond, head of the Wellcome Trust Centre for Gene Regulation and Expression in Dundee, Reinhard Lührmann, director at the Max-Planck-Institute for Biophysical Chemistry in Göttingen, and Iain Mattaj, director general of the European Molecular Biology Laboratory in Heidelberg.

THE DIRECTOR'S REPORT

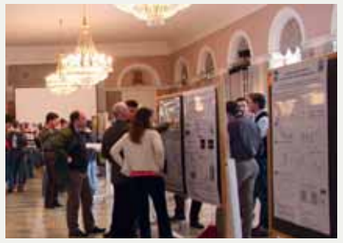
In 2005, we recruited Dierk Niessing, previously at Rockefeller University in New York, who investigates the mechanisms of cellular cargo transport using a combination of biochemistry and structural biology. His research team is co-financed by the Helmholtz Society, which provides 1.3 million euros over five years. In 2006, we succeeded in recruiting Roland Beckmann, also previously at Rockefeller and more recently at the Charité in Berlin. Roland's research on protein sorting has greatly strengthened the cellular biochemistry focus at the Center. He has established a high-end electron microscopy facility unique among German universities to determine the functional architecture of large cellular assemblies which are the beyond reach of classic crystallographic approaches. In the same year, we recruited Klaus Förstemann, who returned to Germany after research in Lausanne and at the Massachusetts Medical School in the USA. He studies the biogenesis and function of micro-RNAs, small RNAs that switch genes off. In 2007, Daniel Wilson joined the Center as a new group leader. His group investigates the mechanisms of action of antibiotics. In 2009, Petra Wendler moves to the Center from London to set up a group that uses electron microscopy to study assisted protein remodeling. Petra received an Emmy Noether startup grant from the German Research Council (DFG). Fortunately, we were able to convince Katja Sträßer and Karl-Peter Hopfner to stay despite offers from other German universities: Katja is extending her work on coupling between different steps of gene expression and is now supported by a starting grant from the European Research Council. Karl-Peter had three outside offers but could be appointed full professor at the Gene Center in 2007. He now expands his research in structural biomedicine and establishes also a new crystallization platform and structural analysis of macromolecular solutions.

To set up computational biology at the Gene Center, we obtained 1.2 million euros from the German national initiative for excellence in research, and carried out two search symposia. We recruited two group leaders, Johannes Söding in 2007 and Achim Tresch in 2008. Johannes develops methods to predict gene function, and Achim concentrates on analysis of cellular networks. Both groups also collaborate with experimental labs in areas including analysis of data from functional genomics. To provide an optimal working environment for the computational biologists, we remodeled the old library to create office space, installed a high-speed computer network, and set up large server rooms.

A second major step towards establishing molecular systems biology at the Gene Center was taken when Ulrike Gaul accepted a professorship in organismic biochemistry. Ulrike returned from the USA after nearly 20 years at top institutions, including the University of California Berkeley and Rockefeller University. Ulrike uses the fruit fly as a model to study gene regulation during developmental processes and the function of glia cells in the nervous system. Beginning in 2009, she will set up advanced Bioimaging and high-throughput facilities at the Gene Center. Her recruitment was made possible by additional funds from the Center for Integrated Protein Science, the Bioimaging Network Munich, and the Humboldt Foundation, which alone will provide 5 million euros over the next five years.

Three principal investigators left the Gene Center during the period of the report. Claudia Petritsch left in 2005 to take up a position at the University of California in San Francisco. Ralf-Peter Jansen left in 2008 to accept a full professorship at the University of Tübingen. Stefan Weiss will be leaving in 2009 to accept a full professorship at Johannesburg University. I would like to thank all of them for their good work and the many important contributions they have made over the years.

THE GENE CENTER HAS DEVELOPED INTO A CENTRAL MEETING PLACE FOR SCIENTIFIC EXCHANGE AND ADVANCED TEACHING AND TRAINING.

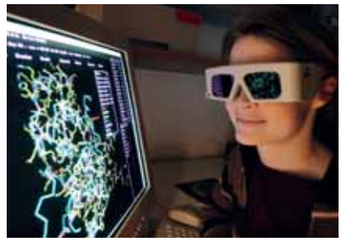
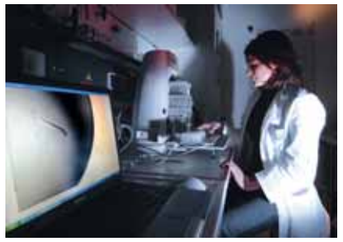


THE DIRECTOR'S REPORT

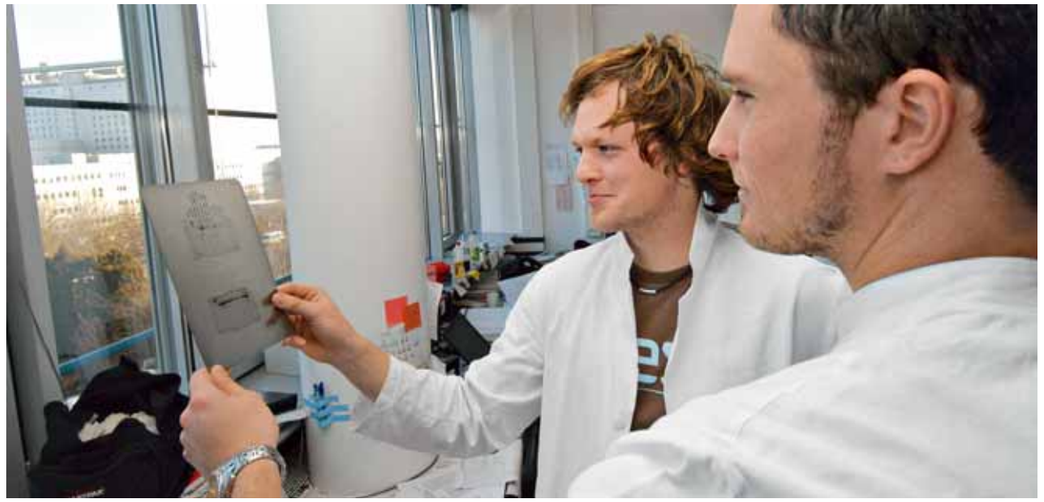
The sustained growth of the Center has been achieved by major extramural funding projects that have helped to establish state-of-the-art research facilities. In particular, a 4.8 million-euro research program to study regulatory networks in genome expression and maintenance (SFB 646) was launched in 2005. This program was positively evaluated in 2008 and has been extended until 2012. In addition, the Gene Center was instrumental in establishing the Munich Cluster of Excellence in Protein Science, CIPSM. The research grant network SFB455 "Viral functions and modulation of the immune system," headed by Ulrich Koszinowski, was successfully extended until 2010. A new technology platform for functional genome analysis (LAFUGA) was set up by Eckhard Wolf, Georg Arnold, and Helmut Blum. Stefan Bauersachs from Eckhard Wolf's group has obtained 1.2 million euros for functional genome analysis within the FUGATO program of the Federal Ministry of Science BMBF. For proteomics, a state-of-the-art orbitrap mass spectrometer is now available. Transcriptomics and genomic profiling is now possible with an Affymetrix gene array platform. The electron microscopy facility was expanded through the addition of a Titan microscope that allows for near-atomic resolution.

The Gene Center has developed into a central meeting place for scientific exchange and advanced teaching and training. Over the last five years, 149 speakers have participated in our international seminar series, and several research symposia were organized, each attracting up to 200 participants. Special lectures have highlighted distinguished scientists, including Tom Steitz from Yale University and the Nobel laureates Günter Blobel from Rockefeller and Erwin Neher from Göttingen. Exchange among the research groups within the Center is fostered by our annual retreats at Wildbad Kreuth in the Bavarian Alps. The Gene Center also works with Bio-M to organize an annual meeting at Castle Ringberg near Tegernsee, where investigators from academia and industry meet each January. Other social events include our Christmas parties. This rich scientific life and the general appeal of the Center and of Munich is what leads the best students and researchers to join us.

A particular highlight was the Open House during the national initiative "Land of Ideas" in 2006. Around 500 people, mostly from the general public, found their way to the Gene Center to listen to lectures and tour laboratories. The former Prime Minister of Bavaria, Dr. Edmund Stoiber, and the former Minister of Science, Dr. Thomas Goppel, the President of the LMU Munich, Prof. Bernd Huber, and the Secretary-General of the European Research Council and founder of the Gene Center, Prof. Ernst-Ludwig Winnacker, all participated in this event.

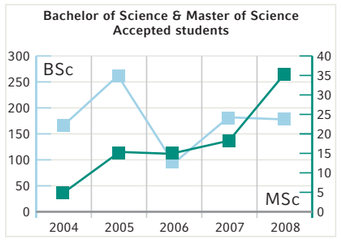





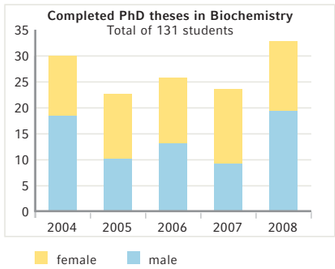
Today's rapid developments in the world of science demand innovative forms of teaching. We are dedicated to optimally preparing the next generation of life scientists for a successful career in academia or the private sector. A central teaching office headed by Heidi Feldmann now coordinates the many lectures and practical courses, maintains web pages for students, and provides all necessary information. The basic annual practical course in biochemistry now accommodates up to 180 undergraduates who are enrolled in the new Bachelor's programme in chemistry and biochemistry. Several newly-designed practical courses in biochemistry place the emphasis on hands-on experience and up-to-date techniques used in current research. A new Master's program taught exclusively in English provides selected students with an interdisciplinary background and critical experimental and theoretical skills. Over the last years, the number of newly accepted students has increased steadily, and we expect about 40 new students every year in the future **(Figure 3)**. The practical training is largely based on internships in research laboratories, and many of our students carry out part of their research training abroad.

FIGURE 3:



Graduate education is at the heart of our activities. Between 2004 and 2008, 131 PhD students completed their graduate studies in Biochemistry, 47% were women **(Figure 4)**. Graduate students and postdoctoral fellows present their research in a weekly seminar series. The annual Gene Center retreat allows for the discussion of ongoing research projects. Graduate education is now being organized in various PhD programs that span several institutions. For example, the graduate programs "Nano-Bio-Technology" and "Proteins in Health and Disease" are funded by a Bavarian elite network. The graduate research training group "Functional Genome Research in Veterinary Medicine" is funded by the German Research Council (DFG). Gene Center groups also work together with the neighboring Max Planck Institutes in a newly created Research School "From Biology to Medicine". The interactions with the Max Planck Society have also been strengthened by appointing Elena Conti and Matthias Mann from the neighboring institute as associate faculty.

FIGURE 4:



THE DIRECTOR'S REPORT

All these activities and successes have required the help of many dedicated investigators, researchers and students. I wish to thank all scientific personnel for their strong contributions and hard work. Also of particular importance, however, are all those who contribute to the effective infrastructure and administration at the Center. My special thanks therefore goes to all the non-scientific personnel who play this essential role in our everyday life.

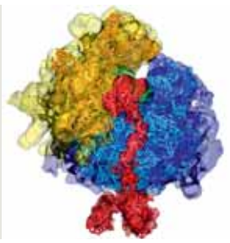
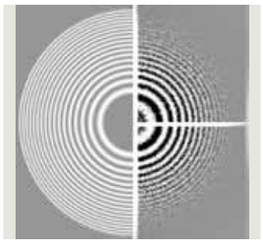
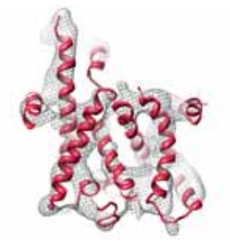
In the coming years, we will extend our research efforts at the organismic and systemic level and will develop promising new technologies. We will seek funding for additional junior groups that study the mechanisms of cell differentiation and organismal development. We will also expand the computational biology and foster close interaction between theoreticians and experimentalists to break new frontiers. Technologies will be developed that allow for seamless bioimaging, from molecules to organisms, and to enable systemic data acquisition. Our central administration will be restructured and extended to match the increased needs of the scientists, teachers, and students.

We will develop research at the Center directed at the emerging field of molecular systems biology. This field aims at predictive descriptions of biological systems based on the underlying molecular mechanisms. To reach this goal, structural, cellular, and organismic analyses of biological systems must be interconnected with the help of computational and new biophysical approaches. These measures will strengthen interactions with biomedicine and nanoscience, and will allow us to stay at the forefront in research and teaching in the life sciences.

I hope this report inspires your interest in the Gene Center. Come and join us in shaping the future!

Patrick Cramer

Roland Beckmann | Molecular machines in protein targeting and translocation

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EMAIL: BECKMANN@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/BECKMANN

SHORT CV

1995 | Ph.D. from the Free University Berlin, Germany;
1995-2000 | Postdoc at The Rockefeller University, New York, USA;
2001-2006 | Group Leader of the VolkswagenStiftung at the Charité, Berlin;
Since 2006 | Professor of Cellular Biochemistry at the Gene Center.

GOAL

To obtain a structural and mechanistic understanding of co-translational protein sorting, translocation and folding.

PERSONAL INTRODUCTION AND BACKGROUND

For biochemists, the usual way of encountering macromolecular complexes of a cell is by handling small amounts of solutions, photometric values or spots on a polyacrylamide gel. By contrast, it was a truly extraordinary experience for me to directly 'see' the actual activity of ion channels by patch-clamping, a method I learned before starting as a postdoc in Günter Blobel's lab in New York. There, however, literally seeing such complexes by electron microscopy (EM) became even more fascinating. As a result, instead of performing electrophysiological experiments I started to study the protein-conducting channel, the Sec61 complex, by EM. In all cells this universally conserved membrane protein complex mediates the membrane translocation or insertion of most secretory and membrane proteins. Reliable sorting of such proteins to their final destination inside or outside the cell is a vital step of gene expression, affecting up to 30% of all genes. These proteins carry a so-called signal sequence at their N-terminus that is recognized by the signal recognition particle (SRP). Upon binding of the signal sequence, the SRP targets the ribosome, the protein synthesis machinery, to the Sec61 complex via the membrane-bound SRP receptor (SR). Here, the ribosome continues translation while translocation or membrane insertion takes place. Since this process involves very large and dynamic macromolecular machines we use cryo-electron microscopy (cryo-EM) in combination with single-particle analysis to investigate the structural basis of protein sorting, translocation, membrane insertion and folding.

RESEARCH HIGHLIGHTS

After determining the first solution structures of the inactive and active 80S ribosome-Sec61 complex we focused on the complexes involved in targeting. We could solve the structure of a eukaryotic targeting complex consisting of an active ribosome (RNC) and SRP. Here, we learned how SRP binds to the signal sequence of a nascent polypeptide while modulating the activity of the ribosome at the same time. Later, we observed a bacterial complex and also the eukaryotic targeting complex at sub-nanometer resolution, allowing the visualization of the signal sequence bound to SRP. We could also show that the signal sequence is positioned on the ribosome in a distinct way for recognition by SRP. Next, a docking complex binding the SRP receptor was solved that revealed how the first membrane contact of the targeted ribosome may occur. Most recently, we succeeded in observing the active monomeric ribosome-bound Sec61 complex as well as the bacterial ribosome-SecYEG complex in its membrane environment, also at sub-nanometer resolution. We were able to explain the mode of binding to the ribosome and the interaction of the protein-conducting channel with the nascent chain. With ever-improving resolution, we are now able to visualize nascent chains in the ribosomal tunnel and study their behavior.

FUTURE PERSPECTIVE

Our aim is to collect more "snapshots" at the highest possible resolution in order to provide as complete a picture as possible of fundamental co-translational events. In the future we will thus concentrate our efforts on four topics: First, we plan to provide a complete molecular model of the 80S ribosome, serving as the basis for a molecular understanding of cotranslational processes in eukaryotes. Second, we will look at different types of nascent polypeptide chains to address questions regarding translational stalling, regulation and secondary structure formation. Third, we will visualize cotranslationally acting chaperons on the active ribosome in order to understand the first steps of protein folding. Fourth, based on our understanding of the ribosome-bound protein-conducting channel we will expand our studies on nascent membrane protein insertion, processing and assembly.

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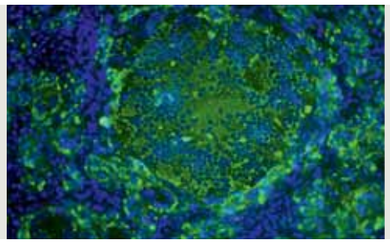
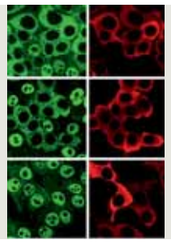
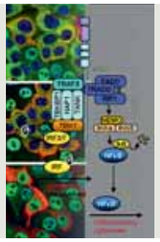
  SRP meets the ribosome.
  Nat. Struct. Mol. Biol. 11, 1049-53 (2004).

PHOTOS AND/OR ILLUSTRATIONS 1: Cryo-EM based molecular model of a targeting complex containing the mammalian SRP (red) bound to an 80S ribosome. 2: Powerspectrum of an electron micrograph. 3: Density and model of an active translocon resolved by single particle cryo-EM.

Karl-Klaus Conzelmann | Molecular biology of (-)RNA viruses

1 2 3

EMAIL: CONZELMA@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/GROUPS/CONZELMANN

SHORT CV

1988 | Ph.D. from the University of Tübingen;
1989-1998 | Federal Research Center for Virus Diseases, Tübingen;
Since 1999 | Associate Professor at the Max von Pettenkofer Institute and Gene Center Munich.

GOAL

To understand the molecular interplay between RNA viruses and host cells.

PERSONAL INTRODUCTION AND BACKGROUND

Co-evolution with their hosts have made viruses into experts in cell biology and host physiology. They have found ways to sneak into cells, switch off alarm systems, re-program cell gene expression and transform cells into virus factories. We are studying rhabdoviruses and paramyxoviruses to learn how they trick the host immune system and exploit cellular machineries for virus replication and assembly. A key technology in this approach is the genetic engineering of these RNA viruses on cDNA level (reverse genetics) which was developed in our laboratory. Recombinant viruses with defined gene defects are being used to reveal the contribution of individual virus proteins or protein domains to virus-host cell interplay. This involves a broad variety of cell biology and biochemistry methods, including state-of-the art fluorescence imaging. Knowledge of the mechanism involved not only tells us how cellular signaling networks function, but also provides means to re-program the viruses in order to use them as biomedical tools.

RESEARCH HIGHLIGHTS

A major topic in the laboratory is the recognition of viruses by immune receptors and the viral mechanisms counteracting the rapid signaling cascades that activate cellular defense. We were involved in the identification of viral triphosphate RNA as a ligand of RIG-I, an important cytoplasmic sensor for viral (i.e. non-self) RNA. We have identified proteins of rhabdo- and paramyxoviruses that can switch off RIG-I- or Toll-like receptor-mediated induction of the antiviral and immune stimulatory type I interferons, as well as JAK/STAT signaling which mediates the effects of interferons. Engineering of the viral interferon-antagonistic proteins renders viruses highly immunogenic and attenuated, by making them visible to the immune system. Another major interest is to elucidate the molecular mechanisms involved in the assembly and budding of virus particles and their entry into new target cells, which requires exploitation of specific cellular vesicle sorting machineries. Engineered fluorescent viruses can be tracked in live cells and allow real-time analysis of the individual steps of virus formation and entry. By further engineering viral envelope proteins and/or cellular receptors, it is possible to re-target viruses to specific cells. Such approaches using the neurotropic rabies virus provide tracers that can be used to identify neurons directly connected by synapses.

FUTURE PERSPECTIVE

We aim to learn from viruses how the immune system can be activated and suppressed. Substances mimicking viral RNAs will be used to develop immune-stimulatory therapies and adjuvants. The mechanisms used by viruses to suppress the activity of the immune system may lead to novel strategies for interference with aberrant immune responses such as autoimmunity. The ability of the rabies virus to find and cross synapses will be employed to study the wiring of neuronal circuits.

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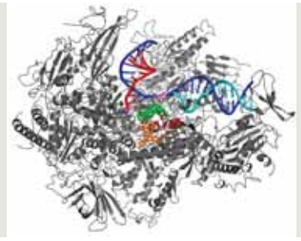
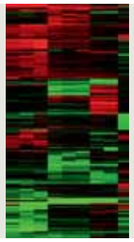
- V. Hornung, J. Ellegast, S. Kim, K. Brzózka, A. Jung, H. Kato, H. Poeck, S. Akira, **K.-K. Conzelmann**, M. Schlee, S. Endres, G. Hartmann. 5'-Triphosphate RNA is the ligand for RIG-I. *Science. 2006 314(5801):994-7.*
- K. Brzózka, S. Finke, **K.-K. Conzelmann**. Inhibition of Interferon Signaling by Rabies Virus Phosphoprotein P: Activation-dependent binding of STAT1 and STAT2. *J Virol. 2006 80(6): 2675-83.*

SELECTED REVIEWS

- K. Brzózka, C. Pfaller, and **K.-K. Conzelmann**. Signal transduction in the type I IFN system and viral countermeasures *Signal Transduction, 2007; 7: 5-19*
- **K.-K. Conzelmann**. Reverse genetics of Mononegavirales. *Curr Top Microbiol Immunol. 2004; 283:1-41.*

PHOTOS AND/OR ILLUSTRATIONS 1: Single virus particles labeled with the autofluorescent proteins eGFP (green), tdTomato (red). A virus containing both appears yellow. 2: Transport of fluorescent rabies virus in axons of culture's neuronal cells. 3: Cells expressing a viral protein (red) that inhibits nuclear import of STAT2 (green). Nuclei are shown in blue.

Patrick Cramer | Gene transcription and regulation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EMAIL: CRAMER@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/CRAMER

SHORT CV

1998 | Ph.D. from the European Molecular Biology Laboratory in Grenoble, France and Heidelberg University;
1999-2000 | Postdoc at Stanford University, USA;
2001-2003 | Tenure-Track Professor at the Gene Center Munich;
Since 2004 | Professor at and Director of the Gene Center.

GOAL

To obtain a three-dimensional movie of the transcription machinery and an understanding of gene regulation at the molecular and systemic level.

PERSONAL INTRODUCTION AND BACKGROUND

To me, one of the most fascinating recent scientific achievements was the reprogramming of differentiated cells to induce stem cell-like behaviour. Such reprogramming can be achieved by expression of a few factors that regulate gene transcription, the first step in the expression of the genetic information. Transcription is the focal point of gene regulation, also during organism development. The central engines of transcription, the RNA polymerases, are multiprotein enzymes that form large functional complexes with nucleic acids and additional proteins. Our laboratory determines three-dimensional structures of these transient polymerase complexes, to elucidate the mechanisms of transcription and its regulation. Structural snapshots in different functional states are combined into movies of the transcription machinery in action. X-ray crystallography and electron microscopy are combined with biochemical and genetic methods to provide complementary functional insights in vitro and in vivo. This leads to structure-function relationships and an understanding of molecular mechanisms. Driven by our desire to understand gene regulation, we also use transcriptomics, genome-wide occupancy profiling, and bioinformatics, to develop new interdisciplinary approaches that can bridge structural biology and functional genomics.

RESEARCH HIGHLIGHTS

Over the past years, our laboratory completed the atomic three-dimensional structure of RNA polymerase II, the 12-subunit 520 kDa complex that produces messenger RNA. Also determined were structures of polymerase complexes with DNA template, RNA product, nucleoside triphosphate substrate, different types of damaged DNA templates, an RNA template, the elongation factor TFIIS, an RNA inhibitor, the mushroom toxin amanitin, and structures of isolated factors that associate with the polymerase. Together with functional data, these structures elucidated many mechanistic aspects of the transcription cycle. The laboratory also identified several submodules of the multiprotein Mediator complex, which is required for transcription regulation, and characterized these modules structurally and functionally. We further provided structural and functional information on the two other eukaryotic RNA polymerases, Pol I and Pol III, which transcribe ribosomal RNA and transfer RNA respectively. To extend our studies to systemic level, functional genomics approaches were established, in particular transcriptomics and genome-wide occupancy profiling by chromatin immunoprecipitation coupled to high-resolution tiling microarray analysis. The combination of structural biology with functional genomics allowed us to identify gene regulatory modules and map multiprotein assemblies on the genome by structure-system correlations.

FUTURE PERSPECTIVE

In the future, we will focus on four major aims. First, we want to understand the molecular basis for RNA polymerase II initiation, including promoter DNA recognition, initial RNA synthesis, and the initiation-elongation transition. Second, we will study on the molecular and systemic level how transcription initiation is regulated via the Mediator complex. Third, we will characterize the cis-acting elements and the trans-acting factors that govern gene transcription in yeast by combining structure-based mutagenesis and functional genomics. Finally, we want to understand the determinants and evolution of gene class-specific transcription by extending our mechanistic analysis of RNA polymerases I and III to functional complexes.

SELECTED ORIGINAL PUBLICATIONS

- L. Larivière, M. Seizl, S. van Wageningen, S. Röther, L. van de Pasch, H. Feldmann, K. Sträßer, S. Hahn, F.C. Holstege, and **P. Cramer**. Structure-system correlation identifies a gene regulatory Mediator submodule. *Genes Dev. 22, 872-877 (2008).*
- E. Lehmann, F. Brueckner, **P. Cramer**. Molecular basis of RNA-dependent RNA polymerase II activity. *Nature 450, 445-449 (2007).*
- C.D. Kuhn, S.R. Geiger, S. Baumli, M. Gartmann, J. Gerber, S. Jennebach, T. Mielke, H. Tschochner, R. Beckmann, and **P. Cramer**. Functional architecture of RNA polymerase I. *Cell 131, 1260-1272 (2007).*
- F. Brueckner, U. Hennecke, T. Carell, **P. Cramer**. CPD damage recognition by transcribing RNA polymerase II. *Science 315, 859-62 (2007).*
- A. Meinhart, **P. Cramer**. Recognition of RNA polymerase II carboxy-terminal domain by 3'-RNA processing factors. *Nature 430, 223-226 (2004).*

SELECTED REVIEWS

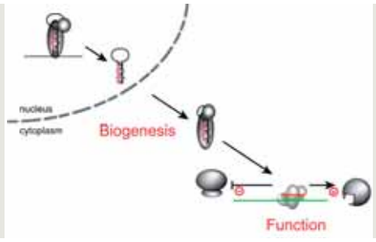
- **P. Cramer** et al. Structure of eukaryotic RNA polymerases. *Annu. Rev. Biophys. 37, 337-352 (2008).*
- **P. Cramer**. Extending the message. *Nature 448, 142-143 (2007).*
- **P. Cramer**. Self-correcting messages. *Science 313, 447-448 (2006).*

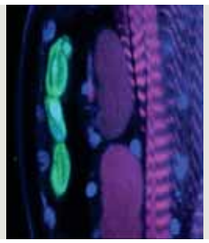
AWARDS

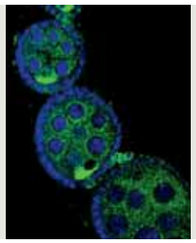
- Jung-Prize for Medicine 2009
- Familie Hansen Award of the Bayer Foundation 2009
- Bijvoet Medal of the University of Utrecht 2008
- Philip Morris Research Award 2007
- Gottfried Wilhelm Leibniz Award of the German Research Foundation (DFG), LMU Munich, 2006
- 10th Eppendorf Award for Young European Researchers 2004

PHOTOS AND/OR ILLUSTRATIONS 1: Structure of the RNA polymerase II elongation complex bound by the mushroom toxin α-amanitin. 2: Clustering of differential genome expression profiles identifies gene regulatory modules. 3: 3D computer graphics allow building of atomic structures based on X-ray analysis.

Klaus Förstemann | Control of gene expression by microRNAs







1 2 3

EMAIL: FOERSTEMANN@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/FOERSTEMANN

SHORT CV

2002 | Ph.D. from the Swiss Institute of Experimental Cancer Research (ISREC) in Lausanne, Switzerland;
2003 | Postdoc at the ISREC in Lausanne, Switzerland;
2004-2005 | Postdoc at the University of Massachusetts Medical School in Worcester, USA;
Since 2006 | Tenure-Track Professor at the Gene Center Munich.

GOAL

To determine the mechanisms and biological significance of small ncRNA-mediated gene regulation.

PERSONAL INTRODUCTION AND BACKGROUND

The unfortunate notion that RNA only serves as an intermediate carrier of information between the genome and the proteome was long generally accepted, and the Nobel laureate James Watson once even called RNA “the lesser cousin of DNA”. Today, we are increasingly aware of the fact that RNA can have many other functions ranging from cellular regulation to catalytic activity. Towards the end of my PhD thesis, in which I examined the non-coding RNA template of yeast telomerase, I was fascinated by the newly emerging field of microRNAs and siRNAs, which are essential for multicellular eukaryotes. This small RNA-silencing system relies on RNAs 21-23 nucleotides in length that mediate the sequence-specific recognition of nucleic acids, thus regulating gene expression on the transcriptional and post-transcriptional levels. The main tasks of microRNAs (miRNAs) are clearance of maternal mRNAs in embryogenesis, setting of thresholds in developmental decisions, fine-tuning of mRNA-levels in response to environmental stimuli and tumor suppression. In addition, short interfering RNAs (siRNAs) and piwi-interacting RNAs (piRNAs) contribute to antiviral defense and the suppression of mobile genetic elements. Starting with my post-doctoral training, I wanted to decipher the biogenesis network for the different classes of small RNAs. Because the system is so complex, it is of great advantage to employ a model organism, such as the fruit fly Drosophila melanogaster, and to use genetic, genomic and biochemical approaches in parallel.

RESEARCH HIGHLIGHTS

There are two central themes in the biogenesis of small regulatory RNAs: First, they derive from longer precursors through nucleolytic processing steps and second, they are sorted and become specifically loaded into protein complexes with distinct biochemical properties. For both the processing and loading steps, it is essential that dedicated protein complexes can distinguish between each class of small RNA precursor. This is certainly important, because the structural differences are small compared to the major functional differences of the mature silencing complexes. During my post-doctoral period I discovered a new co-factor for Drosophila Dicer-1 that confers specificity for miRNA-precursors on this processing enzyme. Furthermore, I could provide in-vivo proof that miRNAs are recognized and sorted into specific protein complexes during their biogenesis according to the structure of an intermediate, leading to distinct functional properties of the resulting complexes. We have since set out to further understand the interrelationships between the miRNA and siRNA biogenesis pathways. In addition, we want to understand more about the role that miRNAs play beyond development, specifically in the metabolic homeostasis during adult life. Why do flies need microRNAs to reach a normal life span? What mechanisms are controlled by miRNAs that confer robustness against environmental changes? Genetic experiments have shown us that these processes depend on the correct dose and timing of miRNA expression, but there are many questions to answer before we can reach a description of the underlying regulatory circuits.

FUTURE PERSPECTIVE

An important future development will be to extend our biochemical and genetic approaches to genome-wide analyses using gene expression arrays and deep sequencing technologies. Because of the pervasive regulatory functions of miRNAs and siRNAs, the classic experiments on individual genes or protein factors simply do not suffice to generate an unbiased, system-wide description. My goal for the coming years is to establish data analysis and modeling approaches that will help us to predict – and subsequently test – the regulatory connections between genetically programmed circuits and environmentally induced responses.

SELECTED ORIGINAL PUBLICATIONS

- C. Shah, **K. Förstemann**.
  Monitoring microRNA-mediated silencing in Drosophila melanogaster S2-cells.
  Biochim Biophys Acta 1779, 766-772 (2008).
- **K. Förstemann**, M.-D. Horwich, L. Wee, Y. Tomari, P.D. Zamore.
  Drosophila microRNAs are sorted into functionally distinct Argonaute complexes after production by dicer-1.
  Cell 130, 287-297 (2007).
- **K. Förstemann**, Y. Tomari, T. Du, V.V. Vagin, A.M. Denli, D.P. Bratu, C. Klattenhoff, W.E. Theurkauf, P.D. Zamore.
  Normal microRNA Maturation and Germ-Line Stem Cell Maintenance Requires Loquacious, a Double-Stranded RNA-Binding Domain Protein.
  PLoS Biol. 3, e236 (2005).
- **K. Förstemann**, J. Lingner.
  Telomerase limits the extent of base pairing between template RNA and telomeric DNA.
  EMBO Rep. 6, 361-366 (2005).

SELECTED REVIEWS

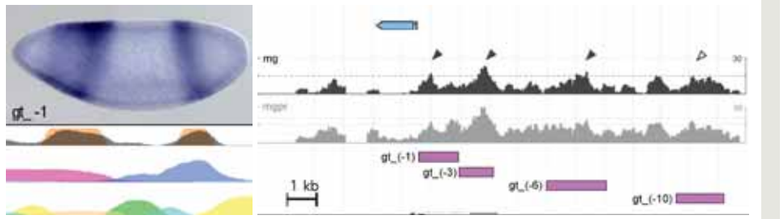
- V. Aumiller, **K. Förstemann**.
  Roles of microRNAs beyond development – Metabolism and neural plasticity.
  Biochim Biophys Acta 1779, 691-696 (2008).
- V. Hartig, Y. Tomari, **K. Förstemann**.
  piRNAs – the ancient hunters of genome invaders.
  Genes Dev. 21, 1707-1713 (2007)

AWARDS

- HFSP Career Development Award 2008
- Boehringer Ingelheim Fonds Doktoranden-Stipendium für J. Hartig (2007)

PHOTOS AND/OR ILLUSTRATIONS 1: Biogenesis of small RNAs takes place in several steps of maturation and sorting. 2: Expression domains of miRNAs can be visualized in transgenic animals. 3: Our model organism Drosophila offers many organ systems that can be genetically manipulated and which are not only understood in their function, but also beautifully structured (here: the oocyte maturation process).

Ulrike Gaul | Systems biology of gene regulation and function of glia in the nervous system



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EMAIL: GAUL@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/GAUL

SHORT CV

1988 | PhD at the Max-Planck-Institute for Developmental Biology, Tübingen;
1989-1993 | Postdoc at the University of Washington, Seattle, and University of California, Berkeley, USA;
1993-2009 | Assistant Professor; since 2000 Associate Professor at the Rockefeller University, New York, USA;
Since 2009 | Humboldt-Professor at the Gene Center Munich.

GOAL

To understand the regulatory gene networks underlying organismal development and homeostasis at the systems level.

PERSONAL INTRODUCTION AND BACKGROUND

My interest in complex systems – how the relationship between components of a given system defines its overall behavior – predates my work in developmental biology. An avid musician in my youth, I was fascinated by the evolution of musical systems and the differences in their emotive power. In twelve-tone music, for example, the notion of any preferential relationship between the notes of the chromatic scale is cast aside: in his novel Doktor Faustus, Thomas Mann ascribes this step to a composer who, making a pact with the devil to achieve musical greatness, seeks to evoke the eerie isolation of the creative individual. The resulting musical universe is indeed uncanny in its ability to express loneliness, mourning and despair. Happily, developing biological systems are more akin to well-tempered music – written in a specific key and with preferred interactions between particular components, yet retaining the facility to modulate into other keys and thus alter the pattern of favored interaction. And of course they are four-dimensional, more opera than fugue.

The central question of developmental biology is how the fertilized egg develops into a complete organism. Thousands of genes have to be active at the right time and the right place to define specific structures like head, trunk, and tail, or cell types like neurons and muscles. We seek to understand how such precise spatio-temporal patterning of gene expression is controlled and coordinated. The relevant information is encoded in the DNA flanking the genes and read off by transcription and translation factors, which induce or inhibit expression. The challenge is to locate and decode these regulatory signals ('cis-regulatory elements') in the genomic sequence and to understand how the participating factors interact to form regulatory networks. The overarching goal of this work is to transcend the analysis of individual components and investigate the developmental processes on network level, by generating quantitative models that describe the behavior of the entire system under normal and perturbed conditions.

RESEARCH HIGHLIGHTS

Over the past five years, we have sought to establish experimental and computational methods for the systems-biological analysis of metazoan development, using the fruit fly Drosophila as our model. In collaboration with physicists and computer scientists, we developed algorithms for the detection and analysis of cis-regulatory elements, both for transcription and microRNA-mediated translation control. Applying these tools to the segmentation paradigm of the Drosophila embryo, we identified many new regulatory elements in this network and elucidated basic rules governing their organization. This effort recently culminated in the first thermodynamic model of pattern formation that captures the mechanistic core of the process – the binding of transcription factors to cis-regulatory sequence and the resulting expression. Our studies on the role of target site accessibility in microRNA-mRNA interactions suggests that thermodynamic principles are equally useful in decoding the rules underlying translation control.

A second research focus in our lab is the study of the role of glial cells in the nervous system, a neglected but important problem of neurobiology. Seeking a principled approach to identify glial genes, we combined emerging technologies into a reverse genetic screen, with genome-wide expression profiling of FAC-sorted glial cells followed by injection-based RNA interference for initial functional analysis. This approach resulted in the discovery of many novel glial genes, including a GPCR pathway involved in blood-brain barrier regulation, and a family of phagocytic receptors required for the clearance of apoptotic neurons. Along the way, we developed an array of cellular markers, drivers, and imaging techniques that help establish Drosophila as a useful paradigm for the study of glial function.

FUTURE PERSPECTIVE

We plan to extend our work on systems biology in several directions, in collaboration with other groups at the Gene Center. The emphasis will be on a more detailed molecular mechanistic analysis of the cis-trans interaction at the regulatory element and the basal promoter, the coupling of these two interactions, and the role of nucleosomes in the process. In addition, we will seek to apply our techniques and concepts to more complex developmental paradigms and regulatory systems. To deepen our analysis of glial cell behavior and glia-neuron interactions, we will further explore the molecular and cellular mechanisms underlying glial phagocytosis and blood-brain barrier functionality, using a combination of functional genomics, physiological, and biochemical approaches, and embark on a study of the role of glia in adult homeostasis.

SELECTED ORIGINAL PUBLICATIONS

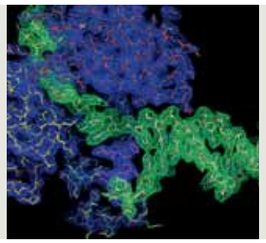
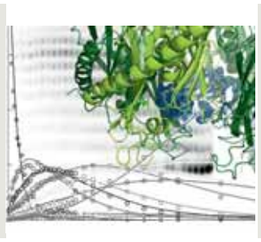
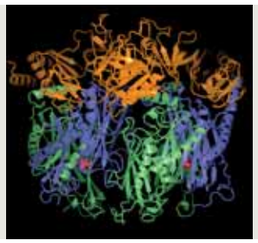
- Kurant E, Axelrod S, Leaman D, and **Gaul U**.
  Six-microns-under acts upstream of Draper in the glial phagocytosis of apoptotic neurons.
  Cell 133, 498-509 (2008).
- Segal E, Raveh-Sadka T, Schroeder M, Unnerstall U, and **Gaul U**.
  Predicting expression patterns from regulatory sequence in Drosophila segmentation.
  Nature 451, 535-540 (2008).
- Kertesz M, Iovino N, Unnerstall U, **Gaul U***, Segal E*.
  The role of site accessibility in microRNA target recognition.
  *Nat Genet 39, 1278-1284. *equal contribution (2007).*
- Schwabe T, Bainton RJ, Fetter RD, Heberlein U, and **Gaul U**.
  GPCR signaling is required for blood-brain barrier formation in Drosophila.
  Cell 123, 133-144 (2005).
- Schroeder M, Pearce M, Fak J, Fan HQ, Unnerstall U, Emberly E, Rajewsky N, Siggia ED, and **Gaul U**.
  Transcriptional control in the segmentation gene network of Drosophila.
  PLoS Biol 2:E271 (2004).

AWARDS

- Alexander von Humboldt Professorship (2008)
- Finalist, NIH Director's Pioneer Award (2007)

PHOTOS AND/OR ILLUSTRATIONS 1: Computational approaches are used to locate cis-regulatory elements in the genomic region DNA surrounding segmentation genes (right) and to predict their expression pattern (top left) based on the regulatory sequence and transcription factor binding preferences (bottom left).

Karl-Peter Hopfner | Mechanisms of DNA repair and virus sensing

1 2 3

EMAIL: HOPFNER@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/HOPFNER

SHORT CV

1997 | Ph.D. Max Planck Institute of Biochemistry and Technical University of Munich;
1998 | Postdoc at The Scripps Research Institute, USA;
2001 | Tenure-Track Professor at the Gene Center Munich;
2005 | Tenured Associate Professor at the Gene Center;
Since 2007 | Professor at the Gene Center;
Since 2009 | Director, Department of Chemistry and Biochemistry.

GOAL

We want to understand the molecular and structural mechanisms of how the cellular DNA-repair and antiviral RNA-sensing protein machineries detect, signal and repair or remove malignant nucleic acids such as damaged DNA and viral RNA.

PERSONAL INTRODUCTION AND BACKGROUND

All cells must maintain the integrity of the genome and remove or repair damaged or foreign nucleic acids to avoid cell death or cell aberration. For both malignant RNA and DNA, cells possess complex, highly specific protein machineries that sense, signal and repair or remove malignant nucleic acids. Defects in these processes are intimately linked with human diseases such as cancer, premature aging and virus infections. It is yet unclear why sensing of damaged or foreign nucleic acids is so highly specific and how single molecules of foreign RNA or single DNA lesions are distinguished from the vast amount of normal cellular DNA or RNA and trigger powerful cellular events such as interferon production, apoptosis or cell cycle arrest. For instance, foreign RNA from viral infections such as influenza and hepatitis C leads to a complex antiviral innate immune response by a class of RNA helicase complexes. Likewise, DNA damage in the form of double-strand breaks is signaled by the multifunctional ATPase-nuclease-kinase complex Mre11-Rad50-NBS1-ATM and repaired to prevent cancer development, cellular senescence and aging. Using a combination of structural, biochemical and molecular biological approaches, we study the molecular and structural mechanisms of how these multicomponent protein machines sense, repair and remove their malignant or foreign nucleic acids. Detailed mechanistic insights into these processes form a basis for understanding human disease and help to guide new therapeutic developments.

RESEARCH HIGHLIGHTS

We were able to achieve a variety of breakthroughs in key concepts of damage recognition and repair as well as sensing of viral RNA epitopes. We determined the first structure of a SWI2/SNF2 remodeling enzyme and its complex with DNA and uncovered that the SWI2/SNF2 ATPase domain uses ATP hydrolysis to translocate on dsDNA, a process that provides the energy to remodel nucleosomes or disrupt other DNA protein complexes. We were furthermore able to show how DNA repair helicases melt the DNA duplex and discovered a new type of small molecule – cyclic diadenosine – associated with DNA-damage signaling in prokaryotes. Finally, in a collaborative effort with the Carell group we showed for the first time how a DNA-repair polymerase can read over a cisplatin DNA adduct, a process that is linked to acquired resistance of cancer cells against cisplatin chemotherapy. Another line of research focused on viral RNA sensing and degradation. We determined the structure and biochemical mechanism of the large nine-subunit RNA exosome, a molecular assembly of exonucleases that degrades RNA in RNA quality control, maturation and turnover processes. Finally, we revealed how the innate immune ATPase RIG-I senses viral RNA via 5′ triphosphates at a unique regulatory domain.

FUTURE PERSPECTIVE

An integrated structural and functional understanding of the molecular mechanisms of DNA damage and viral RNA sensing will require the analysis of transient and regulated macromolecular assemblies. We will use hybrid approaches such as the combination of high resolution X-ray crystallography with electron microscopy and small-angle X-ray scattering, together with our functional in-vitro and in-vivo approaches, to tackle these challenges. Most of the molecular mechanisms of damaged and foreign nucleic acid sensing are unclear, and it will be exciting to see how these machineries translate epitope recognition into signaling.

SELECTED ORIGINAL PUBLICATIONS

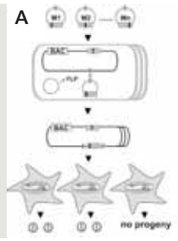
- Cui S, Eisenächer K, Kirchhofer K, Brzózka K, Lammens A, Lammens A, Fujita T, Conzelmann K, Krug A, **Hopfner KP**. The regulatory domain is the triphosphate sensor of RIG-I. *Molecular Cell. 29. 169-179 (2008)*
- Alt A, Lammens K, Chioccini C, Lammens A, Piech K, **Hopfner KP***, Carell T*. Bypass of DNA Crosslink Lesions Generated During Anticancer Treatment with Cisplatin by the Eukaryotic DNA Polymerase eta. *Science. 318, 967 – 970 (2007)*
- Buttner K, Nehring S, **Hopfner KP**. Structural basis for DNA duplex separation by a superfamily-2 helicase. *Nat. Struct. & Mol. Biol. 14, 647-52 (2007)*
- Dürr H, Körner C, Müller M, Hickmann V, **Hopfner KP**. X-Ray structures of the Sulfolobus solfataricus SWI2/SNF2 ATPase core and its complex with DNA. *Cell 121, 363-373 (2005).*
- Büttner K, Wenig K, **Hopfner KP**. Structural Framework for Archaeal Exosomes in RNA Processing. *Mol. Cell 20, 461-71 (2005).*

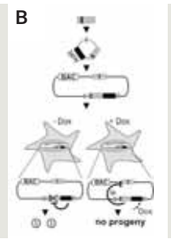
SELECTED REVIEWS

- Büttner, K, Wenig, K and **Hopfner KP**. The Exosome: a macromolecular cage for controlled RNA degradation. *Mol. Microbiology 61, 1372-1379 (2006).*
- Dürr H, **Hopfner KP**. Structural and biochemical analysis of SWI2/SNF2 enzymes. *In Methods of Enzymology: DNA repair. Ed. J Campell, P Modrich, Elsevier. Pending (2006).*
- Assenmacher N, **Hopfner KP**. Mre11/Rad50/Nbs1: Complex activities. *Chromosoma 113, 157-66 (2004).*

PHOTOS AND/OR ILLUSTRATIONS 1: The exosome: a large molecular machine for the controlled degradation and processing of RNA. 2: Hybrid methods to study macromolecular assemblies. 3: Structure of the exosome, a large RNA degradation complex.

Ulrich Koszinowski | Herpesvirus biology and genetics





1 2

EMAIL: KOSZINOWSKI@MVP.UNI-MUENCHEN.DE
INTERNET: WWW.MVP.UNI-MUENCHEN.DE

SHORT CV

1970 | M.D. at University of Göttingen;
1970-1975 | Postdoc at University of Göttingen;
1975 | Habilitation at University of Göttingen;
1976-1977 | Research Associate at London University, UK;
1978 | Heisenberg Award, German Cancer Research Center Heidelberg;
1980 | Director and Professor, Federal Res. Inst. Animal Virus Diseases, Tübingen;
1987 | Chair Virology, University of Ulm;
1992 | Chair Virology, Heidelberg University;
Since 1996 | Chair Virology, LMU Munich.

GOAL

Understanding the principles governing the function of herpesvirus proteins.

PERSONAL INTRODUCTION AND BACKGROUND

Herpesviruses are important pathogens in all vertebrates. Their large genomes (230 Kb for mouse cytomegalovirus) encode about 200 proteins. Only about 25% of the gene content is required to build the virion; the majority of proteins are not essential, serving to modulate the infected cell and/or the immune response of the host. Our laboratory is investigating the function of non-essential and of essential genes. Non-essential genes are studied to reveal principles of co-evolution of species-specific viruses within their natural hosts. Common essential genes are shared between herpesvirus subfamilies. They are studied to dissect aspects of virus morphogenesis in order to identify new targets for therapeutic intervention. The main experimental tools used are forward and reverse genetics. Genes are conditionally expressed from the viral genome to identify loss of function and dominant negative mutants. Non-essential genes are studied in vitro and in vivo after infection of a mouse to identify host functions modulated by viral genes. The group develops new concepts for new genetic screens and methods to elucidate the contribution of individual host and virus genes to infection conditions of individual cell types in vivo.

RESEARCH HIGHLIGHTS

The group applies methods of virus genetics, immunology, and cell biology. The group has proprietarily developed cloning and mutagenesis principles for herpesvirus genomes, e.g. cloning a whole herpesvirus genome as a bacterial artificial chromosome (BAC). Recent additions are random comprehensive virus gene mutagenesis principles. Different methods are developed to study essential and non-essential viral proteins. A. Essential genes: Conditional gene expression identifies the function of dominant mutants of viral genes in the genomic context.
B. Non-essential genes vary between herpesviruses. We have identified many genes that modulate host cell function, such as antigen presentation, cytokine synthesis, apoptosis and NK cell activation. We hypothesize that these functions are needed by the virus at different stages of infection in order to replicate in specific target tissues and to escape immune functions that may act in different ways in specific tissues. Conditional gene switches in vivo serve to trace the infection of specific tissues and to determine and visualize the contribution of individual virus genes.

FUTURE PERSPECTIVE

A. Dominant-negative-mutant identification of essential genes serving as a systemic tool to determine functions of any essential viral protein is presently under development. Procedures work safely but need to be accelerated. Early morphogenesis steps and the nuclear exit of viral capsids are a major focus for chemotherapy target identification. The aim is for dominant-negative mutants to provide access to the engineering of cell, type, specific and systemic viral resistance.
B. The combination of mouse genetics and conditional marker expression is intended to pave the way for study of the role of individual nonessential genes at the level of organs and tissues.

SELECTED ORIGINAL PUBLICATIONS

- Sacher, T.; Podlech, J.; Mohr, C.A.; Jordan, S.; Ruzsics, Z.; Reddehase, M.J.; **Koszinowski, U.H.**
  The Major Virus-Producing Cell Type During Murine Cytomegalovirus Infection, the Hepatocyte, Is Not the Source of Virus Dissemination in the Host.
  Cell Host. Microbe 3, 263-272 (2008).
- Rupp, B.; Ruzsics, Z.; Buser, C.; Adler, B.; Walther, P.; **Koszinowski, U.H.**
  Random Screening for Dominant-Negative Mutants of the Cytomegalovirus Nuclear Egress Protein M50.
  J. Virol., 81, 5508-5517 (2007).
- Lenac, T.; Budt, M.; Arapovic, J.; Hasan, M.; Zimmermann, A.; Simic, H.; Krmpotic, A.; Messerle, M.; Ruzsics, Z.; **Koszinowski, U.H.**; Hengel, H.; Jonjic, S.
  The Herpesviral Fc Receptor Fcr-1 Down-Regulates the NKG2D Ligands MULT-1 and H60.
  J. Exp. Med., 203, 1843-1850 (2006).
- Schnee, M.; Ruzsics, Z.; Bubeck, A.; **Koszinowski, U.H.**
  Common and Specific Properties of Herpesvirus UL34/UL31 Protein Family Members Revealed by Protein Complementation Assay.
  J. Virol., 80, 11658-11666 (2006).
- Rupp B, Ruszics Z, Sacher T, **Koszinowski, U.H.**
  Conditional cytomegalovirus replication in vitro and in vivo.
  J. Virol. 79, 486-494 (2005).
- French, A.R.; Pingel, J.T.; Wagner, M.; Bubic, I.; Yang, L.; Kim, S.; **Koszinowski, U.H.**; Jonjic, S.; Yokoyama, W.M.
  Escape of Mutant Double-Stranded DNA Virus From Innate Immune Control.
  Immunity., 20, 747-756 (2004).

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- Ruzsics, Z. and **Koszinowski, U.H.**
  Mutagenesis of the Cytomegalovirus genome
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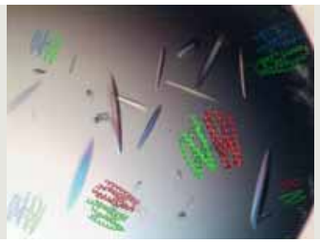
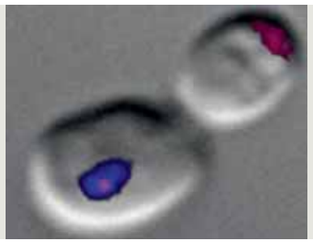
- Hengel H, **Koszinowski U.H.**, Conzelmann KK.
  Viruses know it all: new insights into IFN networks.
  Trends Immunol. 7, 396-401 (2005).
- Wagner, M.; **Koszinowski, U.H.**
  Mutagenesis of Viral BACs with Linear PCR Fragments (ET Recombination).
  Methods Mol. Biol., 256, 257-268 (2004).

AWARDS

- Spiridon Brusina Award (University of Rijeka Croatia)

PHOTOS AND/OR ILLUSTRATIONS 1: Genetic screen for dominant negative mutants of essential viral genes. 2: The role of cell types during virus infection in vivo by cre-recombination.

Dierk Niessing | Motor-protein-dependent translocation of cellular cargo


1 2 3

EMAIL: NIESSING@LMB.UNI-MUENCHEN.DE OR NIESSING@HELMHOLTZ-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/NIESSING

SHORT CV

2000 | Ph.D. at Max Planck Institute for Biophysical Chemistry, Göttingen;
2000-2002 | Postdoc at The Rockefeller University, New York, USA;
2003-2005 | Postdoc at SGX Pharmaceuticals, Inc., San Diego, USA;
Since 2005 | Helmholtz/University Young Investigator (Tenure-Track) at the Gene Center and the Helmholtz Zentrum München.

GOAL

To obtain an integrated understanding of intracellular transport processes and their effect on gene regulation.

PERSONAL INTRODUCTION AND BACKGROUND

Imagine New York City without cars on the road or any mail being delivered. City would grind to a halt within no time. Like cities, eukaryotic cells are complex, crowded, and rely heavily on transportation to organize their inner life. In each cell, large motor-protein-containing complexes move along molecular tracks to deliver specific cargoes to defined destinations. Considering that several heritable diseases have been linked to mutations in transport complexes, it is surprising how little is known about these basic cellular processes. A main focus of our group is thus to understand how such transport events are organized on a molecular level and how they are used to regulate gene expression.

RESEARCH HIGHLIGHTS

The Niessing laboratory is jointly funded by the Helmholtz Zentrum München and the Gene Center. We use a combination of structural biology, biophysics, biochemistry, and in-vivo approaches to understand how mRNAs destined for transport are packaged into larger ribonucleoprotein particles (mRNPs). A main focus of our work is to study the selective transport and localization of the ASH1 mRNA in the yeast S. cerevisiae. Because the ASH1 mRNP is one of few transport complexes where all core factors have been identified, it may provide prototypical information for mRNA transport in general. An initial success in this project was our determination of the crystal structure of the ASH1 mRNA cargo-binding protein She2p. After joining the Gene Center in summer 2005, we addressed the question of how dozens of mRNAs are specifically bound by She2p and characterized the mechanistic requirements of different core factors for transport-complex assembly. We further demonstrated that the type V myosin motor of the ASH1 mRNP fails to form stable dimers. This finding is in stark contrast to other members of this motor family. It raises several mechanistic questions that we are currently addressing. Recently, we have initiated similar studies for related transport processes.

FUTURE PERSPECTIVE

The group's long-term goal is to explain how core factors of large multiprotein transport 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. We have begun to expand our research on transport processes in higher eukaryotes that exhibit direct links to heritable diseases.
We are particularly interested in learning more about mRNA-transport processes in neurons. Localization of transcripts and their localized translation in pre-and postsynaptic areas has been linked to synaptic plasticity, memory, and learning. Patients with neurodegenerative diseases often show alternations or disturbances in neuronal transport events. Because of their complexity and heterogeneity, neuronal mRNPs are inherently difficult to study. In order to deal with this problem, we aim to understand the composition and functional interdependence of core factors from sub-complexes that are common to different neuronal mRNPs. This approach might allow us to get a glimpse on the mechanistic details that govern basic neuronal mRNP function.

SELECTED ORIGINAL PUBLICATIONS

- Du T.G., Jellbauer S., Müller M. Schmid M., **Niessing D.**, Jansen R.P.
  Nuclear transit of the RNA-binding protein She2p is required for translational control of localized ASH1 mRNA.
  EMBO Rep. 9, 781-787 (2008).
- Heuck A., Du T.G., Jellbauer S., Richter K., Kruse C., Jaklin S., Müller M., Buchner J., Jansen R.-P., **Niessing D.**
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  Proc. Natl. Acad. Sci. USA – Track II: 105, 19778-19783 (2007).
- **Niessing D.**, Zenklusen D., Hüttelmaier S., Singer R.H., Burley S.K.
  She2p is a Novel RNA-Binding Protein with a Basic Helical Hairpin Motif.
  Cell 119, 491-502 (2004).

SELECTED REVIEWS

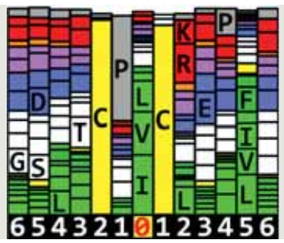
- Müller M., Heuck A., **Niessing D.**
  Directional mRNA transport in eukaryotes: lessons from yeast.
  Cell. Mol. Life Sci. 64, 171-180 (2007)
- **Niessing D**.
  Der Forschungsaufenthalt im Ausland – Should I stay or should I go?
  Biospektrum November 789-790 (2006).
- Cramer P., Sträßer K., **Niessing D.**, Meister G., Jansen R.P.
  RNA as coordinator and regulator of gene expression
  Biospektrum Special Edition 11. Jahrgang, 523-525 (2005).

AWARDS

- Boehringer Ingelheim PhD fellowship to Marisa Müller
- HFSP Long-term fellowship to Dr. Stephane Roche
- Elected to Helmholtz-Leadership Academy (2009)

PHOTOS AND/OR ILLUSTRATIONS 1: Crystals of a transport-complex core factor. 2: Yeast cell in budding stage (blue: nucleus; red: localized mRNA). 3: PhD student pipetting crystallization chemicals.

Johannes Söding | Protein bioinformatics and computational biology



1 2 3

EMAIL: SOEDING@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/SOEDING

SHORT CV

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 at the Boston Consulting Group;
2002-2007 | Scientific staff member at the Max Planck Institute for Developmental Biology in Tübingen;
Since 2007 | Group leader at the Gene Center Munich.

GOAL

- To develop significantly faster and significantly more sensitive algorithms for sequence comparison, in order to exploit the deluge of sequence data that we will see in the future.
- To better understand gene regulation by combining sequence data and high-throughput functional genomics data with quantitative modeling of transcriptional processes and networks.

PERSONAL INTRODUCTION AND BACKGROUND

Computational biology has become my passion since I entered this field 7 years ago. Given my background in experimental physics, computational biology has allowed me to apply my predilection for quantitative reasoning to biology. Whereas most areas of physics are in stagnation, biology is undergoing a revolution, largely brought about by the high rate at which new experimental techniques such as massively parallel sequencing or micro-arrays are being developed. For me, the challenge is to devise methods of analysis that are able to turn the flood of information from these techniques into biological understanding. I originally concentrated on studying protein evolution by developing new methods to detect very remotely homologous relationships. This has led to the development of one of the most successful and widely-used structure and function prediction servers (HHpred). We will continue these efforts by developing sequence search algorithms that transcend the limits of speed and sensitivity of current methods, and will use them to improve protein structure and function prediction as well as the prediction of genomic regulatory motifs. At the Gene Center, I have started to work on transcriptional regulation. This offers the enticing possibility of close collaboration with experimentalists working on the same topic, as well as giving ample opportunity to profit from my background in statistics and sequence analysis.

We have begun to develop novel methods for the discovery of cis-regulatory motifs, to apply thermodynamic models to transcriptional regulation, and to develop more complex and realistic models of transcriptional networks than those proposed so far.

RESEARCH HIGHLIGHTS

During my time as a research assistant in Tübingen, I developed a method for the detection of very remotely homologous proteins (HHsearch) with which we are now able to identify relationships reaching back to the origin of protein domains about 3.5 By ago. We were able to show, for instance, that all bacterial outer-membrane beta barrels are descended from a single beta-beta hairpin by amplification and subsequent diversification [Remmert et al., manuscript in preparation]. Since aligning a protein sequence with the sequence of a protein of known structure is the most important step in protein structure prediction, we could apply this method to protein structure and function prediction: our server HHpred ranked second among the 68 fully automatic servers participating in the 2006 community-wide protein structure prediction benchmark CASP7 [Battey et al., Proteins 2007], while being more than 50 times faster than the other top 20 servers. Recently, we have developed a new paradigm of sequence comparison that is based on sequence-context specificity. This has allowed us to double BLAST's sensitivity at the same speed [Biegert and Söding, PNAS 2009].

FUTURE PERSPECTIVE

We are currently preparing a manuscript describing a method for iterative HMM-HMM search that doubles the sensitivity of PSI-BLAST while producing significantly better alignments, without loss of speed. We believe that this method and the context-specificity paradigm offer great potential for improving all downstream alignment-based analyses (function prediction, functional site prediction, secondary and tertiary structure prediction, sub-cellular localization, phylogeny, protein-protein interactions etc.). To be able to profit from the expected future wealth of sequence data, we are devising methods that should enable database searches to be speeded up by a factor of ~100 at almost no loss of sensitivity. Furthermore, we will strive to completely characterize core promoter elements and classify core promoters in yeast and fly models, to better understand the role of cis-regulatory elements and their interaction with trans-acting factors for transcriptional regulation. In close collaboration with the Cramer and Gaul groups, we will integrate our theoretical analyses with the experimental investigation of the molecular processes underlying transcriptional regulation.

SELECTED ORIGINAL PUBLICATIONS

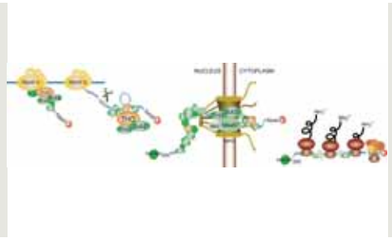
- Jasiak A. J., Hartmann H., Karakasili E., Marian K., Flatley A., Kremmer E., Sträßer K., Martin D. E., **Söding J.** , and Cramer P.
  Genome-associated RNA polymerase II includes the dissociable RPB4/7 subcomplex.
  J. Biol. Chem. 283, 26423-26427 (2008).
- Fischer J., Mayer C. E., and **Söding J.**
  Prediction of protein functional residues from sequence by probability density estimation.
  Bioinformatics 24:613-620 (2008).
- **Söding J.**, Biegert A., and Lupas A. N.
  The HHpred interactive server for protein homology detection and structure prediction.
  Nucleic Acids Res. 33:W244-248 (2005).
- **Söding J.**
  Protein-homology detection by HMM-HMM comparison.
  Bioinformatics 21:951-960 (2005).

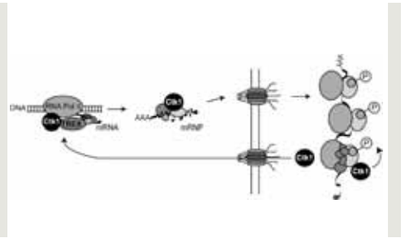
AWARDS

- 3rd place, Heinz Billing Award for the Advancement of Scientific Computation

PHOTOS AND/OR ILLUSTRATIONS 1: Computational biology office space in the former Gene Center library behind the two-storey glass facade on the left. 2: Example of a context profile describing the amino acid distribution of a Zinc finger. 3: The new, bright and friendly open office for Computational Biology in the former library.

Katja Sträßer | Integration of different steps in gene expression





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EMAIL: STRASSER@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/STRAESSER/KS_START.HTM

SHORT CV

2001 | Ph.D. from the University of Heidelberg;
2001-2002 | Postdoc at the University of Heidelberg;
Since 2003 | Group Leader at the Gene Center Munich.

GOAL

To obtain a functional understanding of the different steps in mRNA biogenesis, their interconnection, and thus the intricate network necessary for controlled and efficient gene expression.

PERSONAL INTRODUCTION AND BACKGROUND

Life as we know it is only possible by the action of proteins and protein complexes that mediate all cellular functions. Expression of the genome is one of these fundamental cellular processes and consists of many different steps. I am fascinated by the way in which these different steps are interconnected by large protein complexes and by the interactions between them to ensure controlled and efficient gene expression. My lab uses cell-biological, genetic, and biochemical approaches to unravel the molecular mechanisms linking these different steps. In addition to these "classic" techniques, novel systemic approaches such as gene expression arrays, ChIP-on-chip, and RIP-chip combined with bioinformatics will greatly support us in our endeavor to understand this intricate network. Taken together, the main goal of my lab is to understand how interconnections between the single steps – ranging from transcription to translation – provide quality control as well as efficiency in gene expression.

RESEARCH HIGHLIGHTS

Based on our identification and characterization of the TREX complex that couples transcription to nuclear mRNA export, we identified a novel protein, Swt1, and elucidated the function of Swt1 in transcription. In addition, we showed that the Ctk1-2-3 kinase complex, which plays an important role in transcription elongation, interacts with the TREX complex. Surprisingly, we were able to identify a second cellular function of Ctk1-2-3 in translation: Ctk1-2-3 phosphorylates Rps2, a ribosomal protein of the small subunit, which is necessary for efficient and correct decoding of the mRNA during translation elongation. We also obtained evidence that Ctk1 plays a role in translation initiation. Based on Ctk1-2-3's role in transcription and translation in addition to its interaction with the TREX complex, we hypothesize that Ctk1-2-3 couples correct transcription and processing of the mRNA in the nucleus to efficient translation of the message in the cytoplasm. Third, RNA pol II complexes that are irreversibly stalled on a gene will prevent transcription of the respective gene and thus eventually lead to cell death. We obtained evidence of a novel cellular pathway by which irreversibly stalled RNA pol II is removed from the transcribed gene.

FUTURE PERSPECTIVE

In the future, we aim to uncover a novel mechanism coupling transcription and mRNA biogenesis to translation by the action of Ctk1-2-3 and other proteins. A very recent focus of the lab is the control of translation by phosphorylation of ribosomal proteins. We are currently generating a complete list of all phosphorylated sites on ribosomal proteins and will then identify the functionally significant phosphorylation events and elucidate their function in translation. Third, we will unravel the cellular mechanism by which irreversibly stalled RNA pol II that poses a roadblock to transcription is removed from the transcribed gene as a last-resort mechanism. Our long-term goal is to understand how gene expression is regulated by the cross-communication between its single steps ranging from transcription to translation.

SELECTED ORIGINAL PUBLICATIONS

- S. Röther and **K. Sträßer**. RNA polymerase II CTD kinase Ctk1 functions in translation elongation. *Gen. Dev. 21: 1409-1421 (2007).*
- S. Röther, E. Clausing, A. Kieser, and **K. Sträßer**. Swt1, a novel yeast protein, functions in transcription. *J. Biol. Chem. 281: 36518 - 36525 (2006).*
- L. Larivière, S. Geiger, S. Hoeppner, S. Röther, **K. Sträßer**, and P. Cramer. Structure and TBP binding of the Mediator head subcomplex Med8–Med18–Med20. *Nat Struct Mol Biol. 13: 895 - 901 (2006).*
- E. Hurt, M.J. Luo, S. Röther, R. Reed, and **K. Sträßer**. Cotranscriptional recruitment of the serine-arginine-rich (SR)-like proteins Gbp2 and Hrb1 to nascent mRNA via the TREX complex. *Proc. Natl. Ac. Sc. USA 101: 1858-1862 (2004).*

SELECTED REVIEWS

- S. Röther and **K. Sträßer**. mRNA Export – an integrative component of gene expression. *In: Kehlenbach R, ed. Nuclear Transport. Austin: Landes Bioscience, Epub Ahead of Print (2008).*
- P. Cramer, **K. Sträßer**, D. Niessing, G. Meister, and R.P. Jansen. RNA als Koordinator und Regulator der Genexpression. *BIOspektrum, Sonderausgabe, 11. Jahrgang, 523-525 (2005).*

AWARDS

- Therese von Bayern-Preis, LMU Munich 2009
- ERC Starting Grant 2008
- "Habilitation" Award of the Dr. Klaus Römer-Stiftung, Department of Chemistry and Biochemistry, LMU Munich 2007
- EMBO Young Investigator 2004

PHOTOS AND/OR ILLUSTRATIONS 1: A simplified model of gene expression: The different steps of gene expression are intimately linked. 2: The kinase Ctk1 functions in transcription and translation and might functionally link these two distant steps of gene expression.

Achim Tresch | Computational biology, regulatory networks

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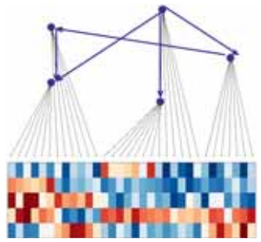

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EMAIL: TRESCH@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/TRESCH

SHORT CV

2002 | Ph.D. at Johannes Gutenberg University, Mainz;
2003-2004 | Postdoc at the Fraunhofer Institute, St. Augustin;
2005 | Postdoc at the German Cancer Research Center, Heidelberg;
2006-2007 | Assistant Professor at Johannes Gutenberg University, Mainz;
Since 2008 | Group Leader at the Gene Center, LMU Munich.

GOAL

To understand the syntax by which the components of the transcription machinery act together and coordinate gene expression.

PERSONAL INTRODUCTION AND BACKGROUND

How does a cell "know" its fate? What makes a murine oocyte become a mouse, and what is the developmental program that is responsible for it? Certainly, transcriptional regulation plays a pivotal role in all these processes. As a mathematician, I am trained to convert observations into equations, and hence try to explain cellular processes in terms of quantitative models. The sheer number of cellular components that potentially interact with each other raises new challenges to us. Network models have proved to offer a natural, comprehensive and interpretable description language. It is fascinating how quickly results from research into the basic principles of computation and statistics make their way into relevant applications in systems biology. I am happy for the opportunity to take part in both these active fields of research at one time.

RESEARCH HIGHLIGHTS

Recent years have seen a qualitative leap in the analysis of high dimensional data. High-density and high-throughput techniques have become broadly available, and the current quality of the data allows data-driven generation of new hypotheses. Starting with basic problems of low-level data analysis such as quality control, preprocessing, removal of bias and assessment of experimental variability, we established guidelines and commonly accepted standard procedures for large-scale biological experiments. This effort greatly enhanced the use of external data as a source of biological evidence. After addressing the most urgent multiple testing and prediction problems that arise in statistical analysis of high dimensional data, we tried to obtain a systems level of understanding of gene regulation. Thus we entered the field of probabilistic graphical models, where we developed the theory of a novel model class (nested-effects models) which proved very successful in the detection of interactions in complex regulatory systems.

FUTURE PERSPECTIVE

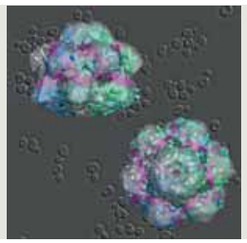
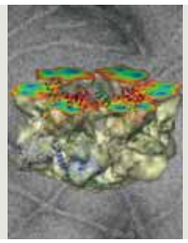
Our future efforts will focus on the integration of multiple sources of experimental data, since the number of experimental techniques is ever-increasing. They all capture different aspects of a transcription event, and it is essential to allow them to contribute altogether to a more detailed, mechanistic global picture.
On the mathematical side, we will develop new network models and refine the search algorithms for their estimation. We particularly need to view the problem of network reconstruction from a perspective of information theory. This will enable us to assess the reliability of our inferences.

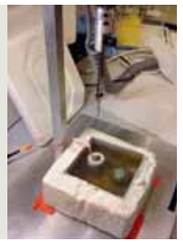
SELECTED ORIGINAL PUBLICATIONS

- **A. Tresch** and F. Markowetz.
  Structure Learning in Nested Effects Models.
  Statistical Applications in Genetics and Molecular Biology, Epub (2008).
- **A. Tresch**, T. Beissbarth, H. Sueltmann, R. Kuner, A. Poustka, A. Buness.
  Discrimination of direct and indirect effects in a network of regulatory effects.
  Journal of Computational Biology 14:1217-28 (2007).
- A. Buness, R. Kuner, M. Ruschhaupt, A. Poustka, H. Sueltmann, **A. Tresch**.
  Identification of aberrant chromosomal regions from gene expression microarray studies applied to human breast cancer.
  Bioinformatics 23:2273-2280 (2007).

PHOTOS AND/OR ILLUSTRATIONS 1: Office 2: Small scale network inference (top) from high dimensional data (bottom). 3: A look behind the scenes: Observations (blue) hint towards hidden regulatory mechanisms (red).

Petra Wendler | Protein remodeling and AAA+ assemblies



1 2 3 4

EMAIL: WENDLER@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/WENDLER

SHORT CV

2004 | Ph.D. at Charité, Humboldt University Berlin;
2004-2009 | Postdoc at Birkbeck College, London, UK;
Since 2009 | Group leader at the Gene Center and within the Emmy-Noether program of the DFG.

GOAL

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

PERSONAL INTRODUCTION AND BACKGROUND

During my academic career in engineering, biochemistry and structural biology I 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-organization 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 lacking. Cryo-electron microscopy is an essential tool for visualizing assemblies of this complexity and size and these 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

During my PhD and postdoctoral research, I have continuously worked on AAA+ complexes and gained the necessary experience to isolate AAA+ machines from yeast or bacteria and characterize them using biochemical and structural analysis. Over the past years I determined the three-dimensional structure of the AAA+ protein-remodeling complex Hsp104 in different functional states using cryo-electron microscopy. The electron density maps of Hsp104 revealed a novel AAA+ subunit packing in the active hexameric assembly and substantial domain movements upon nucleotide binding and hydrolysis. To extend the structural characterization of the functional states, an Hsp104 homology model was fitted into the cryo-EM densities and the fit verified by mutational, biochemical and biophysical analysis. This provided an initial view of the conformational changes during Hsp104's ATPase cycle that underlie its remarkable ability to remodel proteins. Furthermore, an asymmetric three-dimensional reconstruction of the Hsp104 hexamer excludes a concerted hydrolysis in the AAA+ rings, suggesting instead that the observed inter-subunit cooperativity generates a sequential firing order.

FUTURE PERSPECTIVE

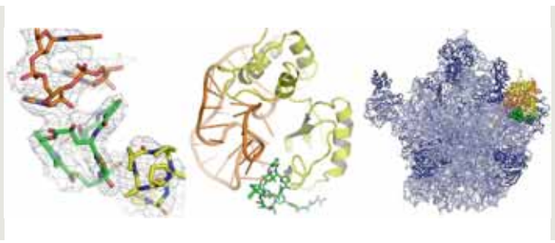
The future goals of my group at the Gene Center Munich are the structural and functional characterization of as yet poorly understood AAA+ assemblies involved in protein remodeling and turnover. The three-dimensional structure of different functional states of the assemblies under native conditions will be resolved using single-particle cryo-electron microscopy. In combination with mutational studies and biophysical analysis the structural data will help to identify functional elements responsible for complex formation, allosteric communication and substrate interaction. Overall, we aspire to understand how accessory domains and proteins facilitate fine tuning of the highly conserved AAA+ domain and allow for the immense functional variety of proteins in this family.

SELECTED ORIGINAL PUBLICATIONS

- **P. Wendler**, J. Shorter, C. Plisson, A. Cashikar, S. Lindquist, H. Saibil.
  Atypical AAA+ subunit packing creates an expanded cavity for disaggregation by the protein-remodeling factor Hsp104.
  Cell 131:1366-77 (2007).
- T. Puri, **P. Wendler**, B. Sigala, H. Saibil, IR. Tsaneva.
  Dodecameric structure and ATPase activity of the human TIP48/TIP49 complex.
  J Mol Biol. 366:179-92 (2007).
- **P. Wendler**, A. Lehmann, K. Janek, S. Baumgart, C. Enenkel.
  The bipartite nuclear localization sequence of Rpn2 is required for nuclear import of proteasomal base complexes via karyopherin alpha/beta and proteasome functions.
  J Biol Chem 279:37751-62 (2004).

PHOTOS AND/OR ILLUSTRATIONS 1: Cryo-EM map of yeast Hsp104 with rigid body fit of atomic structures show unusual AAA+ arrangement and allosteric interactions. The background is a light microscopic image of baking yeast from which Hsp104 was derived. 2: Cut away view of yeast Hsp104 cryo EM map with rigid body fit of atomic structures into two subunits. The background shows negative-stained yeast amyloid fibers, which can be disassembled by Hsp104. 3: Data collection on the FEI Tecnai Polara Microscope. 4: Preparation of macromolecular complexes for cryo-electron microscopy by quick freezing in liquid ethane using a manual plunger.

Daniel N. Wilson | Regulation of gene expression: the ribosome and protein synthesis



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EMAIL: WILSON@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/WILSON

SHORT CV

1999 | Ph.D. at Otago University, Dunedin, New Zealand;
2000-2002 | Alexander von Humboldt Fellow at the Max-Planck Institute for Molecular Genetics, Berlin, Germany;
2002-2006 | Postdoc at the Max Planck Institute for Molecular Genetics, Berlin, Germany;
Since 2007 | Group Leader at the Gene Center Munich.

GOAL

To investigate the mechanism of action of antibiotics in order to (i) develop improved antimicrobial agents to overcome the rise in multi-drug resistant bacteria, and (ii) dissect and understand the fundamental process of protein synthesis.

PERSONAL INTRODUCTION AND BACKGROUND

My fascination with the ribosome and protein synthesis began during my doctoral studies investigating the diverse and multitudinous mechanisms by which the genetic code can be reprogrammed – during translation, ribosomes can "hop, skip and jump" at specific recoding sites, as well as shift frame and insert unusual amino acids. The turn of the century brought with it high-resolution structures of ribosomes and ribosomal complexes which, coupled with the ever-increasing resolution of cryo-electron microcopy reconstructions, has "opened our eyes" to better comprehend the complexity of this macromolecular machine. My group takes a combined biochemical and structural biological approach to investigate how different ligands interact with the ribosome to modulate and regulate translation. This ranges from protein factors that facilitate ribosome biogenesis to stress response proteins and general translation factors that modulate the efficiency of protein synthesis.

RESEARCH HIGHLIGHTS

In the past five years, we have determined a number of structures of antibiotics in complex with the ribosome, for example, the initiation inhibitor kasugamycin in complex with the small subunit, and the oxaizolidinone drug linezolid as well as the thiopeptide antibiotics thiostrepton, nosiheptide, micrococcin, bound to the large subunit. Such structural "snapshots" not only provide insight into the mechanism of action of drugs as well as a basis for development of new improved inhibitors, but also enable specific steps of the fundamental process of translation to be dissected. We have generated homogenous ribosome functional complexes that have been interrogated both biochemically and structurally using X-ray crystallography, and collaboratively via cryo-electron microscopy. Highlights include (i) the first crystal structure of a protein factor (RRF) bound to the large ribosomal subunit, (ii) the identification of a new elongation factor LepA that reverses the translocation reaction catalyzed by EF-G as well as the visualization of LepA during the process of "back-translocation", (iii) the highest-resolution cryo-EM reconstruction of EF-G bound to the ribosome (stalled using non-hydrolysable GTP), (iv) direct visualization of the Shine-Dalgarno helix bound to the small ribosomal subunit by X-ray crystallography, (v) the first structures of assembly factors (RbfA and Era) bound to ribosomal particles (by cryo-EM), and (vi) the first cryo-EM reconstruction of a plant chloroplast, including the identification and correction of a previously mis-assigned plastid specific ribosomal protein as a stress response protein.

FUTURE PERSPECTIVE

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 the biochemical and structural characterization of how various antibiotics interact with ribosomes, as well as understanding the variety of resistance mechanisms that are employed by pathogenic bacteria to overcome these drugs. One important aspect involves the identification and characterization of novel antimicrobial agents, in particular antibiotics that target novel sites on the ribosome in order to avoid cross-resistance. Given the importance of the ribosome and the process of translation for cell viability, the regulation of ribosome biogenesis has been considered as a valid target for novel antimicrobials. Thus, a second major focus for the future is the biochemical and structural characterization of the numerous processing, modification and ancillary factors (many of which are bacteria-specific) that participate in the complicated process of ribosome assembly. Understanding their mechanism of action will be an essential first step to screening for compounds that inhibit their function.

SELECTED ORIGINAL PUBLICATIONS

- Harms JM*, **Wilson DN***, Schlünzen F*, Connell SR, Stachelhaus T, Zaborowska Z, Spahn CMT, Fucini P. Translational regulation via L11: Molecular switches on the ribosome turned on and off by thiostrepton and micrococcin. *Mol. Cell 30: 26-38 (2008).*
- **Wilson DN**, Schlünzen F, Harms JM, Starosta AL, Connell SR, and Fucini P. The oxazolidinone antibiotics perturb the ribosomal peptidyl-transferase center and effect tRNA positioning *Proc. Natl Acad. Sci. USA 105: 13339-44 (2008).*
- Sharma MR*, **Wilson DN***, Datta PP, Barat C, Schluenzen F, Fucini P and Agrawal RK. Cryo-EM study of the spinach chloroplast ribosome reveals the structural and functional roles of plastid-specific ribosomal proteins. *Proc. Natl Acad. Sci. USA 104: 19315-19320 (2007).*
- Datta PP*, **Wilson DN***, Kawazoe M*, Swami NK, Kaminishi T, Sharma MR, Booth TM, Takemoto C, Fucini P, Yokoyama S and Agrawal RK. Structural aspects of RbfA action during small ribosomal subunit assembly. *Mol. Cell 28: 434-445 (2007).*
- **Wilson DN***, Schluenzen F*, Harms JM*, Yoshida T, Ohkubo T, Albrecht A, Buerger J, Kobayashi Y, and Fucini P. X-ray crystallography study on ribosome recycling: the mechanism of binding and action of RRF on the 50S ribosomal subunit. *EMBO J. 24: 251-260 (2005).*

SELECTED REVIEWS

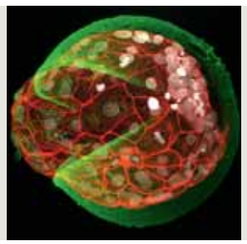
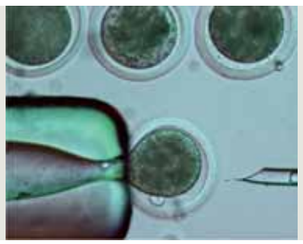
- **D.N. Wilson** and K.H. Nierhaus. The weird and wonderful world of bacterial ribosome regulation. *Crit. Rev. Biochem. Mol. Biol. 42: 187-219 (2007).*
- **D.N. Wilson** and K.H. Nierhaus. The oxazolidinone class of drugs find their orientation on the ribosome. *Mol. Cell 26: 460-462 (2007).*
- **D.N. Wilson**. Antibiotics and the inhibition of ribosome function. *In Protein Synthesis and Ribosome Structure, eds. Nierhaus, KH and Wilson, DN (Wiley-VCH, Weinheim, Germany), pp. 449-527 (2004).*

AWARDS

- Human Frontiers of Science Young Investigator Grant 2008

PHOTOS AND/OR ILLUSTRATIONS 1: From right to left: Overview of the X-ray crystallography structure of the antibiotic thiostrepton bound to the large ribosomal subunit. The binding site of thiostrepton encompasses both protein and RNA. The electron density (mesh) indicates that the drug inserts into a cleft between the ribosomal protein L11 (yellow) and helices 43/44 of the 23S rRNA (orange). 2: Alexandra Dönhöfer (left) and Dr. Viter Marquez use in-vitro translation systems to analyse ribosome function.

Eckhard Wolf | Growth, metabolism and reproduction in mammals

1 2 3, 4

EMAIL: EWOLF@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LMB.UNI-MUENCHEN.DE/GROUPS/MT/MAINMT2.HTM

SHORT CV

1990 | Dr. med. vet. from the LMU Munich;
1991-1993 | Postdoc at the Institute of Animal Breeding, LMU Munich;
1994 | Assistant Professor, University of Veterinary Sciences, Vienna;
Since 1995 | Full Professor for Molecular Animal Breeding and Biotechnology at the Gene Center and at the Faculty of Veterinary Medicine, LMU Munich;
Since 2003 | Director of the Laboratory for Functional Genome Analysis (LAFUGA) at the Gene Center.

GOAL

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

PERSONAL INTRODUCTION AND BACKGROUND

As a veterinarian by training, I was always interested in the pathomechanisms of diseases. Novel techniques for dynamic monitoring of molecular, cellular, and systemic changes during progression of a disease facilitate new insights into its pathogenesis. The availability of whole-genome sequences for a number of mammalian species and powerful techniques for genome-wide association studies provide the basis for unraveling the genetic basis of diseases. Moreover, candidate mechanisms of diseases can be addressed by forward and reverse genetic approaches which are no longer limited to the mouse model, but are also available for large animals which are becoming increasingly important as models for translational biomedical research.

Using this spectrum of tools and techniques, our lab addresses mechanisms of growth regulation, metabolism and fertility and their disturbances. Mammalian reproduction is a complex process which is influenced by multiple genetic and environmental factors. Reproductive success is determined by a cascade of biological processes: maturation and selection of gametes, fertilization, pre- and post-implantation embryonic development, fetal growth regulation, birth and early postnatal development of offspring. The laboratory studies key steps of reproduction, such as the interaction between early embryos and their maternal environment, and analyzes growth factor systems (growth hormone, insulin-like growth factors, EGF receptor ligands) that regulate pre- and postnatal growth. Both mouse and large animal models (cattle, pig) are used to unravel common and species-specific key events in normal and assisted reproduction and consequences for growth and development.

RESEARCH HIGHLIGHTS

At the DFG Research Unit FOR 478, we performed the first systematic study of embryo-maternal interactions in the pre-implantation period (see http://www.ematko.de). Monozygotic bovine twins (one pregnant, one non-pregnant) were used as a unique model to decipher the embryo-maternal cross-talk by dynamic transcriptome and proteome studies in several stages of early pregnancy. A number of key molecules and pathways that define uterine receptivity have already been identified. Another focus was on mechanisms of epigenetic reprogramming in nuclear transfer cloning and their effects on the development of embryos, fetuses and offspring. We showed aberrant DNA-methylation and histone modifications in cloned bovine embryos, resulting in developmental abnormalities such as large offspring syndrome (LOS). We recently found that epigenetic abnormalities may also persist in clinically healthy cloned animals. Endocrine studies of LOS fetuses and offspring revealed abnormal levels of several components of the insulin-like growth factor (IGF)-system. Using transgenic and knockout mouse models we were able to define the specific roles of IGFs, IGF-binding proteins and IGF receptors in prenatal and postnatal growth regulation. More recently, a number of transgenic large animal models were developed to provide new insights into the pathomechanisms of human diseases such as type 2 diabetes mellitus.

FUTURE PERSPECTIVE

Based on the unique animal models that we developed during the last five years, we intend not only to comprehensively describe the progression of diseases, but also to identify, validate and influence pathogenetic processes. This will require a closer collaboration with bioinformaticians which is already under way, for example in the new research network REMEDY, addressing the interactions between fertility and metabolic disorders. The next step will be to view key mechanisms of diseases in the context of genetic variation. The large genetic and phenotypic diversity in large animal species such as pigs and dogs provides an excellent basis for such studies.

SELECTED ORIGINAL PUBLICATIONS

- F. F. Paula-Lopes, M. Boelhauve, F. A. Habermann, F. Sinowatz, and **E. Wolf**.
  Leptin promotes meiotic progression and developmental capacity of bovine oocytes via cumulus cell-independent and -dependent mechanisms.
  Biol. Reprod. 76, 532-541 (2007).
- C. Moerth, M. R. Schneider, I. Renner-Mueller, A. Blutke, M. W. Elmlinger, R. G. Erben, C. Camacho-Hubner, A. Hoeflich, and **E. Wolf**.
  Postnatally elevated levels of insulin-like growth factor (IGF)-II fail to rescue the dwarfism of IGF-I-deficient mice except kidney weight.
  Endocrinology 148, 441-451 (2007).
- S. Bauersachs, S. E. Ulbrich, K. Gross, S. E. Schmidt, H. H. Meyer, H. Wenigerkind, M. Vermehren, F. Sinowatz, H. Blum, and **E. Wolf**.
  Embryo-induced transcriptome changes in bovine endometrium reveal species-specific and common molecular markers of uterine receptivity.
  Reproduction 132, 319-331 (2006).
- M. R. Schneider, M. Dahlhoff, N. Herbach, I. Renner-Mueller, C. Dalke, O. Puk, J. Graw, R. Wanke, and **E. Wolf**.
  Betacellulin overexpression in transgenic mice causes disproportionate growth, pulmonary hemorrhage syndrome, and complex eye pathology.
  Endocrinology 146, 5237-5246 (2005).

SELECTED REVIEWS

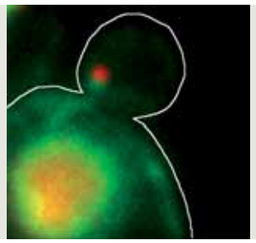
- M. R. Schneider, S. Werner, R. Paus, and **E. Wolf**.
  Beyond wavy hairs: the epidermal growth factor receptor and its ligands in skin biology and pathology.
  Am. J. Pathol. 173, 14-24 (2008).
- T. E. Spencer, O. Sandra, and **E. Wolf**.
  Genes involved in conceptus-endometrial interactions in ruminants: insights from reductionism and thoughts on holistic approaches.
  Reproduction 135, 165-179 (2008).
- B. Aigner, B. Rathkolb, N. Herbach, d. A. Hrabe, R. Wanke, and **E. Wolf**.
  Diabetes models by screening for hyperglycemia in phenotype-driven ENU mouse mutagenesis projects.
  Am. J. Physiol. Endocrinol. Metab. 294, E232-E240 (2007).

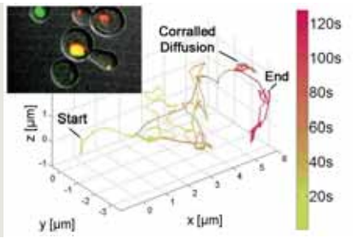
AWARDS

- Member of the Center for Advanced Studies (CAS), LMU Munich (2008)
- Call to the Swiss Federal Institute of Technology (ETH) Zurich – Chair for Animal Breeding (2005)
- Call to the University of Bern – Chair for Veterinary Genetics (2004)

PHOTOS AND/OR ILLUSTRATIONS 1: Hatching bovine blastocyst. 2: Nuclear transfer. 3: Clone of transgenic cattle, expressing a bispecific antibody for tumor therapy. 4: Cloned transgenic pigs for diabetes research.

Ralf-Peter Jansen | Cytoplasmic mRNA localization and translational regulation





1 2

EMAIL: RALF.JANSEN@UNI-TUEBINGEN.DE
INTERNET: HTTP://WWW.IFIB.UNI-TUEBINGEN.DE/JANSEN

SHORT CV

1993 | Ph.D. from the European Molecular Biology Laboratory and Heidelberg University;
1993-1996 | Postdoc at IMP, Vienna, Austria;
1996-1997 | Staff Scientist at IMP, Vienna;
1998-2002 | Independent Research Group Leader at the Center for Molecular Biology Heidelberg (ZMBH);
2002-2008 | Associate Professor at the Gene Center Munich;
Since 2008 | Professor at the Interfaculty Institute for Biochemistry, University of Tübingen.

GOAL

To understand the molecular mechanism leading to localization of specific mRNAs and their local translation.

PERSONAL INTRODUCTION AND BACKGROUND

In my opinion, one of the most fascinating biological phenomena is the organizational power of the cell. Millions of proteins have to be targeted to their correct intracellular locations. One of the key mechanisms for achieving this is the site-specific translation of the corresponding protein from a localized mRNA. mRNA localization occurs as a multi-step process involving a variety of protein factors that bind localized mRNAs, link them to molecular motors that transport these mRNAs. Additional proteins control the translation of the mRNAs by interfering with the translational machinery. Our lab has mainly focused on the elucidation of the mechanisms leading to mRNA localization in budding yeast. To that end, we are combining biochemical strategies such as affinity purification and subcellular fractionation with imaging techniques such as in-situ hybridization and mRNA tracking in living cells to provide insights into the mechanism of mRNA localization.

RESEARCH HIGHLIGHTS

After having defined the major components of the yeast mRNA localization apparatus, we have focused over the last years on the assembly of ribonucleoprotein (RNP) complexes containing localized mRNAs and their targeting mechanisms.
We were able to show that RNPs containing mRNAs coding for specific membrane proteins are co-transported along with special structures of the endoplasmic reticulum, which allows an on-site synthesis of the corresponding proteins (Fig. 1). In addition, in collaboration with other groups within the Collaborative Research Center (SFB) 646, we have developed and applied new methods to track different mRNAs in live cells (Fig. 2). These assays were used to study whether transport of each localized mRNA occurs individually or whether they are co-transported. Our analyses suggest that large RNPs containing several different localized mRNAs constitute the transport intermediates and that unlocalized mRNAs are excluded from these RNPs. When investigating where RNPs with localized mRNAs form, we identified the nucleolus as a putative assembly site. The nucleolus, a large intranuclear compartment, has long been known for its function in ribosome biogenesis but our results indicate that it might also serve during assembly of additional RNP complexes.

FUTURE PERSPECTIVE

In the future, we would like to initiate an in-depth analysis of the mechanisms leading to mRNA localization in yeast and mammalian cells. We will therefore focus 1. on the assembly mechanism for RNPs in the nucleolus, 2. on the mechanisms that allow selective association of mRNPs with membrane structure of the endoplasmic reticulum (ER), 3. on translational control mechanisms for mRNAs at the ER, and 4. on the mechanism that target mRNAs to the periphery of mitochondria.

SELECTED ORIGINAL PUBLICATIONS

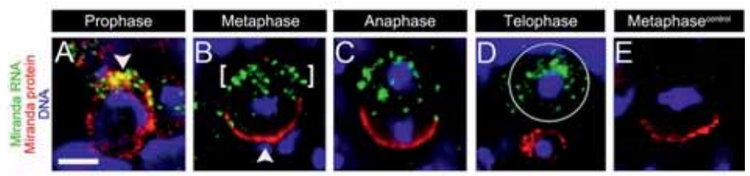
- T.-G. Du, S. Jellbauer, M. Müller, M. Schmid, D. Niessing, and **R.-P. Jansen**.
  Nuclear transit of the RNA-binding protein She2p is required for translational control of localized ASH1 mRNA.
  EMBO Rep. 9, 781-887 (2008).
- S. Lange, Y. Katayama, M. Schmid, O. Burkacky, C. Bräuchle, Don C. Lamb, and **R.-P. Jansen**.
  Simultaneous transport of different localized mRNAs species revealed by live-cell imaging.
  Traffic 9, 1256-1267 (2008).
- A. Heuck, T.-G. Du, S. Jellbauer, K. Richter, C. Kruse, S. Jaklin, M. Müller, J. Buchner, **R.-P. Jansen**, and D. Niessing.
  Monomeric myosin V uses two binding regions for the assembly of stable translocation complexes.
  PNAS 104, 19778-19783 (2007).
- M. Schmid, A. Jaedicke, T.-G. Du, and **R.-P. Jansen**.
  Coordination of endoplasmic reticulum and mRNA localization to the yeast bud.
  Curr. Biol. 16, 1538-1543 (2006).
- C. Juschke, D. Ferring, **R.-P. Jansen**, M. Seedorf.
  A novel transport pathway for a yeast plasma membrane protein encoded by a localized mRNA.
  Curr. Biol. 14, 406-411 (2004).

SELECTED REVIEWS

- T.-G. Du, M. Schmid, and **R.-P. Jansen**.
  Why cells move messages: The biological functions of RNA localization.
  Sem. Cell Dev. Biol. 18, 171-177 (2007).
- **R.-P. Jansen** and M. Kiebler.
  Intracellular RNA sorting, transport and localization. Nat. Struct.
  Mol. Biol. 12, 826-829 (2005).
- M. Lopez de Heredia and **R.-P. Jansen**.
  mRNA localization and the cytoskeleton.
  Curr. Opin. Cell. Biol. 16, 80-85 (2004).

PHOTOS AND/OR ILLUSTRATIONS 1: Fluorescence microscopy image of a living yeast cell. Taken from a movie that follows movement of a localized mRNA (red) and endoplasmic reticulum, the site of membrane protein synthesis (green). 2: 3D-Tracking of mRNA-protein complexes by spinning disc confocal microscopy. Insert in upper left corner shows a yeast cell with the tracked RNP (small yellow dot) containing two localized mRNAs.

Claudia Petritsch | Asymmetric division of neuronal stem cells



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EMAIL: CLAUDIA.PETRITSCH@UCSF.EDU
INTERNET: HTTP://IRM.UCSF.EDU/FACULTY/BIOS/PAGES/PETRITSCH.ASPX

SHORT CV

1996 | PhD from the Institute of Molecular Pathology (IMP) Vienna;
1997-1998 | Postdoctoral Fellow at lab of Prof. Hartmut Beug, Institute of Molecular Pathology (IMP) Vienna;
1999-2003 | Postgraduate Researcher and EMBO and HFSP Postdoctoral at lab of Prof. Yuh Nung Jan, Howard Hughes Medical Institute, University of California San Francisco, USA;
2003-2005 | Group Leader at the Gene Center Munich;
2005-2008 | Associate research biochemist, UCSF, USA;
Since 2008 | Assistant Adjunct Professor, UCSF, USA.

GOAL

My objective is to elucidate defects in cell division and differentiation of brain cancer stem cells and to distinguish them from normal adult neural stem and progenitor cells. The Petritsch lab utilizes transgenic model organisms (Drosophila and mouse) and novel cell culture assays to investigate in particular whether defects in asymmetric division of stem and progenitor cells in response to oncogenic mutations are responsible for their neoplastic transformation and the emergence of brain cancer stem cells. I have previously identified novel regulators of asymmetric cell division essential for proper neurogenesis and stem cell self-renewal. Our lab has recently discovered that normal adult neural stem cells undergo asymmetric cell divisions to generate glial cells and that this process is disrupted in response to oncogenic mutations in premalignant and glioma stem cells.

PERSONAL INTRODUCTION AND BACKGROUND

Studies in mouse models and the recent finding of malignant stem cell-like cells in human brain tumors, the brain cancer stem cells, suggest that stem and progenitor cells are a likely cellular origin of adult brain tumors. Data mainly from invertebrate neuroblasts have shown that stem and progenitor cells use asymmetric cell divisions (ACD) to properly self-renew and differentiate and that ACD might even protect against cancer. During ACD proteins with distinct functions in self-renewal and differentiation are sorted into two distinct protein complexes and are segregated into distinct daughter cells upon cytokinesis. As a result, one daughter cell acquires a more differentiated fate, whereas the other daughter remains similar to the original cell (self-renewal). Since very little is known about ACD in the mammalian adult stem cell lineage, a potential link between ACD and tumor suppression in the adult brain has not yet been fully established. Our recent study in a mouse model of glioma revealed that wild-type glial progenitors undergo ACD and that ACD is disrupted by oncogenic mutations in premalignant glial progenitors, and more severely in murine brain cancer stem cells. We do not know yet whether ACD defects are causing the aberrant self-renewal, differentiation and proliferation which we observed in premalignant glial progenitors and glioma stem cells, or whether these defects are merely by-products. Based on our knowledge of ACD in other systems, we propose that failure to properly separate self-renewal and differentiation factors during asymmetric cell divisions possibly leads to a "tug-of-war" between these opposing activities in neural stem cells and progenitor cells and causes their aberrant self-renewal and differentiation. We further hypothesize that asymmetry-defective stem and progenitor cells generate premalignant lesions and, perhaps by acquiring additional mutations, undergo neoplastic transformation. We are currently testing these hypotheses in my laboratory at UCSF by using tools including genetically engineered asymmetry-defective adult neural stem cells.

FUTURE PERSPECTIVE

It is our overarching goal to elucidate the molecular mechanism of self-renewal, differentiation and cell fate determination in normal and malignant stem cells. We will continue to investigate the molecular basis of asymmetric cell division in normal stem cells of the brain and the mammary gland. We will extend our studies to tumor suppressors and oncogenes as potential regulators of asymmetric stem cell division by utilizing genetically modified mice and flies, orthotopic transplantation models and mammalian cell culture. Ultimately, we would like to translate our studies or normal and malignant stem cells into improved diagnostics and therapies for brain and breast cancer patients.

SELECTED ORIGINAL PUBLICATIONS

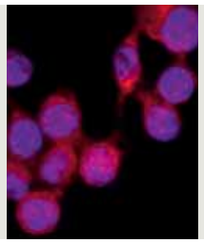
- Erben V., Waldhuber M., Langer D., Fetka I., Jansen R. P., **Petritsch C.**
  Asymmetric localization of the adaptor protein Miranda is achieved by diffusion and sequential interaction of Myosin II and VI.
  Journal of Cell Science (121), 1403-14 (2008).
- Silber J., Lim D.A., **Petritsch C.***, Maunakea A. K.*, Persson A.*, Yu M., Vandenberg S., Ginzinger D. G., James C. D., Costello J. F., Weiss W. A., Bergers G., Alvarez-Buylla A., Hodgson G.
  miR-124a and miR-137 inhibit proliferation of GBM cells and induce differentiation of tumor stem cells.
  BioMedCentral Medicine (2008).
- Du R.*, Lu K.*, **Petritsch C.***, Liu P., Ganss R., Passague E., Song H., VandenBerg S., Werb Z., Bergers G.
  Hif1a induces the recruitment of bone marrow-derived vascular modulatory cells to regulate tumor angiogenesis and invasion. (*authors contributed equally),
  Cancer Cell (3), 206-20 (2008).
- Du R., **Petritsch C.***, Liu P., Lu K., Haller A., Ganss R., Song H., Vandenberg S., Bergers G.
  Matrix metalloproteinase 2 regulates tumor cell survival, invasion and vascular branching in GBM.
  Neuro-oncology Mar 21, (2008).
- Waldhuber M., Emoto K. and **Petritsch C.**
  The Drosophila caspase DRONC is required for metamorphosis and cell death in response to irradiation and developmental signals.
  Mech. Dev. 122 (7-8), 914-27 (2005).

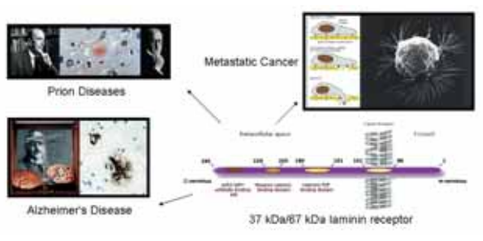
AWARDS

- Award for Outstanding Women in Life Sciences, LMU Munich, 2004 and 2005
- Bavarian California Technology Award (BaCaTec) 2005

PHOTOS AND/OR ILLUSTRATIONS 1: Miranda protein and Miranda mRNA localize asymmetrically to opposite poles during mitosis.

Stefan Weiss | LRP/LR as a therapeutic target in neurodegenerative diseases and cancer





1 2

EMAIL: WEISS@LMB.UNI-MUENCHEN.DE
INTERNET: HTTP://WWW.LMB.UNI-MUENCHEN.DE/WEISS/MAIN_WEISS.HTM

SHORT CV

1992 | Ph.D. from the Ruprecht-Karls University, Heidelberg;
1993-1995 | Postdoc at the Gene Center Munich;
1995-1997 | Group Leader at the Gene Center Munich;
1997-2001 | Assistant Professor at the Gene Center Munich;
1997-2001 | Visiting fellowships at the CEA, Fontenay-aux-Roses, Paris, France;
2002 | Professorship qualification at Ludwig-Maximilians-Universität Munich;
Since 2002 | Private lecturer;
2004-2005 | Associate Professor (Deputyship) at the Gene Center Munich;
2008-2009 | Associate Professor (Deputyship) at the Gene Center Munich;
Since 2009 | Professor at Johannesburg University, South Afrika.

GOAL

Development of therapeutic strategies targeting the 37 kDa/67 kDa laminin receptor for treatment of neurodegenerative diseases (prion diseases, Alzheimer's disease) and metastatic cancer.

PERSONAL INTRODUCTION AND BACKGROUND

The non-integrin 37 kDa laminin receptor (LRP/LR) is a multifunctional protein displaying fundamental roles as a cell surface receptor in (i) cell adhesion, migration, differentiation and communication (ii) prion diseases, (iii) viral infections and (iv) metastatic cancer. Blocking or downregulating the receptor by molecular tools therefore represents an alternative promising strategy for the treatment of neurodegenerative diseases, viral-prone diseases such as dengue virus infections, and cancer. We identified LRP/LR as the cell surface receptor for the cellular prion protein (PrPc) and as a receptor for infectious prions (PrPSc). We proved by in-vitro experiments that (i) siRNAs directed against LRP mRNA, (ii) polysulfated glycanes, (iii) a LRP decoy mutant and (iv) especially antibodies directed against LRP/LR significantly reduced or abolished prion propagation cell culture, recommending these tools as alternative therapeutics in vivo. Anti-LRP/LR-specific antibodies in particular might act as powerful therapeutic antibodies for the treatment of prion diseases, metastatic cancer and viral diseases.

RESEARCH HIGHLIGHTS

We identified LRP/LR as a receptor for infectious prions. A series of therapeutics targeting LRP/LR were proven to have significant effects on the lifespan of scrapie-infected mice. siRNAs directed against LRP mRNA delivered by microinjection of recombinant lentiviral vectors into the brain prolonged the pre-clinical phase of scrapie-infected mice. Transgenic scrapie-infected mice expressing a LRP decoy mutant in the brain also showed a prolonged life span. Antibodies directed against the receptor prolonged the survival of scrapie-infected mice and hampered peripheral prion propagation in the spleen when delivered by passive immunotransfer or recombinant adeno-associated viruses (AAV) gene delivery.
LRP/LR represents a basement membrane receptor overexpressed in metastatic solid tumors. Most strikingly, we showed that antibodies directed against LRP/LR significantly reduce invasion and adhesion, the two key components of metastatic tumors, suggesting that anti-LRP/LR specific antibodies may be further developed as therapeutic antibodies for metastatic cancer treatment. Beside antibodies, pentosan polysulfate and HMs, polysulfated glycanes belonging to the group of cutting-edge glycosaminoglycanes such as hyaluronic acid also have the potential to significantly reduce invasion of tumorigenic cells by blocking LRP/LR. Finally, siRNAs directed against LRP mRNA delivered by recombinant lentiviral plasmids into neoplastic cells also significantly reduced the LRP/LR level concomitant with a significant reduction of invasion.

FUTURE PERSPECTIVE

Anti-LRP/LR antibodies will be applied in animal models to investigate their therapeutic potential for the treatment of metastatic cancer. The role of LRP/LR in further neurodegenerative diseases such as Alzheimer's Disease will be evaluated. The therapeutic potential of anti-LRP/LR tools such as siRNAs and antibodies for the treatment of viral infections such as Dengue Virus infections will be investigated. Clinical trials with anti-LRP/LR specific antibodies for the treatment of metastatic cancer and neurodegenerative diseases are scheduled.

SELECTED ORIGINAL PUBLICATIONS

- Zuber C., Mitteregger G., Schuhmann N., Rey C., Knackmuss S., Rupprecht W., Reusch U., Pace C., Little M., Kretzschmar H.A., Hallek M., Büning H. and **Weiss S.**
  Delivery of single-chain antibodies scFvs directed against the 37 kDa/67 kDa laminin receptor into mice via recombinant adeno-associated viral vectors for prion disease gene therapy.
  Journal of General Virology 89, 2054-2060 (2008).
- Zuber C., Knackmuss S., Zemora G., Reusch U., Vlasova E., Diehl D., Mick V., Hofmann K., Nikles D., Fröhlich T., Arnold G., Brenig B., Wolf E., Lahm H., Little M., **Weiss S.**
  Invasion of tumorigenic HT1080 cells is impeded by blocking or downregulating the 37 kDa/67 kDa laminin receptor.
  Journal of Molecular Biology, 378, 530-539 (2008).
- Vana K., **Weiss S.**
  A trans-dominant negative 37 kDa/67 kDa laminin receptor mutant impairs PrPSc propagation in scrapie-infected neuronal cells.
  Journal of Molecular Biology 358, 57-66 (2006).
- Gauczynski S., Niikles D., El-Gogo S., Papy-Garcia D., Rey C., Alban S., Barritault D., Lasmézas C.I., **Weiss S.**
  The 37 kDa/67 kDa laminin receptor acts as a receptor for infectious prions and is inhibited by polysulfated glycanes.
  Journal of Infectious Diseases, 194, 702-709 (2006).

SELECTED REVIEWS

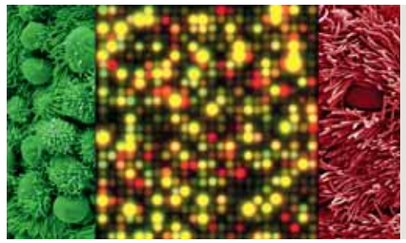
- Ludewigs H., Zuber C., Vana K., Nikles D., Zerr I., **Weiss S.**
  Therapeutic approaches for prion disorders.
  Expert Review of Anti-infective Therapy 5, 613-630 (2007).
- Zuber C., Ludewigs H., **Weiss S.**
  Therapeutic approaches targeting the prion receptor LRP/LR.
  Veterinary Microbiology 123, 387-393 (2007).

AWARDS

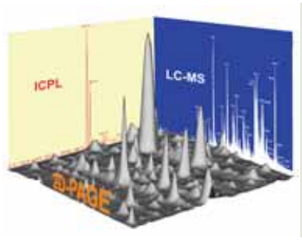
- Dr. Chantal Zuber received the Dr. Klaus Römer Award 2008

PHOTOS AND/OR ILLUSTRATIONS 1: The 37 kDa/67 kDa laminin receptor plays a major role in neurodegenerative diseases and metastatic cancer. 2: Infectious prions (PrP27-30) bind to the 37 kDa/67 kDa laminin receptor on the surface of BHK-cells (adopted from Gauczynski et al., JID, 194, 702-709 (2006)).

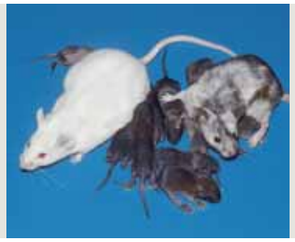
Laboratory for Functional Genome Analysis (LAFUGA)



1



2



3

GOAL

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

HELMUT BLUM (LAFUGA–GENOMICS)

EMAIL: BLUM@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LAFUGA.DE/GENOMICS.HTM

Array-based transcriptome analysis is currently the most sensitive and comprehensive approach to studying expression of all known genes in a highly parallel mode. The genomics unit of LAFUGA is focused on holistic transcriptome studies and is equipped with state-of-the-art Affymetrix technology for genome-wide analyses of gene expression in model organisms and Agilent's open microarray platform. The latter allows for sensitive and versatile approaches independently of the availability of prefabricated microarrays. Current research projects focus on transcriptome changes in the context of host-pathogen interactions in the mammary gland, on embryo-induced transcriptome changes in the maternal environment, and on transcriptome profiles of various human cancer cell lines, which differ in their metastasic, angiogenic and carcinogenic potential.

GEORG J. ARNOLD (LAFUGA–PROTEOMICS)

EMAIL: ARNOLD@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LAFUGA.DE/PROTEOMICS.HTM

Gene expression studies on the protein level have become an indispensable tool for the comprehensive investigation of complex biological processes. The proteomics unit is focused on quantitative holistic proteome approaches using multi-dimensional nano-HPLC-MS-MS in combination with stable isotope labeling techniques and the gel-based 2D-DIGE technology. A strategy to generate highly specific peptide induced antibodies with monoepitopic binding characteristics has been developed (iSEPIA-technology) for cellular localization and functional characterization of relevant proteins. Current projects address key questions in reproductive biology (embryo-endometrium interactions, protein expression kinetics in early embryogenesis, germ cell potential), pathogen-induced proteome alterations in the mammary gland and proteome analysis in neurodegenerative diseases (cooperation with H. Kretzschmar, ZNP).

ECKHARD WOLF (LAFUGA–ANIMAL MODELS)

EMAIL: EWOLF@LMB.UNI-MUENCHEN.DE
INTERNET: WWW.LAFUGA.DE/MODEL.HTM

This unit specializes 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 routinely 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

The LAFUGA units provided the technology platform for a number of research consortia in the fields of biology of reproduction (e.g. DFG FOR 478 “Mechanisms of embryo-maternal communication”, DFG FOR 1041 “Germ cell potential”) and host-pathogen interactions (DFG FOR 585 “Pathogen-specific defense mechanisms in the mammary gland”). Research highlights include a first systematic study of embryo-maternal interactions in the preimplantation period, the use of highly sensitive saturation labeling to determine proteome changes during the process of oocyte maturation, and the generation and characterization of a panel of novel animal models including transgenic pigs for xenotransplantation and for diabetes research.

FUTURE PERSPECTIVE

The challenge for the next years will be to use complex “OMICS” data to build models for developmental and pathogenetic processes. LAFUGA is involved in this enterprise at different levels of complexity, such as the definition of pluripotency switches during early embryonic differentiation and reprogramming of somatic cells (EU project PLURISYS) or the characterization of interactions between fertility and metabolic disorders which is performed in the ongoing BMBF-funded research network REMEDY.

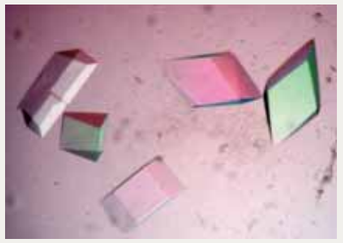
SELECTED ORIGINAL PUBLICATIONS

- K. Mitko, S. E. Ulbrich, H. Wenigerkind, F. Sinowatz, **H. Blum**, **E. Wolf**, and S. Bauersachs. Dynamic changes in messenger RNA profiles of bovine endometrium during the oestrous cycle. *Reproduction 135, 225-240 (2008).*
- T. Frohlich, D. Helmstetter, M. Zobawa, A. C. Crecelius, T. Arzberger, H. A. Kretzschmar, and **G. J. Arnold**. Analysis of the HUPO Brain Proteome reference samples using 2D DIGE and 2D LC-MS/MS. *Proteomics 6, 4950-4966 (2006).*
- F. J. Berendt, T. Frohlich, S. E. M. Schmidt, H. D. Reichenbach, **E. Wolf**, and **G. J. Arnold**. Holistic differential analysis of embryo-induced alterations in the proteome of bovine endometrium in the preattachment period. *Proteomics 5, 2551-2560 (2005).*

SELECTED REVIEWS

- S. Bauersachs, K. Mitko, S. E. Ulbrich, **H. Blum**, and **E. Wolf**. Transcriptome studies of bovine endometrium reveal molecular profiles characteristic for specific stages of estrous cycle and early pregnancy. *Exp. Clin. Endocrinol. Diabetes 116, 371-384 (2008).*
- T. Frohlich, and **G. J. Arnold**. Proteome research based on modern liquid chromatography – tandem mass spectrometry: separation, identification and quantification. *Journal of Neural Transmission 113, 973-994 (2006).*

PHOTOS AND/OR ILLUSTRATIONS 1: Transcriptome profiling of oviduct epithelial cells at estrus (red) vs. diestrus (green). 2: Proteomics technologies for high-throughput identification and quantification. 3: Chimeric mouse with offspring.



New research facilities

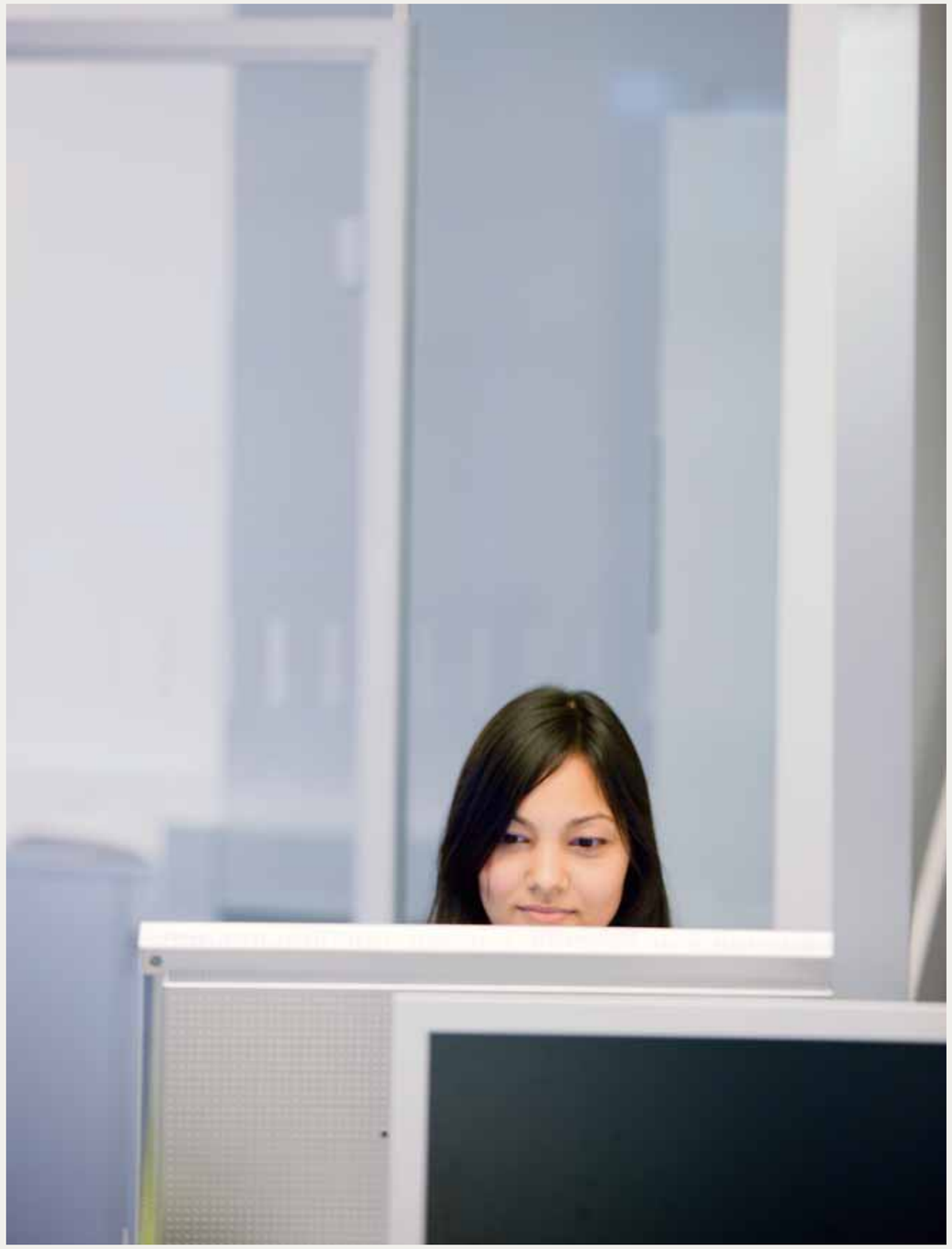
IN RECENT YEARS, GENE CENTER SCIENTISTS HAVE SET UP SEVERAL NEW RESEARCH FACILITIES.

ELECTRON MICROSCOPY

The Beckmann group has now completed the setup of a state-of-the-art cryo-electron microscopy facility. The facility is managed by Dr. Otto Berninghausen and technically supported by Charlotte Ungewickel. In 2007, two electron microscopes were installed in dedicated new rooms in the neighboring Biocenter. First, a 100-kV Morgagni routine transmission electron microscope with a CCD camera allows for rapid screening of samples and the analysis of standard biological specimens. Second, a 120-kV Spirit electron microscope with cryo-capabilities enables rapid collection of single particle data for medium-resolution structural analysis. In December 2008 a 80-300 kV high-resolution cryo-electron microscope, the Titan Krios from FEI, was installed. Currently, the most advanced electron microscope on the market, this 3.5-million-euro machine is equipped with a 4K CCD camera. Finally, a small 5-kV low-voltage transmission and scanning electron microscope, the LVEM from DeLong, is available at the Gene Center for early characterization of samples. A carbon evaporator, microwave-based glow discharge device, ultramicrotome, Ultracut E, and Vitrobot Marc III, FEI, are available for sample preparation. High-resolution drum scanners from Heidelberg are used for digitizing micrographs. Ten dual/triple screen work stations with 4 CPUs for image processing and model building and a Linux cluster comprising several hundred CPUs have been set up for data processing and structural reconstruction. The new facility was financed by a combined effort of the German Research Foundation (DFG), LMU Munich, and the State of Bavaria, and now allows for competitive research work in electron microscopy at the highest international level.

CRYSTALLIZATION

To cope with the strongly increased demands for crystallographic structure determination by groups at the Gene Center and external collaboration partners, Karl-Peter Hopfner successfully negotiated funding and support from the LMU Munich for a new crystallization core facility with state of the art crystallization instrumentation. Additional funds were obtained from LMUexcellent to embed new nano-crystallization techniques. The crystallization facility is coordinated by Dr. Gregor Witte and is located in the basement of the Gene Center. The facility is expected to be fully operational by the end of 2009. The focus of this new facility is to provide a broad platform for semi-automated crystallization using different approaches, rather than a high-throughput automated approach. State-of-the art liquid-handling systems enable fast and easy preparation of crystallization screens and setups. A free interface diffusion system (Fluidigm Topaz) is available for crystallization setups at the nanoliter scale. The results of various crystallization experiments can be monitored using an automated crystallization-plate imaging and incubation system (2x Thermo Rhombix Vision). The new facility is temperature-stabilized and provides lab space and microscopes for manual setups, manipulation and preparation of protein crystals for synchrotron measurements and different temperature-controlled incubators and storage possibilities. The new facility ensures that the Gene Center remains highly competitive in the X-ray structure determination of ever more challenging fragile and scarce macromolecular complexes.



COMPUTATIONAL BIOLOGY

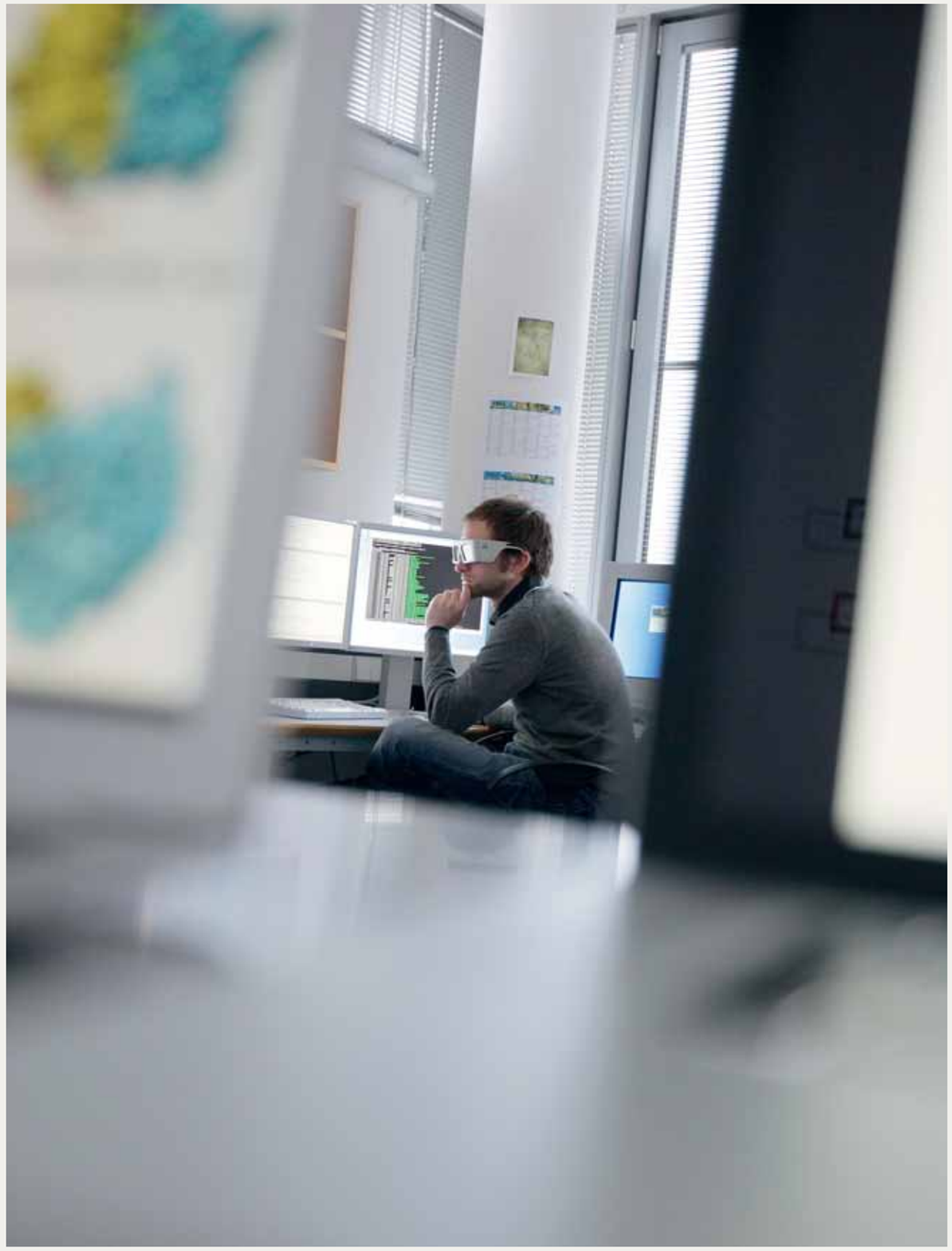
To prepare the infrastructure for computational biology, the entire Gene Center computing network was replaced by a modern 1 Gbit/s network. Further, the former Gene Center Library has been transformed into a modern open office space for up to 30 computational biologists. With its two-storey glass facade, welcoming interior design and open layout, the new Computational Biology Labs create a warm and interactive atmosphere fostering team work and creativity. By the end of 2008, the two new group leaders, Johannes Söding and Achim Tresch, together with around ten new students, had transformed the new facilities into a lively and productive research space. A dedicated server room for Computational and Systems Biology was also set up and will be capable of housing six full-size racks with up to 80 kW of power consumption. With these measures, the Gene Center successfully created the infrastructure required to perform cutting-edge research in Computational Biology and to provide bioinformatics services.

MICROARRAY PLATFORM

Funds from the LMUexcellent programme enabled the Cramer lab to establish an Affymetrix microarray facility. The facility is coordinated by Dr. Dietmar Martin and provides state-of-the-art instrumentation and protocols for gene expression analysis. It includes a complete Affymetrix microarray working station consisting of a GeneChip Hybridization Oven, a GeneChip Fluidics Station and a GeneChip Scanner. The aim of the new facility is to provide a platform for transcriptome and genome-wide protein-DNA interaction studies (ChIP-chip profiling) for the Gene Center and two research networks (SFB646 and TR5). The facility also provides instrumentation and protocols for quality assessment of DNA and RNA samples - a crucial step for microarray-based applications - using the Biorad Experion Analyzer. Labeling of RNA and DNA samples is performed using tested and reproducible protocols to maximize sensitivity and minimize experimental noise. Bioinformatical tools and software are available for statistical data analysis. In combination with the expertise available in the computational biology labs, the new microarray facility enables state-of-the-art gene expression analysis, genome occupancy profiling and analysis and interpretation of genome-wide data to be carried out.

PROTEOMICS

The Laboratory for Functional Genome Analysis LAFUGA has secured funds from the LMUexcellent programme to set up an orbitrap mass spectrometer for improved protein identification and proteomics. The new facility is coordinated by Dr. Georg Arnold, with proteomics services provided by Dr. Thomas Fröhlich. The new mass spectrometry facility enables protein identification with highly increased sensitivity and semi-automated sample handling. The proteomics services are essential for almost any research project in molecular biology.



Administration and service personnel

Of great importance are all those non-scientific coworkers who contribute to the effective infrastructure and administration at the Center. They are essential to maintaining our daily routine. Heidi Feldmann and Johanna Turck run the central students' office and organize our teaching efforts. Brigitta Beatrix and Timo Weiler contribute extensively to teaching coordination. Our secretaries Sieglinde Einödshofer, Stephanie Wolf, Petra Fulde, and Sabine Hörske take care of general administrational and organizational issues. Jutta Hohmann and Ricarda Grünauer provide financial services. IT services are provided by Reinhold Härtel, Andreas Hauser, and Dirk Kostrewa. Michael Englschall and Gabriele Bittner are in charge of general supplies and waste management. Our workshops are run by Michael Till and Dieter Zech. Last but not least, Homa Popal, Dorchanai Schams, Zorica Stojanovic, and Bozica Radojevic maintain the laboratory glassware.

Publications and invited lectures

Roland Beckmann
PUBLICATIONS

2008

A. Kusser, M. Bertero, S. Naji, M. Thomm, **R. Beckmann**, P. Cramer.
Structure of an archaeal RNA polymerase.
J. Mol. Biol., 376, 303-307 (2008).

2007

C.-D. Kuhn, S. R. Geiger, S. Baumli, M. Gartmann, J. Gerber, S. Jennebach, T. Mielke, H. Tschochner, **R. Beckmann**, P. Cramer.
Functional Architecture of RNA Polymerase I.
Cell, 131, 1260-1272 (2007).

2006

M. Halic, M. Blau, T. Becker, T. Mielke, M.R. Pool, K. Wild, I. Sinning and **R. Beckmann**.
Following the signal sequence from ribosomal tunnel exit to signal recognition particle.
Nature, 444, 507-511 (2006).

C.B.F. Andersen, T. Becker, M. Blau, M. Anand, M. Halic, B. Balar, T. Mielke, T. Boesen, J.S. Pedersen, C.M.T. Spahn, T.G. Kinzy, G.R. Andersen, **R. Beckmann**.
Structure of eEF3 and the mechanism of tRNA release from the E-site.
Nature, 443, 663-668 (2006).

M. Halic, M. Gartmann, O. Schlenker, T. Mielke, M.R. Pool, I. Sinning and **R. Beckmann**.
Signal recognition particle receptor exposes the ribosomal translocon binding site.
Science, 312, 745-747 (2006).

2005

M. Blau, S. Mullapudi, T. Becker, J. Dudek, R. Zimmermann, P. A. Penczek, **R. Beckmann**.
ERj1p uses a universal ribosomal adaptor site to coordinate the 80S ribosome at the membrane.
Nat. Struct. Mol. Biol., 12, 1015-1016 (2005).

M. Halic, T. Becker, C.M.T. Spahn, J. Frank and **R. Beckmann**.
Localization and dynamic behavior of ribosomal protein L30e.
Nat. Struct. Mol. Biol., 12, 467-468 (2005).

R. Beckmann.
Cryo-EM: single particle reconstruction,
In: Ganten et al. (Ed.).
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M. Halic and **R. Beckmann**.
The Signal recognition particle and its dynamic interactions during protein targeting.
Curr. Op. Struct. Biol., 15, 1-10 (2005).

2004

S. Mullapudi, L. Pullan, O.T. Bishop, H. Khalil, J.K. Stoops, **R. Beckmann**, P.-M. Kloetzel, E. Krueger and P.A. Penczek.
Rearrangement of the 16S precursor subunits is essential for the formation of the active 20S proteasome.
Biophys J., 87, 4098-105 (2004).

K. Wild1, M. Halic[1], I. Sinning and **R. Beckmann**.
SRP meets the ribosome.
Nat. Struct. Mol. Biol., 11, 1049-53 (2004). 1: contributed equally

M. Halic, T. Becker, M. Pool, C.M.T. Spahn, R. Grassucci, J. Frank and **R. Beckmann**.
Structure of the signal recognition particle interacting with the elongation-arrested ribosome.
Nature, 427, 808-14 (2004).

C.M.T. Spahn, M.G. Gomez-Lorenzo, R.A. Grassucci, R. Jorgensen, G.R. Andersen, **R. Beckmann**, P.A. Penczek, J.P.G. Ballesta and J. Frank.
Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation.
EMBO J., 23, 1008-1019 (2004).

INVITED LECTURES

2008

- 9th Int. School on Crystallography, Como, Italy
- DGZ Annual Meeting, Marburg
- European Microscopy Congress, Aachen
- CECAM Meeting, Lyon, France
- Gordon Conference on cryo-EM, II Ciocco, Italy
- IMPRS Lecture, Martinsried
- Gordon Conference on Bacterial Cell Surface, New Hampshire, USA
- CIPSM Symposium, Elmau
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2007

- Regensburg University
- Retreat, Wildbad Kreuth
- Biozentrum, Martinsried
- Strasbourg University, France
- Ribosome Conference, Cape Cod, USA
- Gordon Conference on Protein Translocation, II Ciocco, Italy
- TU Munich
- IMPRS Lecture, Martinsried
- EBSA Meeting, London, UK
- Birkbeck College, London, UK
- Horizons Meeting, Göttingen
- Stockholm University, Sweden
- Biozentrum Basel, Switzerland
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2006

- SFB 594 Colloquium, LMU Munich
- Bioquant, University of Heidelberg
- Gordon Conference on cryo-EM, II Ciocco, Italy
- DNA Workshop, LMU Munich
- University of Masschusetts, Amherst, USA
- SFB 449 International Symposium, Berlin
- Hybrid Methods Meeting, Lake Tahoe, USA
- Homburg University
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2005

- Microscopy Conference, Davos, Switzerland
- Gordon Conference on Protein Transport, New London, USA
- VW-Foundation Blomberg
- University of Heidelberg
- GBM Meeting, Berlin
- SFB 646 seminar, Munich
- Biophysical Society 49th Annual Meeting, Long Beach, USA
- Gene Center Retreat, Wildbad Kreuth
- Rockefeller University, New York, USA

2004

- EMBO Conference on Structures in Biology, EMBL, Heidelberg
- SFB 367, University of Lübeck
- Nobel Symposium 130, Tällberg, Sweden
- ETH Zurich, Switzerland
- SFB542, University of Aachen
- RNA-Meeting 2004, Blaubeuren
- Rockefeller University, New York, USA
- EMBO Course, EMBL Grenoble, France

Karl-Klaus Conzelmann
PUBLICATIONS

2008

Marschalek A., Finke S., Schwemmle M., Mayer D., Heimrich B., Stitz L., and **Conzelmann KK**.
Attenuation of rabies virus replication and virulence by picornavirus IRES elements.
J Virol., 2009, 83, 1911-9. Epub 2008 Dec 10.

Pfaller C., and **Conzelmann KK**.
Measles virus V protein is a decoy substrate for the kinase IKK-alpha and prevents Toll-like receptor 7/9-mediated IFN induction.
J Virol. 2008 82(24):12365-73. (2008)

Cui S, Eisenächer K, Kirchhofer A, Brzózka K, Lammens A, Lammens K, Fujita T, **Conzelmann KK**, Krug A, Hopfner KP.
The C-terminal regulatory domain is the RNA 5' triphosphate sensor of RIG-I.
Mol Cell. 29(2):169-179. (2008)

Klingen Y, **Conzelmann KK** , Finke S.
Double-Labeled Rabies Virus – Live tracking of enveloped virus transport.
J Virol. 82(1):237-45. (2008)

2007

Wickersham I, Lyon DC, Barnard RJO, Mori T, Finke S, **Conzelmann KK**, Young JAT, Callaway EM.
Monosynaptic restriction of transsynaptic tracing from single, genetically targeted neurons.
Neuron, 53(5):639-47. (2007)

Marston DA, McElhinney LM, Johnson N, Miller T, **Conzelmann KK**, Tordo N, and Fooks AR.
Comparative analysis of the full genome sequence for European Bat Lyssavirus
J Gen Virol. 88(Pt 4):1302-14. (2007)

Brzózka K, Pfaller C, and **Conzelmann KK**.
Signal transduction in the type I IFN system and viral countermeasures
Signal Transduction 7:5-19 (2007).

Wickersham I, Finke S, **Conzelmann KK**, Callaway EM.
Retrograde neuronal tracing with a deletion-mutant rabies.
Nat. Methods 4(1):47-49 (2007).

2006

Hornung V, Ellegast J, Kim S, Brzozka K, Jung A, Kato H, Poeck H, Akira S, **Conzelmann KK** , Schlee M, Endres S, Hartmann G.
5'-Triphosphate RNA is the ligand for RIG-I.
Science. 314(5801):994-7 (2006).

Brzózka K, Finke S, **Conzelmann KK**.
Inhibition of Interferon Signaling by Rabies Virus Phosphoprotein P: Activation-dependent binding of STAT1 and STAT2
J Virol. 80(6): 2675-83 (2006).

2005

Brzózka K, Finke S, **Conzelmann KK**.
Identification of the rabies virus alpha/beta interferon antagonist: phosphoprotein P interferes with phosphorylation of interferon regulatory factor 3
J Virol. 79(12):7673-81 (2005).

Schlender J, Hornung V, Finke S, Gunthner-Biller M, Marozin S, Brzozka K, Moghim S, Endres S, Hartmann G, **Conzelmann KK**.
Inhibition of toll-like receptor 7- and 9-mediated alpha/beta interferon production in human plasmacytoid dendritic cells by respiratory syncytial virus and measles virus.
J Virol. 79(9):5507-15 (2005).

Finke S, **Conzelmann KK**.
Recombinant rhabdoviruses: vectors for vaccine development and gene therapy.
Curr Top Microbiol Immunol. 292:165-20 (2005).

Hengel H, Koszinowski UH, **Conzelmann KK**.
Viruses know it all: new insights into interferon networks.
Trends Immunol. 26(7):396-401 (2005).

Finke S, **Conzelmann KK**.
Replication strategies of rabies virus.
Virus Research 111(2): 120-131 (2005).

Conzelmann KK.
Transcriptional activation of alpha/beta interferon genes: interference by non-segmented negative-strand RNA viruses.
J Virol. 79(9):5241-8 (2005).

2004

Hornung V, Schlender J, Guenthner-Biller M, Rothenfusser S, Endres S, **Conzelmann KK**, Hartmann G.
Replication dependent potent IFN-a induction in human plasmacytoid dendritic cells by a single-stranded RNA virus
J. Immunol. 173(10):5935-43 (2004).

Finke S, Brzózka K, **Conzelmann KK**.
Tracking Fluorescence-Labeled Rabies Virus: eGFP-tagged Phosphoprotein P Supports Virus Gene Expression and Formation of Infectious Particles.
J. Virol. 78(22):12333-43 (2004).

Conzelmann KK.
Reverse genetics of Mononegavirales.
Curr Top Microbiol Immunol. 283:1-41 (2004).

INVITED LECTURES

2008

- Seminar, IDT Dessau
- Seminar, University Geneva
- NSV Meeting, Northwestern University, Evanston, USA
- Seminar, Institute Pasteur, Paris
- Seminar, Universität Erlangen
- 7th Meeting of the German Neuroscience Society, Göttingen

2006

- Ernst-Klenk Symposium, Köln
- Seminar, Universität Heidelberg

2005

- Seminar, FLI Tübingen
- Symposium "RNA viruses shuttling between animal and men", Marburg
- Intl. RSV Symposium 2005, Oxford, UK
- Europ. IFN Minisymposium, University Brussels

2004

- Seminar, Univ. Freiburg
- Workshop NSV, Northwestern University, Evanston, USA
- International Symposium of SFB 587, MHH Hannover

Patrick Cramer
PUBLICATIONS

2008

A. Muschielok, J. Andrecka, A. Jawhari, F. Brückner, **P. Cramer**, and J. Michaelis.
A nano-positioning system for macromolecular structural analysis.
Nature Methods 5(11), 965-71 (2008).

A.J. Jasiak, H. Hartmann, E. Karakasili, M. Kalocsay, A. Flatley, E. Kremmer, K. Sträßer, D.E. Martin, J. Söding, and **P. Cramer**.
Genome-associated RNA polymerase II includes the dissociable RPB4/7 subcomplex.
J. Biol. Chem. 283(39), 26423-7 (2008).

F. Brueckner, and **P. Cramer**.
Structural basis of transcription inhibition by α-amanitin and implications for RNA polymerase II translocation.
Nature Struct. Mol. Biol. 15(8), 811-18 (2008).

P. Cramer, K.J. Armache, S. Baumli, S. Benkert, F. Brueckner, C. Buchen, G.E. Damsma, S. Dengl, S.R. Geiger, A.J. Jasiak, A. Jawhari, S. Jennebach, T. Kamenski, H. Kettenberger, C.-D. Kuhn, E. Lehmann, K. Leike, J.F. Sydow, and A. Vannini.
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Annu. Rev. Biophys. 37, 337-352 (2008).

S.R. Geiger, C.D. Kuhn, C. Leidig, J. Renkawitz and **P. Cramer**.
Crystallization of RNA polymerase I sub-complex A14/A43 by iterative prediction, probing and removal of flexible regions.
Acta Cryst. F64, 413-418 (2008).

S. Mohammed, K. Lorenzen, R. Kerkhoven, B.V. Breukelen, A. Vannini A, **P. Cramer**, and A. J. Heck.
Multiplexed Proteomics Mapping of Yeast RNA Polymerase II and III Allows Near-Complete Sequence Coverage and Reveals Several Novel Phosphorylation Sites.
Analytical Chem. 80, 3584-92 (2008).

L. Larivière, M. Seizl, S. van Wageningen, S. Röther, L. van de Pasch, H. Feldmann, K. Sträßer, S. Hahn, F.C.P. Holstege and **P. Cramer**.
Structure-system correlation identifies a gene regulatory Mediator submodule.
Genes Dev. 22, 872-877 (2008).

J. Andrecka, R. Lewis, F. Brückner, E. Lehmann, **P. Cramer**, and J. Michaelis.
Single-molecule tracking of mRNA exiting from RNA polymerase II.
Proc. Natl. Acad. Sci. USA, 105, 135-140 (2008).

J. Gerber, A. Reiter, R. Steinbauer, S. Jakob, C.D. Kuhn, **P. Cramer**, J. Griesenbeck, P. Milkereit and H. Tschochner.
Site specific phosphorylation of yeast RNA polymerase I.
Nucl. Ac. Res. 36, 793-802 (2008).

S. Naji, M. G. Bertero, P. Spitalny, **P. Cramer**, M. Thomm.
Structure-function analysis of the RNA polymerase cleft loops elucidates initial transcription, DNA unwinding, and RNA displacement.
Nucl. Ac. Res. 36, 676-87 (2008).

A. Kusser, M. Bertero, S. Naji, M. Thomm, R. Beckmann, **P. Cramer**.
Structure of an archaeal RNA polymerase.
J. Mol. Biol. 376, 303-307 (2008).

2007

C.-D. Kuhn, S. R. Geiger, S. Baumli, M. Gartmann, J. Gerber, S. Jennebach, T. Mielke, H. Tschochner, R. Beckmann, **P. Cramer**.
Functional Architecture of RNA Polymerase I.
Cell, 2007, 131, 1260-1272.

E. Lehmann, F. Brueckner, **P. Cramer**.
Molecular basis of RNA-dependent RNA polymerase II activity.
Nature 2007, 450, 445-449.

G. E. Damsma, A. Alt, F. Brueckner, T. Carell, **P. Cramer**.
Mechanism of transcriptional stalling at cisplatin-damaged DNA.
Nature Struct. Mol. Biol. 2007, 14, 1127-1133.

M. Micorescu, S. Grünberg, A. Franke, **P. Cramer**, M. Thomm, M. Bartlett.
Archaeal transcription: function of an alternative transcription factor B from Pyrococcus furiosus.
J. Bacteriol 2007, 190, 157-167.

K. Lorenzen, A. Vannini, **P. Cramer**, A. J. R. Heck.
Structural Biology of RNA Polymerase III: Mass Spectrometry Elucidates Subcomplex Architecture.
Structure 2007, 15, 1237-1245.

P. Cramer.
Finding the right spot to start transcription.
Nature Struct. Mol. Biol. 2007, 14, 686-687.

P. Cramer.
Extending the message.
Nature 2007, 448, 142-143.

E. Kashkina, M. Anikin, F. Brueckner, E. Lehmann, S.N. Kochetkov, W.T. McAllister, **P. Cramer**, D. Temiakov.
Multisubunit RNA polymerases melt only a single DNA base pair downstream of the active site.
J. Biol. Chem. 2007, 282, 21578-21582

F. Brueckner, **P. Cramer**.
DNA photodamage recognition by RNA polymerase II.
FEBS Lett. 2007, 581, 2757-2760

F. Brueckner, U. Hennecke, T. Carell, **P. Cramer**.
CPD Damage Recognition by Transcribing RNA Polymerase II.
Science 2007, 315, 859-862.

2006

P. Cramer.
Deciphering the RNA polymerase II structure: a personal perspective.
Nature Struct. Mol. Biol. 2006, 13, 1042-1044.

P. Cramer.
Recent structural studies of RNA polymerases II and III.
Biochem. Soc. Transact. 2006, 34, 1058-1061.

E. Kashkina, M. Anikin, F. Brueckner, R.T. Pomerantz, W.T. McAllister, **P. Cramer** & D. Temiakov.
Template Misalignment in Multisubunit RNA Polymerases and Transcription Fidelity.
Mol. Cell 2006, 24, 257-266.

L. Larivière, S. Geiger, S. Hoeppner, S. Roether, K. Straesser & **P. Cramer**.
Structure and TBP binding of the Mediator head subcomplex Med8-Med18-Med20.
Nature Struct. Mol. Biol. 2006, 13, 895-901.

P. Cramer.
Self-Correcting Messages.
Science 2006, 313, 447-448.

A. Jasiak, K.-J. Armache, B. Martens, R.-P. Jansen & **P. Cramer**.
Structural Biology of RNA Polymerase III: Subcomplex C17/25 X-Ray Structure and 11 Subunit Enzyme Model.
Mol. Cell 2006, 23, 71-81.

P. Cramer.
Mechanistic studies of the mRNA transcription cycle.
Biochem. Soc. Symp. 2006, 73, 41-47.

E. Vojnic, B. Simon, B.D. Strahl, M. Sattler and **P. Cramer**.
Structure and CTD binding of the Set2 SRI domain that couples histone H3 K36 methylation to transcription.
J. Biol. Chem. 2006, 281, 13–15.

H. Kettenberger, A. Eisenführ, F. Brueckner, M. Theis, M. Famulok & **P. Cramer**.
Structure of an RNA polymerase II-RNA inhibitor complex elucidates transcription regulation by non-coding RNAs.
Nature Struct. Mol. Biol. 2006, 13, 44-48.

H. Kettenberger & **P. Cramer**.
Fluorescence detection of nucleic acids and proteins in multicomponent crystals.
Acta Cryst. 2006, D62, 146–150.

2005

A. Meinhart, T. Kamenski, S. Hoeppner, S. Baumli and **P. Cramer**.
A structural perspective of CTD function.
Genes Dev. 19: 1401-1415 (2005)

P. Cramer, K. Straesser, D. Niessing, G. Meister und R.-P. Jansen.
RNA als Koordinator und Regulator der Genexpression
Biospekt. Special 523-525 (2005)

S. Hoeppner, S. Baumli and **P. Cramer**.
Structure of the Mediator Subunit Cyclin C and its Implications for CDK8 Function.
J. Mol. Biol 350, 833-842 (2005)

K.-J. Armache, H. Kettenberger and **P. Cramer**.
The dynamic machinery of mRNA elongation.
Curr. Op. Struct. Biol. 15, 197-203 (2005).

P. Cramer and W. Baumeister.
Macromolecular assemblages – from molecules to functional modules.
Curr. Op. Struct. Biol. 15, 185-187 (2005)

S. Baumli, S. Hoeppner & **P. Cramer**.
A conserved mediator hinge revealed in the structure of the MED7/MED21 (Med7/Srb7) heterodimer.
J. Biol. Chem 280, 18171-18178 (2005)

K.-J. Armache, S. Mitterweger, A. Meinhart & **P. Cramer**.
Structures of Complete RNA Polymerase II and Its Subcomplex, Rpb4/7.
J. Biol. Chem. 280, 7131-7134 (2005)

2004

H. Kettenberger, K.-J. Armache & **P. Cramer**.
Complete RNA Polymerase II Elongation Complex Structure and Its Interactions with NTP and TFIIS.
Mol. Cell, 16, 955-965 (2004)

P. Cramer.
Gene expression in eukaryotes: RNA polymerase II structure.
Encyc. Biol. Chem., 3 (2004)

T. Kamenski, S. Heilmeier, A. Meinhart & **P. Cramer**.
Structure and mechanism of RNA polymerase II CTD phosphatases.
Mol. Cell, 15, 399-407 (2004).

A. Meinhart & **P. Cramer**.
Recognition of RNA polymerase II carboxy-terminal domain by 3'-RNA processing factors.
Nature 430, 223-226 (2004).

M. Cikala, O. Alexandrova, C. David, M. Proeschel, B. Stiening, **P. Cramer** and A. Boettger.
The phosphatidylserine receptor from Hydra is a nuclear protein with potential Fe(II) dependent oxygenase activity.
BMC Cell Biology 5, 26 (2004).

P. Cramer.
Transiente RNA-Polymerase-Komplexe.
Biospektrum 4, 378-380 (2004)

P. Cramer.
RNA polymerase structure: from core to functional complexes.
Curr. Op. Genet. Dev. 14, 218-226 (2004).

P. Cramer.
Structure and function of RNA polymerase II.
Adv. Prot. Chem. 67,1-42 (2004).

G. Lipps, A. Weinzierl, G. von Scheven, C. Buchen, **P. Cramer**.
Structure of a bifunctional DNA primase/polymerase.
Nature Struct. Mol. Biol. 11, 157-162 (2004).

INVITED LECTURES

2008

- Sanofi-Aventis, Frankfurt
- Wellcome Trust Center for cell biology, Edinburgh, UK
- CIPSM symposium, Elmau
- EU summer school on chromatin and transcription, Spetsai, Greece
- EMBO transcription meeting, Heidelberg
- Symposium on structural biology, Hamburg
- EMBO workshop on yeast transcription, St. Feliu, Spain
- Annual meeting of the Swedish structural biology network, Tällberg, Sweden
- FASEB research conference on nucleic acid enzymes, Saxton rivers, USA
- Meeting on RNA polymerases, Quebec, Canada
- Gordon Conference on Nucleic Acids, Newport, USA
- Bayer-Schering Pharma, Berlin
- Bijvoet symposium, Utrecht, Netherlands
- Max Planck Institute for Developmental Biology, Tübingen
- Annual meeting of the German Crystallographic Society, Erlangen
- Workshop Graduate school Conformational transitions, Halle
- Annual meeting of the Swiss bioscience societies, Lausanne, Switzerland

2007

- Hans Fischer Symposium TUM, Munich
- Münchner Wissenschaftstage, Munich
- RNA polymerase I international symposium, Regensburg
- GBM Fall Meeting, Hamburg
- Horizons in Biology PhD Symposium, Göttingen
- 24th European Crystallographic Meeting, Marrakech, Marocco
- 16. Symposium Bioorganische Chemie, Dortmund
- Mechanisms of Eukaryotic Transcription Meeting, Cold Spring Harbor, USA
- FEBS 2007 Congress, Vienna, Austria
- SFB 610 Symposium, Leipzig
- Harvard, Dept of Molecular Biology, Boston, MA, USA
- FASEB Meeting on prokaryotic transcription, Saxtons River, Vermont, USA
- Albany 2007 - the 15th conversation, Albany, NY, USA
- UMDNJ, School of Osteopathy, Stratford, NJ, USA
- National Cancer Institute NCI, Frederick, MD, USA
- Steinhofer Lecture 2007, Freiburg
- Gene Center Annual Retreat, Wildbad Kreuth
- Leibniz-Graduate School of Molecular Biophysics, Berlin
- EMBL - Macromolecular Crystallography@PETRA, Hamburg
- Roche Diagnostics, Penzberg
- ADNAT Symposium, Hyderabad, India
- MPI of Molecular Cell Biology, Dresden
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2006

- University of Utrecht, Utrecht, NL
- University of Aarhus, Dept. of Structural Biology, Aarhus, DK
- Institute for Molecular Biology IBMB, Barcelona, ES
- Center for Genome Regulation CRG, Barcelona, ES
- NCCR Symposium "New trends in structural biology", ETH Zürich, CH
- Münchner Wissenschaftstage 2006, Munich
- 23rd European Crystallographic Meeting, Leuven, BL
- Bioscience 2006, Glasgow, UK
- EU workshop "Structural biology of DNA repair processes", Munich
- University of Giessen, Institute of Biochemistry, Giessen
- University of Regensburg, Institute of Biochemistry, Regensburg
- ESF-EMBO symposium on gene transcription in yeast, St. Feliu, ES
- SFB473 symposium "Molecular control of gene expression", Erlangen
- Structure and function of large molecular assemblies, Erice, Italy
- Monod Conference "Functions of RNA in gene regulation", Roscoff, F
- University of Michigan Department of Chemistry, Ann Arbor, USA
- Keystone symposium "Regulation of eukaryotic transcription", Taos, USA
- University of Oxford Department of Biochemistry, Oxford, UK
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2005

- MPI für Immunbiologie, Freiburg
- MRC Laboratory for Molecular Biology LMB, Cambridge, UK
- Biocenter LMU Munich
- SFB TR5 Annual Meeting, Heidelberg
- Münchner Wissenschaftstage „Licht und Leben", Munich
- SKMB Transcription Workshop, Lausanne, CH
- ELSO Symposium, Dresden
- Cold Spring Harbor Conference "Transcription in Eukaryotes", Cold Spring Harbor, USA
- CeNS ENB NanoBioTech, Munich
- FEBS Meeting 2005, Budapest, HU
- MPI für Biophysik, Frankfurt
- IRCM Lecture, Montreal, Canada
- Biozentrum der Universität Würzburg, Würzburg
- Netherlands Cancer Institute NKI, Amsterdam, NL
- Transcription Meeting at Imperial College, London, UK
- ASBMB Meeting, San Diego, USA
- 3'-RNA processing Meeting, Oxford, UK
- BioM Campus Open day, Martinsried
- Deutsche Gesellschaft für Kristallographie Annual Meeting, Köln
- University of Regensburg
- BASF Ludwigshafen
- University of Bonn

2004

- Chemische Gesellschaft Heidelberg
- GZMB Göttingen
- Biozentrum Basel, Switzerland
- EMBO Conference "Structures in Biology", Heidelberg
- Münchner Wissenschaftstage „Leben und Technik", Munich
- Faculty of Biology LMU Munich
- Instituto Gulbenkian de Ciencia, Lisbon, Portugal
- CeNS international summer school, Venice, Italy
- 30 years EMBL Hamburg: Structural Biology at Crossroads, Hamburg
- Wacker Consortium Munich
- Technische Universität München, Weihenstephan
- FASEB Research conference on nucleic acid enzymes, Saxton Rivers, USA
- SPINE Conference on Structural Proteomics, Amsterdam, Netherlands
- EURESCO Conference: Gene transcription in yeast, St. Feliu, Spain
- EMBO Workshop on Macromolecular Complexes, Grenoble, France
- Transregio 5 Spring Meeting, Munich
- ZMBH Universität Heidelberg
- Retreat SFB455, Garmisch
- Freie Universität Berlin
- Universität Bayreuth

Klaus Förstemann
PUBLICATIONS

2008

C. Shah, **K. Förstemann**.
Monitoring microRNA-mediated silencing in Drosophila melanogaster S2-cells.
Biochim Biophys Acta 1779, 766-772 (2008).

V. Aumiller, **K. Förstemann**.
Roles of microRNAs beyond development – Metabolism and neural plasticity.
Biochim Biophys Acta 1779, 691-696 (2008).

2007

V. Hartig, Y. Tomari, **K. Förstemann**.
piRNAs – the ancient hunters of genome invaders.
Genes Dev. 21, 1707-1713 (2007)

K. Förstemann, M.-D. Horwich, L. Wee, Y. Tomari, P.D. Zamore.
Drosophila microRNAs are sorted into functionally distinct argonaute complexes after production by dicer-1.
Cell 130, 287-297 (2007).

2006

A. Eugster, C. Lanzuolo, M. Bonneton, P. Luciano, A. Pollice, J.F. Pulitzer, E. Stegberg, A.S. Berthiau, **K. Förstemann**, Y. Corda, J. Lingner, V. Géli, E. Gilson.
The finger subdomain of yeast telomerase cooperates with Pif1p to limit telomere elongation.
Nat Struct Mol Biol. 13, 734-739 (2006)

2005

K. Förstemann, Y. Tomari, T. Du, V.V. Vagin, A.M. Denli, D.P. Bratu, C. Klattenhoff, W.E. Theurkauf, P.D. Zamore.
Normal microRNA Maturation and Germ-Line Stem Cell Maintenance Requires Loquacious, a Double-Stranded RNA-Binding Domain Protein.
PLoS Biol. 3, e236 (2005).

K. Förstemann, J. Lingner.
Telomerase limits the extent of base pairing between template RNA and telomeric DNA.
EMBO Rep. 6, 361-366 (2005).

INVITED LECTURES

2008

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- Institute of Clinical Biochemistry, LMU Munich
- ICGEB, Trieste / Italien
- Helmholtz Zentrum München, Garching

2007

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- Butenandt-Institute, LMU Munich

2006

- Forschergruppen-Meeting "Cytoplasmic Regulation of Gene Expression", Wildbad Kreuth

2005

- EMBO workshop "Regulation of mRNA turnover", Arolla/Schweiz

Ulrike Gaul
PUBLICATIONS

2008

Kurant E, Axelrod S, Leaman D, and **Gaul U**.
Six-microns-under acts upstream of Draper in the glial phagocytosis of apoptotic neurons.
Cell 133, 498-509. (2008).

Segal E, Raveh-Sadka T, Schroeder M, Unnerstall U, and **Gaul U**.
Predicting expression patterns from regulatory sequence in Drosophila segmentation.
Nature 451, 535-540. (2008).

Kertesz M, Iovino N, Unnerstall U, **Gaul U***, Segal E*.
The role of site accessibility in microRNA target recognition.
Nat Genet 39, 1278-1284 (2007).
**equal contribution*

2005

Schwabe T, Bainton RJ, Fetter RD, Heberlein U, and **Gaul U**.
GPCR signaling is required for blood-brain barrier formation in Drosophila.
Cell 123, 133-144 (2005).

Bainton R, Tsai LT, Schwabe T, DeSalvo M, **Gaul U**, Heberlein U.
moody encodes two GPCRs that regulate cocaine behaviors and blood-brain barrier permeability in Drosophila.
Cell 123, 145-156 (2005).

Leaman D, Chen PY, Fak J, Yalcin A, Pearce M, Unnerstall U, Marks DS, Sander C, Tuschl T, and **Gaul U**.
Antisense-mediated depletion reveals essential and specific functions of microRNAs in Drosophila development.
Cell 121, 1097-1108 (2005).

2004

Sinha S, Schroeder M, Unnerstall U, **Gaul U**, and Siggia ED.
Cross-species comparison significantly improves genome-wide prediction of cis-regulatory modules in Drosophila.
BMC Bioinformatics 5:129 (2004).

Schroeder M, Pearce M, Fak J, Fan HQ, Unnerstall U, Emberly E, Rajewsky N, Siggia ED, and **Gaul U**.
Transcriptional control in the segmentation gene network of Drosophila.
PLoS Biol 2:E271 (2004).

INVITED LECTURES

2008

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- "The Logic of Gene Regulation", Janelia Conference, Janelia Farm Research Campus, Ashburn, VA
- "Glia in Health & Disease", CSHL meeting, Cold Spring Harbor, NY, USA
- Institute for Molecular Pathology (IMP), VBC Seminar, Vienna, Austria
- Deutsches Krebsforschungszentrum (DKFZ), Heidelberg
- University of Pennsylvania, Dept. of Biology
- Columbia University, Dept. of Genetics and Development
- Johns Hopkins University, Dept. of Neuroscience
- LMU Munich, Germany, Institute for Informatics
- Washington University, St. Louis, Developmental Biology Retreat (Keynote Speaker), USA
- Technische Universität München, Dept. of Surgery
- Gene Center Munich

2007

- "Molecular Pharmacology", Gordon Research Conference, Ventura, CA
- 48th Annual Drosophila Research Conference, Philadelphia, PA (Plenary Lecture), USA
- "Systems Biology and Regulatory Networks", Keystone meeting, Steamboat Springs, CO, USA
- "Visual Processing in Insects: From Anatomy to Behavior", Janelia Conference, Janelia Farm Research Campus, Ashburn, VA, USA
- "Glial Cells in Health and Disease", European Glial Cell meeting, London, UK
- "Neurobiology of Drosophila", CSHL meeting, Cold Spring Harbor, NY, USA
- Recomb Satellite Conference on Systems Biology, University of California, San Diego, USA
- European Molecular Biology Laboratory (EMBL), Heidelberg
- Max Planck Institute for Developmental Biology, Tübingen
- Technion – Israel Institute of Technology, Haifa, Israel, Faculty of Medicine
- Weizmann Institute of Science, Rehovot, Israel, Dept. of Molecular Genetics
- HHMI Janelia Farm Research Campus, Ashburn, VA, USA
- University College London, UK, MRC Laboratory for Molecular Cell Biology (LMCB)
- University of Cambridge, UK, Wellcome Trust/Cancer Research UK Gurdon Institute
- National Institute for Medical Research, Mill Hill, London, UK
- Max Planck Institute for Biophysical Chemistry, Göttingen
- Max Planck Institute for Molecular Genetics, Berlin
- Max Delbrück Center for Molecular Medicine (MDC), Berlin
- Max Planck Institute for Neurobiology, Munich
- Gene Center Munich
- Max Planck Institute for Brain Research, Frankfurt
- University of Cologne, Institute for Genetics
- Max Planck Institute for Medical Research, Heidelberg
- Max Planck Institute for Experimental Medicine, Göttingen
- Max Planck Institute for Molecular Cell Biology and Genetics, Dresden
- Max Planck Institute for Immunobiology, Freiburg
- Stanford University School of Medicine, Dept. of Neurobiology, USA
- Stanford University, Frontiers in Biological Research Seminar Series, USA
- Northwestern University, Dept. of Biochemistry, Molecular Biol. and Cell Biology, USA

2006

- "Systems Biology: Global regulation of gene expression", CSHL meeting, Cold Spring Harbor, NY, USA
- "Glia in Health & Disease", CSHL meeting, Cold Spring Harbor, NY, USA
- University of California, San Francisco, Neuroscience Seminar Series, USA
- City College, City University of New York, Dept. of Biology, USA
- Skirball Institute, New York, Developmental Genetics Seminar, USA
- University of California, Berkeley, Cell and Developmental Biology Seminar Series, USA

2005

- 46th Annual Drosophila Research Conference, San Diego, CA, USA
- "Structural, Functional & Evolutionary Genomics", Gordon Research Conference, Lewiston, ME, USA
- "Neurobiology of Drosophila", CSHL meeting, Cold Spring Harbor, NY, USA
- Duke University, Developmental Biology Colloquium, USA
- New York University, Dept. of Biology, USA
- New York Academy of Sciences, RNAi Discussion Group, USA
- University of Colorado, Denver; Cells, Development and Cancer Seminar Series, USA
- Columbia University, Dept. of Genetics and Development, USA
- Harvard Medical School, Dept. of Systems Biology, USA
- Princeton University, Dept of Molecular Biology, USA
- Harvard Medical School, Dept. of Cell Biology, USA
- Northwestern University, Dept. of Biochemistry, Molecular Biol. and Cell Biology, USA
- University of Chicago, Dept. of Molecular Genetics and Cell Biology, USA

2004

- "Systems Biology: Genomic Approaches to Transcriptional Regulation", CSHL meeting, Cold Spring Harbor, NY, USA
- 45th Annual Drosophila Research Conference, Washington, DC, USA
- "siRNAs and miRNAs", Keystone meeting, Keystone, CO, USA
- Crete International Workshop on the Molecular and Developmental Biology of Drosophila, Kolymbari, Greece
- University of Minnesota, Dept. of Genetics, Cell Biology and Development, USA
- State University of New York, Stony Brook, Dept of Biochemistry and Cell Biology, USA
- University of California, Berkeley, Computational Biology and Genomics Seminar, USA

Karl-Peter Hopfner
PUBLICATIONS

2008

Gack MU, Kirchhofer A, Shin YC, Inn KS, Liang C, Cui S, Myong S, Ha T, **Hopfner KP**, Jung JU.
Roles of RIG-I N-terminal tandem CARD and splice variant in TRIM25-mediated antiviral signal transduction.
Proc Natl Acad Sci U S A 105, 16743-8.

Witte G, Hartung S, Büttner K, **Hopfner KP**.
Structural biochemistry of a bacterial checkpoint protein reveals di-adenylate cyclase activity regulated by recombination intermediates.
Molecular Cell 30. 167-178

Hopfner KP, Bemeleit D, Lammens K.
The Mre11 nuclease complex.
Handbook of Metalloproteins (editor A Messerschmidt). In press.

Hartung S, **Hopfner KP**.
Lessons from structural and biochemical studies on the archaeal exosome.
Biochem. Soc. Trans. In press.

Lewis R, Dürr H, **Hopfner KP**, Michaelis J.
Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle.
Nucleic Acids Res 36. 1881-90.

Karcher, A., Schele A, **Hopfner KP**.
X-ray structure of the complete ABC enzyme ABCE1 from Pyrococcus abyssi,
J Biol Chem. 283. 7962-71

2007

Alt A, Lammens K, Chioccini C, Lammens A, Piech K, **Hopfner KP***, Carell T*.
Bypass of DNA Crosslink Lesions Generated During Anticancer Treatment with Cisplatin by the Eukaryotic DNA Polymerase eta.
Science. 318, 967 – 970

Carell, T., Cramer P, **Hopfner KP**.
The chemistry of transcription through damaged DNA and of translesion synthesis at atomic resolution.
Nucleic Acids Symp Ser (Oxf) 51. 103.

Buttner K, Nehring S, **Hopfner KP**.
Structural basis for DNA duplex separation by a superfamily-2 helicase.
Nat. Struct. & Mol. Biol. 14, 647-52

Hopfner KP and Michaelis J.
Mechanisms of nucleic acid translocases: lessons from structural biology and single molecule biophysics.
Curr. Op. Struct. Biol. 17. 87-95

Hartung S, **Hopfner KP**.
The exosome, plugged.
EMBO Rep. 8. 456-7.

2006

Lengronne A, McIntyre J, Katou Y, Kanoh Y, **Hopfner KP**, Shirahige K, Uhlmann F.
Establishment of sister chromatid cohesion at the S. cerevisiae replication fork.
Mol. Cell 23, 1-13

Reindl C, Bagrintseva K, Schnittger S, Ellwart JW, Wenig K, **Hopfner KP**, Hiddemann W, Spiekermann K.
Point Mutations found in the JM-S and JM-Z juxtamembrane region of FLT3 define a new class of activating mutations in AML.
Blood 107, 3700-7.

Assenmacher N, Wenig K, Lammens A, **Hopfner KP**.
Structural basis for transcription coupled repair: the N-terminus of Mfd resembles UvrB with degenerate ATPase motifs.
J. Mol. Biol. 355. 675-83.

Büttner, K, Wenig, K and **Hopfner KP**.
The Exosome: a macromolecular cage for controlled RNA degradation.
Mol. Microbiology 61, 1372-1379.

Dürr, H and **Hopfner KP**.
SWI2/SNF2 ATPase and DExx box helicases: Differences and Unifying concepts from high resolution crystal structures.
Nucleic Acids Research 409, 375-88.

Uhlmann, F and **Hopfner KP**.
Chromosome Cohesion: The Crux with the Ring.
Curr. Biol. 16. R102-5.

Dürr, H and **Hopfner KP**.
Structural and biochemical analysis of SWI2/SNF2 enzymes.
In Methods of Enzymology: DNA repair. Ed. J Campell, P. Modrich, Elsevier.

Hopfner KP.
Structural Aspects of Rad/SMC Proteins.
In Facets of Genome Integrity, Ed. D. Lankenau, Springer Heidelberg.

2005

Dürr H, Körner C, Müller M, Hickmann V, **Hopfner KP**.
X-Ray Structures of the Sulfolobus solfataricus SWI2/SNF2 ATPase Core and Its Complex with DNA.
Cell 121. 363-373.

Büttner K, Wenig K, **Hopfner KP**.
Structural Framework for Archaeal Exosomes in RNA Processing.
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Karcher A, Büttner K, Märtens B, Jansen RP, **Hopfner KP**.
X-Ray Structure of RLI, an Essential Twin Cassette ABC ATPase Involved in Ribosome Biogenesis and HIV Capsid Assembly.
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Simeoni F, Arvai A, Bello P, Gondeau C, **Hopfner KP**, Neyroz P, Heitz F, Tainer J, Divita G.
Biochemical Characterization and Crystal Structure of a Dim1 Family Associated Protein: Dim2.
Biochemistry 44. 11997-12008.

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The Mre11/Rad50/Nbs1 Complex.
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2004

Lammens, A, Schele, A, **Hopfner KP**.
Structural biochemistry of ATP-driven dimerization and DNA-stimulated activation of SMC ATPases.
Current Biology 14,1778-82

Manzan A, Pfeiffer G, Hefferin ML, Cara EL, Carney JP, **Hopfner KP**.
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EMBO Reports 5. 54-9.

Pannicke U, Ma Y, **Hopfner KP**, Niewolik D, Lieber MR, Schwarz K.
Functional and biochemical dissection of the structure-specific nuclease ARTEMIS.
EMBO J 23.1987-97.

De Jager M, Trujillo KM, Sung P, **Hopfner KP**, Carney JP, Tainer JA, Connelly JC, Leach DR, Kanaar R, Wyman C.
Differential Arrangements of Conserved Building Blocks among Homologs of the Rad50/Mre11 DNA Repair Protein Complex.
J Mol Biol 339. 937-49.

Arthur LM, Gustausson K, **Hopfner KP**, Carson CT, Stracker TM, Karcher A, Felton D, Weitzman MD, Tainer J, Carney JP.
Structural and functional analysis of Mre11-3.
Nucl. Acids. Res. 32. 1886-93.

Moncalian G, Lengsfeld B, Bhaskara V, **Hopfner KP**, Karcher A, Alden E, Tainer JA, Paull TT.
The Rad50 signature motif: essential to ATP binding and biological function.
J Mol Biol 335. 937-51.

Assenmacher N, **Hopfner KP**.
Mre11/Rad50/Nbs1: Complex activities.
Chromosoma 113,157-66.

INVITED LECTURES

2008

- FASEB Summer Research School "RNA decay", Lucca, Italy
- Young Scientists Meeting of the German Society of Cell Biology, Heidelberg
- Technical University Munich Colloquium, "DNA Repair", Munich
- Biochemical Society Meeting "Molecular Biology of Archaea", St. Andrews, Scottland
- Graduate School "DNA enzymes" Giessen, Invited external expert lecture
- Ringberg Meeting (Ringberg/ Tegernsee) "Molecular Mechanism of DNA double-strand break repair"
- International ASM Conference "DNA Repair", Rotterdam
- Biocenter Basel "DNA Replication and Repair", Graduate Student Program Lecture Series

2007

- Lawrence National Laboratory, Lecture on "DNA Helicases", Berkeley, USA
- Gordon Research Conference "Genetic Toxicology", Oxford, UK
- French-German conference on "DNA repair", Toulouse, France
- FEBS Congress "Molecular Machines", Vienna, Austria
- International ASM Conference "DNA Repair", Berkeley, USA
- Ringberg Meeting (Ringberg/ Tegernsee) "Molecular Mechanism of DNA double-strand break repair"

2006

- "International Symposium on X-ray/ Electron microscopy Hybrid Methods" Lake Tahoe, USA
- International ASM Conference "DNA Repair", Amsterdam
- International Seeberg Symposion "DNA Repair", Lofoten Islands, Norway
- FASEB Conference "Nucleic Acid Enzymes", Vermont, USA
- University of Göttingen: "Structural Biology of Genome Integrity Processes"
- Max Planck Institute for Molecular Physiology Dortmund: "Structural Biology of Genome Integrity Processes"
- Biocenter Basel "DNA Replication and Repair", Graduate Student Program Lecture Series

2005

- Ringberg Meeting (Ringberg/ Tegernsee) "Structural biology of RLI1 in Ribosome Biogenesis and HIV Capsid Assembly"
- 8th GBS Annual Meeting, Buxtehude "Chromatin Remodeling and DNA Repair"
- 1st Annual Meeting, EU Integrated Project "DNA Repair", Rotterdam
- Gordon Research Conference "Protein Nucleic Acid Interactions" Rhode Island, USA "Structural Mechanism of SWI2/SNF2 enzymes"
- FASEB conference "Helicases and NTP driven nucleic acid machines" Arolla, Switzerland "Structural Mechanism of SWI2/SNF2 enzymes"
- University of the Saarland, Bad Homburg. "Tales of Tails: Structural Biology of Rad50/SMC Proteins in Genome Integrity"
- Winterschool Center For Nanoscience (CENS), Mauterndorf. "Tales of Tails: Structural Biology of Rad50/SMC Proteins in Genome Integrity"
- Summerschool Center For Nanoscience (CENS), Munich "Tales of Tails: Structural Biology of Rad50/SMC Proteins in Genome Integrity"
- University of Aarhus, Aarhus, Denmark: "Structural Mechanism of the RNase-L inhibitor"
- University of Dresden: "Molecular Machines in Genome Integrity Processes"

2004

- Ringberg Meeting (Ringberg/Tegernsee) "Structural biology of ABC ATPase: atomic insights into human disease"
- EMBO Workshop Mechanism of Genomic Integrity, Galway, Ireland "ATP-driven association of SMC proteins with DNA"
- Meeting of the DNA Repair Network, Ulm, Germany "ATP-driven association of SMC proteins with DNA"
- International Centre for Genetic Engineering and Biotechnology, Trieste, Italy "The Mre11/Rad50 complex: a tale of tails"
- International Max Planck Research School Seminar Series, Max Planck Institute for Terrestrial Microbiology, Marburg "Tales of Tails: Structural Biology of Rad50/SMC Proteins"
- Biocenter Basel "Tales of Tails: Structural Biology of Rad50/SMC Proteins in Genome Integrity"
- Biocenter Basel "DNA Replication and Repair", Graduate Student Program Lecture Series
- ASM Conference on DNA Repair & Mutagenesis: From Molecular Structure to Biological Consequences (Bermuda) "X-ray structures of a Rad54/SNF2 ATPase and its complex with DNA" (EMBO Young Investigator Lecture)

Ulrich Koszinowski PUBLICATIONS

2008

Cicin-Sain, L.; Ruzsics, Z.; Podlech, J.; Bubic, I.; Menard, C.; Jonjic, S.; Reddehase, M. J.; **Koszinowski, U. H.**
Dominant-Negative FADD Rescues the in Vivo Fitness of a Cytomegalovirus Lacking an Antiapoptotic Viral Gene.
J. Virol. 2008, 82, 2056-2064.

Jiang, X. J.; Adler, B.; Sampaio, K. L.; Digel, M.; Jahn, G.; Ettischer, N.; Stierhof, Y. D.; Scrivano, L.; **Koszinowski, U.H.**; Mach, M.; Sinzger, C.
UL74 of Human Cytomegalovirus Contributes to Virus Release by Promoting Secondary Envelopment of Virions.
J. Virol. 2008, 82, 2802-2812.

Jonjic, S.; Krmpotic, A.; Arapovic, J.; **Koszinowski, U. H.**
Dissection of the Antiviral NK Cell Response by MCMV Mutants.
Methods Mol. Biol. 2008, 415, 127-149.

Mages, J.; Freimuller, K.; Lang, R.; Hatzopoulos, A. K.; Guggemoos, S.; **Koszinowski, U. H.**; Adler, H.
Proteins of the Secretory Pathway Govern Virus Productivity During Lytic Gammaherpesvirus Infection.
J. Cell Mol. Med. 2008.

Mohr, C. A.; Cicin-Sain, L.; Wagner, M.; Sacher, T.; Schnee, M.; Ruzsics, Z.; **Koszinowski, U. H.**
Engineering of Cytomegalovirus Genomes for Recombinant Live Herpesvirus Vaccines.
Int. J. Med. Microbiol. 2008, 298, 115-125.

Sacher, T.; Jordan, S.; Mohr, C. A.; Vidy, A.; Weyn, A. M.; Ruszics, Z.; **Koszinowski, U. H.**
Conditional Gene Expression Systems to Study Herpesvirus Biology in Vivo.
Med. Microbiol. Immunol. 2008, 197, 269-276.

Sacher, T.; Podlech, J.; Mohr, C. A.; Jordan, S.; Ruzsics, Z.; Reddehase, M. J.; **Koszinowski, U. H.**
The Major Virus-Producing Cell Type During Murine Cytomegalovirus Infection, the Hepatocyte, Is Not the Source of Virus Dissemination in the Host.
Cell Host. Microbe 2008, 3, 263-272.

Sinzger, C.; Hahn, G.; Digel, M.; Katona, R.; Sampaio, K. L.; Messerle, M.; Hengel, U.; **Koszinowski, U. H.**; Brune, W.; Adler, B.
Cloning and Sequencing of a Highly Productive, Endotheliotropic Virus Strain Derived From Human Cytomegalovirus TB40/E.
J. Gen. Virol. 2008, 89, 359-368.

2007

Cicin-Sain, L.; Bubic, I.; Schnee, M.; Ruzsics, Z.; Mohr, C.; Jonjic, S.; **Koszinowski, U. H.**
Targeted Deletion of Regions Rich in Immune-Evasive Genes From the Cytomegalovirus Genome As a Novel Vaccine Strategy.
J. Virol. 2007, 81, 13825-13834.

Dolken, L.; Perot, J.; Cognat, V.; Alioua, A.; John, M.; Soutschek, J.; Ruzsics, Z.; **Koszinowski, U. H.**; Voinnet, O.; Pfeffer, S.
Mouse Cytomegalovirus MicroRNAs Dominate the Cellular Small RNA Profile During Lytic Infection and Show Features of Posttranscriptional Regulation.
J. Virol. 2007, 81, 13771-13782.

Robbins, S. H.; Bessou, G.; Cornillon, A.; Zucchini, N.; Rupp, B.; Ruzsics, Z.; Sacher, T.; Tomasello, E.; Vivier, E.; **Koszinowski, U. H.**; Dalod, M.
Natural Killer Cells Promote Early CD8 T Cell Responses Against Cytomegalovirus.
PLoS. Pathog. 2007, 3, e123.

Rupp, B.; Ruzsics, Z.; Buser, C.; Adler, B.; Walther, P.; **Koszinowski, U. H.**
Random Screening for Dominant-Negative Mutants of the Cytomegalovirus Nuclear Egress Protein M50.
J. Virol. 2007, 81, 5508-5517.

2006

Adler, B.; Scrivano, L.; Ruzcics, Z.; Rupp, B.; Sinzger, C.; **Koszinowski, U. H.**
Role of Human Cytomegalovirus UL131A in Cell Type-Specific Virus Entry and Release.
J. Gen. Virol. 2006, 87, 2451-2460.

Lenac, T.; Budt, M.; Arapovic, J.; Hasan, M.; Zimmermann, A.; Simic, H.; Krmpotic, A.; Messerle, M.; Ruzsics, Z.; **Koszinowski, U. H.**; Hengel, H.; Jonjic, S.
The Herpesviral Fc Receptor Fcr-1 Down-Regulates the NKG2D Ligands MULT-1 and H60.
J. Exp. Med. 2006, 203, 1843-1850.

Lotzerich, M.; Ruzsics, Z.; **Koszinowski, U. H.**
Functional Domains of Murine Cytomegalovirus Nuclear Egress Protein M53/P38.
J. Virol. 2006, 80, 73-84.

Mintern, J. D.; Klemm, E. J.; Wagner, M.; Paquet, M. E.; Napier, M. D.; Kim, Y. M.; **Koszinowski, U. H.**; Ploegh, H. L.
Viral Interference With B7-1 Costimulation: a New Role for Murine Cytomegalovirus Fc Receptor-1.
J. Immunol. 2006, 177, 8422-8431.

Pinto, A. K.; Munks, M. W.; **Koszinowski, U. H.**; Hill, A. B.
Coordinated Function of Murine Cytomegalovirus Genes Completely Inhibits CTL Lysis.
J. Immunol. 2006, 177, 3225-3234.

Ruzsics, Z.; Wagner, M.; Osterlehner, A.; Cook, J.; **Koszinowski, U.H.**; Burgert, H. G.
Transposon-Assisted Cloning and Traceless Mutagenesis of Adenoviruses: Development of a Novel Vector Based on Species D.
J. Virol. 2006, 80, 8100-8113.

Schnee, M.; Ruzsics, Z.; Bubeck, A.; **Koszinowski, U. H.**
Common and Specific Properties of Herpesvirus UL34/UL31 Protein Family Members Revealed by Protein Complementation Assay.
J. Virol. 2006, 80, 11658-11666.

2005

Cicin-Sain, L.; Podlech, J.; Messerle, M.; Reddehase, M. J.; **Koszinowski, U. H.**
Frequent Coinfection of Cells Explains Functional in Vivo Complementation Between Cytomegalovirus Variants in the Multiply Infected Host.
J. Virol. 2005, 79, 9492-9502.

Gillet, L.; Daix, V.; Donofrio, G.; Wagner, M.; **Koszinowski, U. H.**; China, B.; Ackermann, M.; Markine-Goriaynoff, N.; Vanderplasschen, A.
Development of Bovine Herpesvirus 4 As an Expression Vector Using Bacterial Artificial Chromosome Cloning.
J. Gen. Virol. 2005, 86, 907-917.

Hasan, M.; Krmpotic, A.; Ruzsics, Z.; Bubic, I.; Lenac, T.; Halenius, A.; Loewendorf, A.; Messerle, M.; Hengel, H.; Jonjic, S.; **Koszinowski, U. H.**
Selective Down-Regulation of the NKG2D Ligand H60 by Mouse Cytomegalovirus M155 Glycoprotein.
J. Virol. 2005, 79, 2920-2930.

Hengel, H.; **Koszinowski, U. H.**; Conzelmann, K. K.
Viruses Know It All: New Insights into IFN Networks.
Trends Immunol. 2005, 26, 396-401.

Krmpotic, A.; Hasan, M.; Loewendorf, A.; Saulig, T.; Halenius, A.; Lenac, T.; Polic, B.; Bubic, I.; Kriegeskorte, A.; Pernjak-Pugel, E.; Messerle, M.; Hengel, H.; Busch, D. H.; **Koszinowski, U. H.**; Jonjic, S.
NK Cell Activation Through the NKG2D Ligand MULT-1 Is Selectively Prevented by the Glycoprotein Encoded by Mouse Cytomegalovirus Gene M145.
J. Exp. Med. 2005, 201, 211-220.

Redwood, A. J.; Messerle, M.; Harvey, N. L.; Hardy, C. M.; **Koszinowski, U. H.**; Lawson, M. A.; Shellam, G. R.
Use of a Murine Cytomegalovirus K181-Derived Bacterial Artificial Chromosome As a Vaccine Vector for Immunocontraception.
J. Virol. 2005, 79, 2998-3008.

Rupp, B.; Ruzsics, Z.; Sacher, T.; **Koszinowski, U. H.**
Conditional Cytomegalovirus Replication in Vitro and in Vivo.
J. Virol. 2005, 79, 486-494.

Zimmermann, A.; Trilling, M.; Wagner, M.; Wilborn, M.; Bubic, I.; Jonjic, S.; **Koszinowski, U.H.**; Hengel, H. A
Cytomegaloviral Protein Reveals a Dual Role for STAT2 in IFN-(Gamma) Signaling and Antiviral Responses.
J. Exp. Med. 2005, 201, 1543-1553.

2004

Andreansky, S.; Liu, H.; Adler, H.; **Koszinowski, U. H.**; Efstathiou, S.; Doherty, P. C.
The Limits of Protection by "Memory" T Cells in Ig-/- Mice Persistently Infected With a Gamma-Herpesvirus.
Proc. Natl. Acad. Sci. U. S. A 2004, 101, 2017-2022.

Bubeck, A.; Wagner, M.; Ruzsics, Z.; Lotzerich, M.; Iglesias, M.; Singh, I. R.; **Koszinowski, U. H.**
Comprehensive Mutational Analysis of a Herpesvirus Gene in the Viral Genome Context Reveals a Region Essential for Virus Replication.
J. Virol. 2004, 78, 8026-8035.

Bubic, I.; Wagner, M.; Krmpotic, A.; Saulig, T.; Kim, S.; Yokoyama, W. M.; Jonjic, S.; **Koszinowski, U. H.**
Gain of Virulence Caused by Loss of a Gene in Murine Cytomegalovirus.
J. Virol. 2004, 78, 7536-7544.

French, A. R.; Pingel, J. T.; Wagner, M.; Bubic, I.; Yang, L.; Kim, S.; **Koszinowski, U. H.**; Jonjic, S.; Yokoyama, W. M.
Escape of Mutant Double-Stranded DNA Virus From Innate Immune Control.
Immunity. 2004, 20, 747-756.

Gold, M. C.; Munks, M. W.; Wagner, M.; McMahon, C. W.; Kelly, A.; Kavanagh, D. G.; Slifka, M. K.; **Koszinowski, U. H.**; Raulet, D. H.; Hill, A. B.
Murine Cytomegalovirus Interference With Antigen Presentation Has Little Effect on the Size or the Effector Memory Phenotype of the CD8 T Cell Response.
J. Immunol. 2004, 172, 6944-6953.

Hahn, G.; Revello, M. G.; Patrone, M.; Percivalle, E.; Campanini, G.; Sarasini, A.; Wagner, M.; Gallina, A.; Milanesi, G.; **Koszinowski, U.H.**; Baldanti, F.; Gerna, G.
Human Cytomegalovirus UL131-128 Genes Are Indispensable for Virus Growth in Endothelial Cells and Virus Transfer to Leukocytes.
J. Virol. 2004, 78, 10023-10033.

Karrer, U.; Wagner, M.; Sierro, S.; Oxenius, A.; Hengel, H.; Dumrese, T.; Freigang, S.; **Koszinowski, U. H.**; Phillips, R. E.; Klenerman, P.
Expansion of Protective CD8+ T-Cell Responses Driven by Recombinant Cytomegaloviruses.
J. Virol. 2004, 78, 2255-2264.

Lembo, D.; Donalisio, M.; Hofer, A.; Cornaglia, M.; Brune, W.; **Koszinowski, U. H.**; Thelander, L.; Landolfo, S.
The Ribonucleotide Reductase R1 Homolog of Murine Cytomegalovirus Is Not a Functional Enzyme Subunit but Is Required for Pathogenesis.
J. Virol. 2004, 78, 4278-4288.

Nagaike, K.; Mori, Y.; Gomi, Y.; Yoshii, H.; Takahashi, M.; Wagner, M.; **Koszinowski, U.**; Yamanishi, K.
Cloning of the Varicella-Zoster Virus Genome As an Infectious Bacterial Arti ficial Chromosome in Escherichia Coli.
Vaccine 2004, 22, 4069-4074.

Wagner, M.; **Koszinowski, U. H.**
Mutagenesis of Viral BACs with Linear PCR Fragments (ET Recombination).
Methods Mol. Biol. 2004, 256, 257-268.

INVITED LECTURES

2008

- Retreat of Gene Center, Wildbad Kreuth
- Symposium Graduate College, Erlangen

2007

- Lecture Spiridon Brusina Award, Rijeka, Croatia
- Waldthausen Symposium, Mainz
- DGHM Jahrestagung, Göttingen
- Annual Meeting of the German Society of Virology, Heidelberg
- Summer School, Bozava, Croatia
- Embo Meeting, Heidelberg

2006

- CMV-Symposium, Iowa, USA
- SFB 455, Westerham
- Workshop Organtransplantation, Niederpöcking
- University of Göttingen, (Prof. Wienands)
- University of Zurich, (A. Vögtlein)

2005

- ASM Conference, Acapulco, Mexico
- Int. Conference on Herpesvirus Infections, Osaka, Japan
- Int. Titisee Conference
- University of Greifswald (Prof. Gürtler)
- Conference on Vaccine Development, Berlin
- European Congress of Virology, Paris, France
- Gesellschaft für Genetik, Braunschweig

2004

- Keystone Symposium, Taos, Mexiko
- Int. Herpesvirus Workshop, Reno, Nevada, USA
- EMBL, Heidelberg
- Virology Meeting, University of Glasgow, Scotland
- SPP New Vaccine Strategies, Bonn
- Leopoldina Conference, Heidelberg
- Benjamin-Lipschütz-Symposium, Jena
- Hans-Fischer-Symposium, Garching
- Vortrag University of Marburg (Prof. Lohoff)

Dierk Niessing PUBLICATIONS

2008

Du T.G., Jellbauer S., Müller M. Schmid M., **Niessing D.**, Jansen R.P.
Nuclear transit of the RNA-binding protein She2p is required for translational control of localized ASH1 mRNA.
EMBO Rep. 9, 781-787 (2008).

2007

Heuck A., Du T.G., Jellbauer S., Richter K., Kruse C., Jaklin S., Müller M.,

Buchner J., Jansen R.-P., **Niessing D.**
Monomeric myosin V uses two binding regions for the assembly of stable translocation complexes.
Proc. Natl. Acad. Sci. USA – Track II: 105, 19778-19783 (2007).

Müller M., Heuck A., **Niessing D.**
Directional mRNA transport in eukaryotes: lessons from yeast.
Cell. Mol. Life Sci. 64, 171-180 (2007)

2006

Niessing D.
Der Forschungsaufenthalt im Ausland – Should I stay or should I go?
Biospektrum November 789-790 (2006).

2005

Cramer P., Sträßer K., **Niessing D.**, Meister G., Jansen R.P.
RNA as coordinator and regulator of gene expression
Biospektrum Special Edition 11. Jahrgang, 523-525 (2005).

2004

Niessing D., Zenklusen D, Hüttelmaier S, Singer RH, Burley SK.
She2p is a Novel RNA-Binding Protein with a Basic Helical Hairpin Motif.
Cell 119, 491-502 (2004).

INVITED LECTURES

2008

- Students-invited lecture, IDG, Helmholtz Zentrum München
- CIPSM symposium, Schloss Elmau
- DFG-Forschergruppenmeeting FOR855, Halle
- 2nd Internatl. Conf. on Protein-Protein Interactions, Dubrovnik, Croatia
- Institute of Molecular Immunology, Helmholtz Zentrum München
- Max Planck Institute, Dresden
- Ringberg Meeting "Academia Meets Industry", Ringberg/Tegernsee

2007

- DFG-Forschergruppenmeeting FOR855, Fuldatal
- Internatl. Meeting of DFG SFB646, Munich
- Internatl. Max Planck Research School (IMPRS), Munich
- EMBO Conference on "Intracellular RNA Localization", Il Ciocco, Italy
- DFG-Forschergruppenmeeting FOR855, Würzburg
- Institute of Molecular Immunology, Helmholtz Zentrum München
- Ringberg Meeting "Academia Meets Industry", Ringberg/Tegernsee

2006

- Workshop "Infection and Immunity" of the Helmholtz Association, Munich
- DFG-Graduiertenkolleg 1026, Halle
- Internatl. Meeting DFG SFB646, Wildbad Kreuth
- Annual GAIN conference at MIT, Boston, USA
- DFG-Forschergruppenmeeting FOR855, Rauischholzhausen
- Genome-Analysis-Center, GSF, Munich
- GBF – Structural Biology Department, Braunschweig
- Institute of Molecular Immunology, Helmholtz Zentrum München
- DFG-Forschergruppenmeeting FOR426, Würzburg
- Workshop "Infection and Immunity" of the Helmholtz Association, Munich
- European Career Fair, MIT, Boston, USA
- Ringberg Meeting "Academia Meets Industry", Ringberg/Tegernsee

2005

- DKFZ, Heidelberg
- Ringberg Meeting "Academia Meets Industry", Ringberg/Tegernsee
- Gene Center Munich (as guest)
- Max Planck Institute, Heidelberg
- Max Planck Society, Berlin

2004

- Gene Center Munich (as guest)
- Fritz-Lippmann Institute for Age Research, Jena
- EMBO Conference on Structures in Biology, Heidelberg
- Natl. Institute for Medical Research, London, UK
- Biozentrum Heidelberg
- Boehringer-Ingelheim North-America Workshop
- IGBMC, Strassbourg, France
- University of Bonn, Institute of Developmental Biology
- EMBL, Heidelberg
- Keystone Symposium on Structural Biology/Structural Genomics, Snowbird, USA

Johannes Söding
PUBLICATIONS

2008

Bateman, A., Finn, R. D., Sims, P. J., Wiedmer, T., Biegert, A., and **Söding, J.**
Phospholipid scramblases and Tubby like proteins belong to a new superfamily of membrane tethered transcription factors.
Bioinformatics. 2009, 25, 159-62. Epub 2008 Nov 13.

Agarwal, V., Remmert, M., Biegert, A., and **Söding, J.**
PDBalert: automatic, recurrent remote homology tracking and protein structure prediction.
BMC Struct Biol. 8:51 (2008)

Jasiak, A. J., Hartmann, H., Karakasili, E., Marian, K., Flatley, A., Kremmer, E., Sträßer, K., Martin, D. E., **Söding, J.**, and Cramer, P.
Genome-associated RNA polymerase II includes the dissociable RPB4/7 subcomplex.
J. Biol. Chem. 283, 26423-26427. (2008).

Biegert, A. and **Söding, J.**
De novo identification of highly diverged protein repeats by probabilistic consistency.
Bioinformatics 24:807-814 (2008).

Fischer, J., Mayer, C. E., and **Söding, J.**
Prediction of protein functional residues from sequence by probability density estimation.
Bioinformatics 24:613-620 (2008).

2007

Chaudhuri, I., **Söding, J.**, and Lupas, A. N.
Evolution of the beta-propeller fold.
Proteins 71:795-803 (2007).

Hsiao, N. H., **Söding, J.**, Linke, D., Lange, C., Hertweck, C., Wohlleben, W., and Takano, E.
ScbA from Streptomyces coelicolor A3(2) has homology to fatty acid synthases and is able to synthesize gamma-butyrolactones.
Microbiology 153:1394-1404 (2007).

Alva, V., Ammelburg, M., **Söding, J.**, and Lupas, A. N.
On the origin of the histone fold.
BMC Struct Biol. 7:17 (2007).

Karpenahalli, M. R., Lupas, A. N., and **Söding, J.**
TPRpred: a tool for prediction of TPR-, PPR and SEL1-like repeats from protein sequences.
BMC Bioinformatics 8:2 (2007).

2006

Gruber, M., **Söding, J.**, and Lupas, A. N.
Comparative analysis of coiled-coil prediction methods.
J. Struct Biol. 155:140-145 (2006).

Söding, J., Remmert, M., and Biegert, A.
HHrep: de novo protein repeat detection and the origin of TIM barrels.
Nucleic Acids Res. 34:W137-142 (2006).

Söding, J., Remmert M., Biegert A., Lupas A. N.
HHsenser: exhaustive transitive profile search using HMM-HMM comparison.
Nucleic Acids Res. 34:W374-378 (2006).

Biegert A., Mayer C., Remmert M., **Söding, J.**, Lupas A. N.
The MPI Bioinformatics Toolkit for protein sequence analysis.
Nucleic Acids Res. 34:W335-339 (2006).

Albrecht, R., Zeth, K., **Söding, J.**, Lupas, A. N., and Linke, D.
Expression, crystallization and preliminary X-ray crystallographic studies of the outer membrane protein OmpW from Escherichia coli.
Acta Crystallogr Sect F Struct Biol Cryst Commun. 62:415-418 (2006).

2005

Moussian, B., **Söding, J.**, Schwarz, H., and Nusslein-Volhard, C.
Retroactive, a membrane-anchored extracellular protein related to vertebrate snake neurotoxin-like proteins, is required for cuticle organization in the larva of Drosophila melanogaster.
Dev Dyn. 233:1056-1063 (2005).

Söding, J., Biegert, A., and Lupas, A. N.
The HHpred interactive server for protein homology detection and structure prediction.
Nucleic Acids Res. 33:W244-248 (2005).

Gruber, M., **Söding, J.**, and Lupas, A. N.
REPPER--repeats and their periodicities in fibrous proteins.
Nucleic Acids Res. 33:W239-243 (2005).

Coles, M., Djuranovic, S., **Söding, J.**, Frickey, T., Koretke, K., Truffault, V., Martin, J., and Lupas, A. N.
AbrB-like transcription factors assume a swapped hairpin fold that is evolutionarily related to double-psi beta barrels.
Structure 13:919-928 (2005).

Söding, J.
Protein homology detection by HMM-HMM comparison.
Bioinformatics 21:951-960 (2005).

INVITED LECTURES

2008

- 24th Ringberg Meeting, Ringberg/Tegernsee
- ECM 24 European Crystallography Meeting, Marrakech, Morocco
- Biozentrum, University Basel, Switzerland
- Critical Assessment of Techniques for Protein Structure Prediction (CASP), Structural Genomics Session, Sardinia, Italy

2007

- Intelligent Systems in Molecular Biology (ISMB), Vienna, Austria

2006

- Workshop on Systems Biology, MPG, Berlin
- Retreat of the Max Planck Institute for Developmental Biology, Tübingen
- Retreat of the Max Planck Institute for Biological Cybernetics, Tübingen
- University Zurich, Switzerland
- National Center for Biotechnology Information (NCBI), National Institutes of Health, Bethesda, MD, USA
- Bioinformatisches Colloquium, LMU Munich and TU Munich
- Gene Center Search Symposium

2005

- One-week seminar "Evolution and Development" of the Studienstiftung des Deutschen Volkes
- Intelligent Systems in Molecular Biology (ISMB) 2005, Detroit, USA, software demonstration
- Seminar at the University of Tübingen

2004

- Intelligent Systems in Molecular Biology (ISMB), Glasgow

Katja Strässer
PUBLICATIONS

2008

Röther, S. and **Sträßer, K.**
mRNA Export – an integrative component of gene expression.
In: Kehlenbach R, ed. Nuclear Transport. Austin: Landes Bioscience, Epub Ahead of Print (2008)

Jasiak, A.J., Hartmann, H., Karakasili, E., Marian, K., Flatley, A., Kremmer, E., **Sträßer, K.**, Martin, D.E., Söding, J., Cramer, P.
Genome-associated RNA polymerase II includes the dissociable RPB4/7 subcomplex.
J. Biol. Chem., 283: 26423-7 (2008)

Larivière, L., Seizl, M., van Wageningen, S., Roether, S., Feldmann, H., **Sträßer, K.**, Hahn, S., Holstege, F., Cramer, P.
Structure-system correlation identifies a gene regulatory Mediator submodule.
Genes Dev. 22: 872-877 (2008)

2007

Röther, S. and **Sträßer, K.**
The RNA polymerase II CTD kinase Ctk1 functions in translation elongation.
Gen. Dev. 21: 1409-1421 (2007)
Covered by the perspective "Synchronicity: policing multiple aspects of gene expression by Ctk1" by M. Hampsey and T. G. Kinzy in the same issue of Gen. Dev.

Krebs, S., Medugorac, I., Röther, S., **Sträßer, K.**, and Förster, M.
A missense mutation in the 3-ketodihydrosphingosine reductase FVT1 as candidate causal mutation for bovine spinal muscular atrophy.
Proc. Natl. Ac. Sc. USA, 104: 6746-51 (2007)

2006

Röther, S., Clausing, E., Kieser, A., and **Sträßer, K.**
Swt1, a novel yeast protein, functions in transcription.
J. Biol. Chem. 281: 36518 – 36525 (2006)

Larivière, L., Geiger, S., Hoeppner, S., Röther, S., **Sträßer, K.**, and Cramer, P.
Structure and TBP binding of the Mediator head subcomplex Med8–Med18–Med20.
Nat Struct Mol Biol. 13: 895 – 901 (2006)

2005

Cramer, P., **Sträßer, K.**, Niessing, D., Meister, G., and Jansen, R.P.
RNA als Koordinator und Regulator der Genexpression.
BIOspektrum, Sonderausgabe, 11. Jahrgang, 523-525 (2005)

2004

Hurt, E., Luo, M.J., Röther, S., Reed, R., and **Sträßer, K.**
Cotranscriptional recruitment of the serine-arginine-rich (SR)-like proteins Gbp2 and Hrb1 to nascent mRNA via the TREX complex.
Proc. Natl. Ac. Sc. USA 101: 1858-1862 (2004)

INVITED LECTURES

2008

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- Department of Biology, LMU Munich
- DFG Workshop "ERC Starting Grants", Bonn
- Forschergruppe (FOR 855), Munich, Halle and Berlin
- EU summer school on chromatin and transcription, Spetses, Greece
- BMBF, EU-Forum, Berlin

2007

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- Max Planck Institute for Biochemistry, Munich
- Center for Integrative Genomics (CIG), Lausanne, Switzerland
- Biozentrum Würzburg

2006

- Herbsttreffen Schloss Hochhausen
- Friedrich-Mischer-Institute, Basel, Switzerland
- EMBO-YIP meeting, Vienna, Austria

2005

- Chromatin/Transcription workshop, MRCI, London, UK
- University of Göttingen
- Physikalisch-Chemisches Kolloquium, LMU Munich
- Institut für Mikrobiologie und Genetik, Universität Göttingen
- EMBO-YIP Meeting, Heidelberg
- Fakultät für Chemie und Pharmazie der Universität Würzburg
- Scientific meeting of the Japanese Biochemical Society, Kobe, Japan

2004

- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee
- Kolloquiumsreihe des SFBs 473 „Schaltvorgänge der Transkription", Erlangen
- Gene Center Retreat
- RNA-Biochemie-Tagung, Blaubeuren
- Biocenter Basel, Switzerland

Achim Tresch
PUBLICATIONS

2008

A. May, R. Kirchner, H. Müller, P. Hartmann, N. El Hajj, **A. Tresch**, U. Zechner, W. Mann, T. Haaf.
Multiplex RT-PCR Expression Analysis of Developmentally Important Genes in Individual Mouse Preimplantation Embryos and Blastomeres.
Biology of Reproduction (2008)

H. Fröhlich, T. Beißbarth, **A. Tresch**, D. Kostka, J. Jacob, R. Spang, F. Markowetz.
Analyzing Gene Perturbation Screens With Nested Effects Models in R and Bioconductor.
Bioinformatics Applications Notes (2008)

J. Fassunke, M. Majores, **A. Tresch**, P. Niehusmann, A. Grote, S. Schoch, A.J. Becker.
Array analysis of epilepsy-associated gangliogliomas reveals expression patterns related to aberrant development of neuronal precursors.
Brain (2008)

Korf U, Derdak S, **Tresch A**, Henjes F, Schumacher S, Schmidt C, Hahn B, Lehmann WD, Poustka A, Beissbarth T, Klingmüller U.
Quantitative protein microarrays for time-resolved measurements of protein phosphorylation.
Proteomics (2008)

U. Korf, F. Henjes, C. Schmidt, **A. Tresch**, H. Mannsperger, C. Löbke, T. Beissbarth, A. Poustka.
Antibody Microarrays as an Experimental Platform for the Analysis of Signal Transduction Networks.
Advances in Biochemical Engineering/Biotechnology. Springer Berlin/Heidelberg (2008).

A. Tresch and F. Markowetz
Structure Learning in Nested Effects Models.
Statistical Applications in Genetics and Molecular Biology (2008)

T. Haaf, A. Hahn, A. Lambrecht, B. Grossmann, E. Schwaab, O. Khanaga, T. Hahn, **A. Tresch**, M. Schorsch.
A high oocyte yield for intracytoplasmic sperm injection treatment is associated with an increased chromosome error rate.
Fertility and Sterility, Epub (2008)

A. Hofmann, U. Ritz, M.H. Hessmann, C. Schmid, **A. Tresch**, J.D. Rompe, A. Meurer, P.M. Rommens.
Cell viability, osteoblast differentiation, and gene expression are altered in human osteoblasts from hypertrophic fracture non-unions.
Bone (2008)

2007

A. Tresch, T. Beissbarth, H. Sueltmann, R. Kuner, A. Poustka, A. Buness.
Discrimination of direct and indirect effects in a network of regulatory effects.
Jounal of Computational Biology (2007)

A. Buness, R. Kuner, M. Ruschhaupt, A. Poustka, H. Sueltmann, **A. Tresch**.
Identification of aberrant chromosomal regions from gene expression microarray studies applied to human breast cancer.
Bioinformatics (2007)

A. Tresch.
Soluble groups with their centralizer factor groups of bounded rank.
Journal of Pure and Applied Algebra (2007)

K. U. Klein, K. Engelhard, M. Glaser, R. Reisch, **A. Tresch**, C. Werner.
Monitoring of Cerebral Blood Flow and Oxygen Saturation during Craniotomies.
J. Neurosurg Anesthesiol (2007)

2005

A. Tresch, K. Samol.
On a conjecture on algebras that are locally embeddable into finite dimensional algebras.
Illinois Journal of Mathematics (2005)

A. Tresch.
Hyperabelian groups with finite co-central rank.
Journal of Algebra (2005)

INVITED LECTURES

2008

- University of Stuttgart. Markov Chain Monte Carlo without likelihoods
- LMU Munich. Network Reconstruction
- München, Heidelberg. Courses in Practical Microarray Analysis
- DGMP 2008, Oldenburg. Rekonstruktion von Signalwegen aus Microarraydaten und Interventionseffekten mit Hilfe von Nested Effects Modellen
- University of Mainz. Gene Expression Microarray Analysis

2007

- ETH Zürich. Extensions of Nested Effects Models
- University of Münster. Nested Efffects Models, RNAi screens and Microarrays
- Ascona, Workshop in statistics for biomolecular integration and modeling, Nested Effects Models for the Reconstruction of Signalling Pathways
- University of Regensburg. Nested Effects Models
- Lewis-Sigler Institute, Princeton University, USA. Maximum Likelihood Estimation in Nested Effects Models
- München, Heidelberg, Dortmund, Berlin, Saarbrücken. Courses in Practical Microarray Analysis

2006

- Video lecture of the national genome research initiative (NGFN). Good statistical practice in microarray analysis. Quality control, Preprocessing, Normalization
- DGKL 2006, Mannheim. Detection of differentially expressed genes in microarray measurements of mixed tissues
- University of Applied Sciences, Remagen. Bestimmung differentiell exprimierter Gene in Mischgeweben
- University of Applied Sciences, Bingen. Klassifikation von Gen-expressionsdaten
- EURANDOM 2006, Eindhoven. Methods for the detection of gene regulatory networks using RNAi microarray data

Petra Wendler
PUBLICATIONS

Wendler, P., J. Shorter, C. Plisson, A. Cashikar, S. Lindquist, H. Saibil.
Atypical AAA+ subunit packing creates an expanded cavity for disaggregation by the protein-remodeling factor Hsp104.
Cell 131(7):1366-77 (2007).

Puri, T., **P. Wendler**, B. Sigala, H. Saibil, IR. Tsaneva.
Dodecameric structure and ATPase activity of the human TIP48/TIP49 complex.
J Mol Biol. 366(1):179-92 (2007).

Wendler, P., A. Lehmann, K. Janek, S. Baumgart, C. Enenkel.
The bipartite nuclear localization sequence of Rpn2 is required for nuclear import of proteasomal base complexes via karyopherin alpha/beta and proteasome functions.
J Biol Chem 279(36):37751-62 (2004).

INVITED LECTURES

- DFG Symposium, Berlin, 2008
- 63rd Harden Conference, Ambleside, UK, 2007 (selected poster presentation)
- Molecular Chaperone Club Meeting, Cambridge, UK, 2006

Daniel N. Wilson
PUBLICATIONS

2008

Harms JM*, **Wilson DN***, Schlünzen F*, Connell SR, Stachelhaus T, Zaborowska Z, Spahn CMT, Fucini P.
Translational regulation via L11: Molecular switches on the ribosome turned on and off by thiostrepton and micrococcin.
Mol. Cell 30(1): 26-38 (2008).

Wilson DN, Schlünzen F, Harms JM, Starosta AL, Connell SR, and Fucini P.
The oxazolidinone antibiotics perturb the ribosomal peptidyl-transferase center and effect tRNA positioning
Proc. Natl Acad. Sci. USA 105(36): 13339-44 (2008).

Connell SR, Topf M, Qin Y, **Wilson DN**, Mielke T, Fucini P, Nierhaus KH, Spahn CMT.
A new tRNA intermediate revealed on the ribosome during EF4-mediated

back-translocation.
Nat. Struct. Mol. Biol., 15, 910-915 (2008).

Di Giacco V*, Márquez V*, Qin Y, Pech M, Triana-Alonso FJ, **Wilson DN**, Nierhaus KH.
Shine–Dalgarno interaction prevents incorporation of noncognate amino acids at the codon following the AUG.
Proc. Natl Acad. Sci. USA 105(31): 10715-10720 (2008)

Szaflarski W*, Vesper O*, Teraoka Y, Plitta B, **Wilson DN**, Nierhaus KH.
New features of the ribosome and ribosomal inhibitors: Non-enzymatic recycling, misreading and back-translocation.
J. Mol. Biol. 380(1): 193-205 (2008).

Lang K*, Erlacher M*, **Wilson DN**, Micura R, Polacek N.
The role of 23S rRNA residue A2451 in ribosomal peptide bond synthesis revealed by atomic mutagenesis.
Chem. Biol. 15(5): 485-492 (2008).

2007

Sharma MR*, **Wilson DN***, Datta PP, Barat C, Schluenzen F, Fucini P and Agrawal RK.
Cryo-EM study of the spinach chloroplast ribosome reveals the structural and functional roles of plastid-specific ribosomal proteins.
Proc. Natl Acad. Sci. USA 104(49): 19315-19320 (2007).

Datta PP*, **Wilson DN***, Kawazoe M*, Swami NK, Kaminishi T, Sharma MR, Booth TM, Takemoto C, Fucini P, Yokoyama S and Agrawal RK.
Structural aspects of RbfA action during small ribosomal subunit assembly.
Mol. Cell 28(3): 434-445 (2007).

Kaminishi T*, **Wilson DN***, Takemoto C*, Harms J*, Kawazoe M, Schluenzen F, Hanawa-Suetsugu K, Shirouzu M, Fucini P and Yokoyama S.
Structural basis of mRNA capture via Shine-Dalgarno interaction of the 30S ribosomal subunit.
Structure 15(3): 289-297 (2007).

Connell SR*, Takemoto C*, **Wilson DN**, Wang H, Murayama K, Terada T, Rost M, Schüler M, Giesebrecht J, Dabrowski M, Mielke T, Fucini P, Yokoyama S, and Spahn CMT.
Structural basis for interaction of the ribosome with the switch regions of GTP-bound elongation factors.
Mol. Cell 25(5): 751-764 (2007).

D.N. Wilson and K.H. Nierhaus.
The weird and wonderful world of bacterial ribosome regulation.
Crit. Rev. Biochem. Mol. Biol. 42(3): 187-219 (2007).

D.N. Wilson and K.H. Nierhaus.
The oxazolidinone class of drugs find their orientation on the ribosome.
Mol. Cell 26(4): 460-462 (2007).

2006

Qin Y, Polacek N, Vesper O, Staub E, Einfeldt E, **Wilson DN** and Nierhaus KH
The highly conserved LepA is a ribosomal elongation factor that back-translocates the ribosome.
Cell 127(4), 721-733 (2006).

Schluenzen*, Takemoto C*, **Wilson DN***, Kaminishi T*, Harms J, Hanawa-Suetsugu K, Szaflarski W, Kawazoe M, Nierhaus KH, Yokoyama S and Fucini P.
The antibiotic kasugamycin mimics mRNA nucleotides to destabilize tRNA binding and inhibit canonical translation initiation.
Nat. Struct. Mol. Biol. 13(10):871-878 (2006).

Fucini P., Schlünzen F, **Wilson DN**, Tian PS, Harms JM, McInnes SJ, Hansen H, Albrecht R, Buerger J, Wilbanks S.
The binding mode of the trigger factor on the ribosome: Implications for protein folding and SRP interaction.
FASEB J. 20(5): A965-A965 Part 2 (2006).

Karahalios P, Kalpaxis DL, Fu H, Katz L, **Wilson DN** and Dinos G.
On the mechanism of action of 9-O-arylalkyloxime derivatives of 6-O-mycaminosyltylonolide, a new class of 16-membered ketolide antibiotics.
Mol. Pharmacol. 70(4): 1271-1280 (2006).

Seo H, Abedin S, Kamp D, **Wilson DN**, Nierhaus KH, Cooperman BS.
EF-G-dependent GTPase on the ribosome. Conformational change and fusidic acid inhibition.
Biochemistry 45(8): 2504-2514 (2006).

Wilson DN and Nierhaus KH.
The E site story: The importance of maintaining two tRNAs on the ribosome during translation.
Curr. Mol. Life Sci. 63(23):2725-37 (2006).

2005

Wilson DN, Harms JM, Nierhaus KH, Schlünzen F, Fucini P.
Species-specific antibiotic-ribosome interactions: Importance for drug development.
Biol. Chem. 386(12): 1239-1252 (2005).

Schlünzen F*, **Wilson DN***, Tian P, Harms JM, McInnes SJ, Hansen HAS, Albrecht R, Buerger J, Wilbanks SM, Fucini P.
The binding mode of the trigger factor on the ribosome: Implications for protein folding and SRP interaction.
Structure 13(11): 1685-1694 (2005).

Dinos G, Kalpaxis D, **Wilson DN**, and Nierhaus KH.
Deacylated tRNA is released from the E site upon A site occupation but before GTP is hydrolysed by EF-Tu.
Nucleic Acids Res. 33(16): 5291-5296 (2005).

Sharma MR*, Barat C*, **Wilson DN***, Booth TM, Kawazoe M, Hori-Takemoto C, Shirouzu M, Yokoyama S, Fucini P, and Agrawal, RK.
Interaction of the highly conserved bacterial GTPase, Era, with the 30S ribosomal subunit: Functional implications for small subunit assembly.
Mol. Cell 18(3):319-329 (2005).

Giavalisco P*, **Wilson DN***, Kreitler T, Lehrach H, Klose J, Gobom J and Fucini P.
High heterogeneity within the ribosomal proteins of the Arabidopsis thaliana 80S ribosome.
Plant Mol. Biol. 57: 577-591 (2005).

Wilson DN*, Schluenzen F*, Harms JM*, Yoshida T, Ohkubo T, Albrecht A, Buerger J, Kobayashi Y, and Fucini P.
X-ray crystallography study on ribosome recycling: the mechanism of binding and action of RRF on the 50S ribosomal subunit.
EMBO J. 24(2): 251-260 (2005).

Wilson DN and Nierhaus KH.
Ribosomal Proteins in the Spotlight.
Crit. Revs. Biochem. Mol. Biol. 40(5): 243-267 (2005).

Wilson DN and Nierhaus KH.
RelBE or not to be.
Nat. Struct. Mol. Biol. 12(4): 282-284 (2005).

Wilson DN and Nierhaus KH.
Functional Roles for Ribosomal Proteins.
In: Encyclopedia of Life Sciences, John Wiley & Sons, Ltd: Chichester http://www.els.net/ [doi:10.1038/npg.els.0004200] (2005).

Nierhaus KH and **Wilson DN**.
Peptide Chain Elongation: Models of the Elongation Cycle.
In: Encyclopedia of Life Sciences, John Wiley & Sons, Ltd: Chichester http://www.els.net/ [doi:10.1038/npg.els.0003949] (2005)

Nierhaus KH and **Wilson DN**.
Peptidyl Transfer on the Ribosome.
In: Encyclopedia of Life Sciences, John Wiley & Sons, Ltd: Chichester http://www.els.net/ [doi:10.1038/npg.els. 0003951] (2005)

Wilson DN, Stelzl U and Nierhaus KH.
Protein Synthesis Inhibitors.
In: Encyclopedia of Life Sciences, John Wiley & Sons, Ltd: Chichester http://www.els.net/ [doi:10.1038/npg.els.0000550] (August 2005)

2004

Márquez V, **Wilson DN**, Tate WP, Triana-Alonso F, Nierhaus KH.
Maintaining the ribosomal reading frame: The influence of the E site during translational regulation of release factor 2.
Cell 117(8): 45-55 (2004).

Petropoulos AD, Xaplanteri MA, Dinos GP, **Wilson DN**, Kalpaxis DL.
Polyamines affect diversely the antibiotic potency: insight gained from kinetic studies of the blasticidin S and spiramycin interactions with functional ribosomes.
J. Biol. Chem. 279(25): 26518-26525 (2004).

Dinos G*, **Wilson DN***, Teraoka Y, Szaflarski W, Fucini P, Kalpaxis D, Nierhaus KH.
Dissecting the ribosomal inhibition mechanisms of edeine and pactamycin: the universally conserved residues G693 and C795 regulate P-site RNA binding.
Mol. Cell 13(1): 113-24 (2004).

Sharma MR*, Barat C*, **Wilson DN***, Booth TM, Hori-Takemoto C, Yokoyama S, Fucini P, and Agrawal, RK.
ERA protein binds in a functionally important region of the 30S ribosomal subunit.
Biophys. J. 86(1): 316A-317A (Part 2 Suppl. S) (2004)

Wilson DN and Nierhaus KH.
The how and Y of cold shock.
Nat. Struct. Mol. Biol. 11(11): 1026-1028 (2004).

Wilson DN.
Antibiotics and the inhibition of ribosome function.
In Protein Synthesis and Ribosome Structure, eds. Nierhaus, KH and Wilson, DN (Wiley-VCH, Weinheim, Germany), pp. 449-527 (2004).

Wilson DN.
Initiation of protein synthesis.
In Protein Synthesis and Ribosome Structure, eds. Nierhaus, KH and Wilson, DN (Wiley-VCH, Weinheim, Germany), pp. 219-239 (2004).

Wilson DN.
Termination and ribosome recycling.
In Protein Synthesis and Ribosome Structure, eds. Nierhaus, KH and Wilson, DN (Wiley-VCH, Weinheim, Germany), pp. 367-395 (2004)

INVITED LECTURES

2008

- Eidgenössische Technische Hochschule (ETH), Zurich, Switzerland
- Wadsworth Center, Department of Health, Albany, USA
- CSH Translational Control Meeting, New York, USA
- Weill Medical College of Cornell University, New York, USA
- Gene Center Retreat, Wildbad Kreuth

2007

- Vienna Biocenter, Austria
- Institute of Technology, University of Tartu, Estonia
- Nabriva Therapeutics Forschungs GmbH, Vienna, Austria
- Institute of Molecular and Cell Biology, University of Tartu, Estonia
- Center for Molecular Biosciences, Leopold Franzens University, Innsbruck, Austria
- Department of Microbiology, University of Regensburg
- IMPRS Seminar, MPI for Biochemistry, Munich

2006

- Rib-X Pharmaceuticals, New Haven, USA
- CSH Translational control conference, New York, USA
- 14th Engelhardt Conference, Moscow, Russia
- 39th IUCr crystallography meeting, Erice, Italy
- 14th Experimental Strategies in Ribosome Research, Patras, Greece
- Institut de Biologie Physico-Chimique, Paris, France
- Wellcome Trust Centre for Cell Biology, Edinburgh University, UK
- Gene Center Munich
- Manchester Interdisciplinary Centre, United Kingdom.
- MRC Laboratory of Molecular Biology, United Kingdom

Eckhardt Wolf
PUBLICATIONS

2008

S. Bauersachs, K. Mitko, S. E. Ulbrich, H. Blum, and **E. Wolf**.
Transcriptome studies of bovine endometrium reveal molecular profiles characteristic for specific stages of estrous cycle and early pregnancy.
Exp. Clin. Endocrinol. Diabetes 116, 371-384 (2008).

M. Bielohuby, M. Sawitzky, I. Johnsen, D. Wittenburg, F. Beuschlein, **E. Wolf**, and A. Hoeflich.
Decreased p44/42 MAPK phosphorylation in gender- or hormone-related but not during age-related adrenal gland growth in mice.
Endocrinology. 2009, 150, 1269-77. Epub 2008 Oct 23.

M. Dahlhoff, D. Horst, M. Gerhard, F. T. Kolligs, **E. Wolf**, and M. R. Schneider.
Betacellulin stimulates growth of the mouse intestinal epithelium and increases adenoma multiplicity in Apc+/Min mice.
FEBS Lett. 582, 2911-2915 (2008).

A. A. Gratao, M. Dahlhoff, F. Sinowatz, **E. Wolf**, and M. R. Schneider.
Betacellulin overexpression in the mouse ovary leads to MAPK3/MAPK1 hyperactivation and reduces litter size by impairing fertilization.
Biol. Reprod. 78, 43-52 (2008).

N. Herbach, B. Goke, **E. Wolf**, and R. Wanke.
Diets influence the diabetic phenotype of transgenic mice expressing a dominant negative glucose-dependent insulinotropic polypeptide receptor (GIPRdn).
Regul. Pept. 146, 260-270 (2008).

N. Klymiuk, **E. Wolf**, and B. Aigner.
Concise classification of the genomic porcine endogenous retroviral gamma1 load to defined lineages.
Virology 371, 175-184 (2008).

K. Lepikhov, V. Zakhartchenko, R. Hao, F. Yang, C. Wrenzycki, H. Niemann, **E. Wolf**, and J. Walter.
Evidence for conserved DNA and histone H3 methylation reprogramming in mouse, bovine and rabbit zygotes.
Epigenetics Chromatin 1, 8 (2008).

T. S. Lisse, F. Thiele, H. Fuchs, W. Hans, G. K. Przemeck, K. Abe, B. Rathkolb, L. Quintanilla-Martinez, G. Hoelzlwimmer, M. Helfrich, **E. Wolf**, S. H. Ralston, and M. Hrabé de Angelis.
ER stress-mediated apoptosis in a new mouse model of osteogenesis imperfecta.
PLoS Genet. 4, e7 (2008).

J. Manolopoulou, M. Bielohuby, S. J. Caton, C. E. Gomez-Sanchez, I. Renner-Mueller, **E. Wolf**, U. D. Lichtenauer, F. Beuschlein, A. Hoeflich, and M. Bidlingmaier.
A highly sensitive immunofluorometric assay for the measurement of aldosterone in small sample volumes: validation in mouse serum.
J. Endocrinol. 196, 215-224 (2008).

K. Mitko, S. E. Ulbrich, H. Wenigerkind, F. Sinowatz, H. Blum, E. **E. Wolf**, and S. Bauersachs.
Dynamic changes in messenger RNA profiles of bovine endometrium during the oestrous cycle.
Reproduction 135, 225-240 (2008).

O. Puk, J. Loster, C. Dalke, D. Soewarto, H. Fuchs, B. Budde, P. Nurnberg, **E. Wolf**, M. Hrabé de Angelis, and J. Graw.
Mutation in a novel connexin-like gene (Gjf1) in the mouse affects early lens development and causes a variable small-eye phenotype.
Invest Ophthalmol. Vis. Sci. 49, 1525-1532 (2008).

N. S. Reim, B. Breig, K. Stahr, J. Eberle, A. Hoeflich, **E. Wolf**, and R. G. Erben.
Cortical bone loss in androgen-deficient aged male rats is mainly caused by increased endocortical bone remodeling.
J. Bone Miner. Res. 23, 694-704 (2008).

M. R. Schneider, B. Mayer-Roenne, M. Dahlhoff, V. Proell, K. Weber, **E. Wolf**, and R. G. Erben.
High cortical bone mass phenotype in betacellulin transgenic mice is EGFR-dependent.
J. Bone Miner. Res., in press

M. R. Schneider, S. Werner, R. Paus, and **E. Wolf**.
Beyond wavy hairs: the epidermal growth factor receptor and its ligands in skin biology and pathology.
Am. J. Pathol. 173, 14-24 (2008).

M. R. Schneider, **E. Wolf**, J. Braun, H. J. Kolb, and H. Adler.
Canine embryo-derived stem cells and models for human diseases.
Hum. Mol. Genet. 17, R42-R47 (2008).

M. R. Schneider, M. Antsiferova, L. Feldmeyer, M. Dahlhoff, P. Bugnon, S. Hasse, R. Paus, **E. Wolf**, and S. Werner.
Betacellulin regulates hair follicle development and hair cycle induction and enhances angiogenesis in wounded skin.
J. Invest Dermatol. 128, 1256-1265 (2008).

M. R. Schneider and **E. Wolf**.
The epidermal growth factor receptor and its ligands in female reproduction: insights from rodent models.
Cytokine Growth Factor Rev. 19, 173-181 (2008).

M. Schwab, B. Kessler, **E. Wolf**, G. Jordan, S. Mohl, and G. Winter.
Correlation of in vivo and in vitro release data for rh-INFalpha lipid implants.
Eur. J. Pharm. Biopharm. 70, 690-694 (2008).

T. E. Spencer, O. Sandra, and **E. Wolf**.
Genes involved in conceptus-endometrial interactions in ruminants: insights from reductionism and thoughts on holistic approaches.
Reproduction 135, 165-179 (2008).

D. C. von Waldthausen, M. R. Schneider, I. Renner-Muller, D. N. Rauleder, N. Herbach, B. Aigner, R. Wanke, and **E. Wolf**.
Systemic overexpression of growth hormone (GH) in transgenic FVB/N inbred mice: an optimized model for holistic studies of molecular mechanisms underlying GH-induced kidney pathology.
Transgenic Res. 17, 479-488 (2008).

M. Wohr, M. Dahlhoff, **E. Wolf**, F. Holsboer, R. K. Schwarting, and C. T. Wotjak.
Effects of genetic background, gender, and early environmental factors on isolation-induced ultrasonic calling in mouse pups: an embryo-transfer study.
Behav. Genet. 38, 579-595 (2008).

C. Zuber, S. Knackmuss, G. Zemora, U. Reusch, E. Vlasova, D. Diehl, V. Mick, K. Hoffmann, D. Nikles, T. Frohlich, G. J. Arnold, B. Brenig, **E. Wolf**, H. Lahm, M. Little, and S. Weiss.
Invasion of tumorigenic HT1080 cells is impeded by blocking or downregulating the 37-kDa/67-kDa laminin receptor.
J. Mol. Biol. 378, 530-539 (2008).

2007

B. Aigner, B. Rathkolb, N. Herbach, d. A. Hrabe, R. Wanke, and **E. Wolf**.
Diabetes models by screening for hyperglycemia in phenotype-driven ENU mouse mutagenesis projects.
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INVITED LECTURES

2008

- Walter-Brendel-Kolleg für Transplantationsmedizin, Wildbad Kreuth
- DGFZ-Workshop "Biotechnologie bei Nutztieren – heute und morgen", Mariensee
- Distinguished Lecturer Series, Animal Molecular and Cellular Graduate Program, University of Florida, Gainesville, FL, USA
- 43. Jahrestagung der Deutschen Diabetes-Gesellschaft, Munich
- FUGATO-Statusseminar, Potsdam
- PIG GENOME II Second European Conference on Pig Genomics, Ljubljana, Slovenia
- Seminar Universität Hohenheim
- 3rd Pfizer Bovine Reproduction Consortium Meeting, Orlando, FL, USA
- 1st COST-GEMINI Meeting, Volos, Greece
- University College Dublin, Ireland
- Jahrestagung der Deutschen Gesellschaft für Reproduktionsmedizin (DGRM), Frankfurt

2007

- Symposium "Academia meets Industry – Industry meets Academia", Schloss Ringberg
- Experts Meeting of EU COST action 861, Brussels, Belgium
- Tierwissenschaftliches Seminar, Universität Hohenheim
- 51. Jahreskongress der Saarländisch-Pfälzischen Internistengesellschaft e.V., Neustadt an der Weinstrasse
- Walter-Brendel-Kolleg für Transplantationsmedizin, Wildbad Kreuth
- Workshop "The Challenges of High-Throughput DNA-Sequencing", GSF-National Research Center for Environment and Health, Munich-Neuherberg
- International Conference on Farm Animal Reproduction, Rolduc, The Netherlands
- Third Weissenburg Symposium – Briciana "Medicine at the Interface between Science and Ethics", Weissenburg
- Robust Cows Workshop, Animal Science Group of Wageningen, Lelystad, The Netherlands
- Roche Seminar, Penzberg
- Emma Thaler Research Weekend des Dr. v. Hauner'schen Kinderspitals, Herrsching
- Pfizer, Sandwich, UK
- Symposion "The Feto-Maternal Dialogue in Domestic Animals: From Conception to Placental Release", Schloss Rauischholzhausen
- Feriensemінar für vielseitig begabte und interessierte Gymnasiasten, Hohenschwangau
- 5. Berliner Genetik-Workshop "Molekulare Genetik in Zellbiologie und Ernährung", Berlin
- Joint Conference of the Cell Transplant Society (CTS), the International Pancreas and Islet Transplant Association (IPITA), and the International Xenotransplantation Association (IXA), Minneapolis, USA
- 2nd Congress of the German Society for Stem Cell Research, Würzburg
- 2nd International Meeting on Mammalian Embryogenomics, Paris, France
- 2nd Obihiro-Bern Joint Workshop on Animal and Food Hygiene, Bern, Switzerland
- 2nd Pfizer Bovine Reproduction Consortium Meeting, Utrecht, The Netherlands

2006

- Symposium "Academia meets Industry – Industry meets Academia", Schloss Ringberg
- Minitube of America, Inc., Verona, WI, USA
- Graduiertenkolleg 455 "Molekulare Veterinärmedizin", Gießen
- GSF-LMU Stem Cell Seminar Series, Munich
- 4. Interdisziplinäre TIZ-BIFO Tagung und 13. Seminar für Tierschutzbeauftragte, Munich
- EU Chimbrids Opening Conference, Mannheim
- BayGene Symposium "Functional Genomics in Bavaria", Martinsried
- Workshop "Manipulation of mammalian and avian embryos", Jastrz˙biec, Poland
- Statusseminar "FUGATO-Forschung", Dipperz-Friesenhausen
- UMR Biologie du Développement et Reproduction, INRA-CNRS-ENVA, Jouy en Josas, France
- International Symposium on Xenotransplantation, Berlin
- 22nd Scientific Meeting of the Association Europeenne de Transfert Embryonnaire (AETE), Zug, Switzerland
- Jahrestagung der Deutschen Gesellschaft für Reproduktionsmedizin (DGRM), Regensburg
- Symposium der Deutschen Akademie der Naturforscher Leopoldina und der Deutschen Veterinärmedizinischen Gesellschaft „Zur Rolle der Veterinärmedizin in Forschung und Gesellschaft", Berlin
- Jahrestagung der Deutschen Transplantationsgesellschaft, Munich
- Verleihung des Ursula M. Händel-Tierschutzpreises der DFG, Bonn
- Tierärztliche Hochschule Hannover

2005

- Vortragsreihe „Wissenschaft für Jedermann", Deutsches Museum, Munich
- AfT-Frühjahrssymposium „Stand und Perspektiven von Tierzucht und Tierhaltung bei landwirtschaftlichen Nutztieren, Wiesbaden
- EMBO Focus Meeting "The importance of the use of animals in scientific research", Madrid, Spain
- Séminaire AGENAE (Analyse du Genome des Animaux d'Elevage), St. Malo, France
- 26. Kongreß der Deutschen Veterinärmedizinischen Gesellschaft „Tierschutz, Leistung und Gesundheit", Berlin
- Fachforum Medizin „Medizinische und ethische Gesichtspunkte zum Konfliktfeld der Organtransplantation", Hanns-Seidel-Stiftung e.V., Wildbad Kreuth
- Deutsches Krebsforschungszentrum (DKFZ), Heidelberg
- Deutsche Akademie der Naturforscher Leopoldina, Halle (Saale)
- 3rd International Conference on the Female Reproductive Tract, Frauenchiemsee
- 2nd Forum of German-French Research Cooperation, Potsdam
- Meeting "Nuclear and Cell Plasticity: Progress in Basics and Applications", Alghero, Italy
- SFB 535 "Invasionsmechanismen und Replikationsstrategien von Krankheitserregern", Gießen
- 50th Anniversary of the Institute of Genetics and Animal Breeding, Polish Academy of Sciences, Jastrz˙biec, Poland
- Münchner Wissenschaftstage
- International Symposium on Biotechnology: Newer Tools for a Newer Era. Santiago de Compostela, Spain

2004

- Symposium 'Academia meets industry – Industry meets Academia', Schloss Ringberg
- ANIMBIOGEN Winter School, Sucha Beskidzka, Poland
- Walter-Brendel-Kolleg für Transplantationsmedizin, Wildbad Kreuth
- 7th Symposium on Growth and Development in Children with Chronic Kidney Disease, Heidelberg
- Jubiläumsveranstaltung 50 Jahre Verband deutscher Biologen in Bayern: Stammzellen – Heiler der Zukunft, Munich
- 3. Wissenschaftliches Symposium Tecniplast Deutschland, Varese, Italy
- 3rd European Congress of Andrology, Münster
- EFPIA workshop on "Safeguarding quality biomedical research in Europe – Health, Science, Jobs, Ethics", Brussels, Belgium
- 16th Meeting of European Artificial Insemination Veterinaries, Berlin
- Symposium Genetik der Individualität – Entwicklung der Gestalt. Charité

Campus Virchow Klinikum, Berlin
- Arbeitsgemeinschaft Reproduktionsbiologie des Menschen e.V., Berlin
- Münchner Wissenschaftstage
- Course "Manipulation of Mammalian and Avian Embryos", Institute of Genetics and Animal Breeding, Polish Academy of Sciences, Jastrzebiec, Poland
- ETH Zurich, Switzerland

Ralf-Peter Jansen
PUBLICATIONS

2008

T.-G. Du, S. Jellbauer, M. Müller, M. Schmid, D. Niessing, and **R.-P. Jansen**.
Nuclear transit of the RNA-binding protein She2p is required for translational control of localized ASH1 mRNA.
EMBO Rep. 9, 781-887 (2008).

S. Lange, Y. Katayama, M. Schmid, O. Burkacky, C. Bräuchle, Don C. Lamb, and **R.-P. Jansen**.
Simultaneous transport of different localized mRNAs species revealed by live-cell imaging.
Traffic 9, 1256-1267 (2008).

Jellbauer, S. and **R.-P. Jansen**.
A putative function of the nucleolus in the assembly or maturation of specialized messenger ribonucleoprotein complexes.
RNA Biology 5, 9-13 (2008).

2007

A. Heuck, T.-G. Du, S. Jellbauer, K. Richter, C. Kruse, S. Jaklin, M. Müller, J. Buchner, **R.-P. Jansen**, and D. Niessing.
Monomeric myosin V uses two binding regions for the assembly of stable translocation complexes.
PNAS 104, 19778-19783 (2007).

M. Lopez de Heredia and **R.-P. Jansen**.
Novel approaches for the identification and study of mRNA protein complexes.
In Leading-Edge Messenger RNA Research Communications (Ed.: M.H. Ostrovskiy). Nova Science Publishers (2007).

T.-G. Du, M. Schmid, and **R.-P. Jansen**.
Why cells move messages: The biological functions of RNA localization.
Sem. Cell Dev. Biol. 18, 171-177 (2007).

2006

M. Schmid, A. Jaedicke, T.-G. Du, and **R.-P. Jansen**.
Coordination of endoplasmic reticulum and mRNA localization to the yeast bud.
Curr. Biol. 16, 1538-1543 (2006).

A. Jasiak, K. Armache, B. Maertens, **R.-P. Jansen**, and P. Cramer.
Structural Biology of RNA Polymerase III: Subcomplex C17/25 X-ray Structure and 11 Subunit Enzyme Model,
Mol. Cell 23, 71-81 (2006).

2005

A. Karcher, K. Buttner, B. Maertens, **R.-P. Jansen**, and K.-P. Hopfner.
X-ray structure of RLI, an essential twin cassette ABC ATPase involved in ribosome biogenesis and HIV capsid assembly.
Structure 13, 649-659 (2005).

G.R. de Andrade and **R.-P. Jansen**.
Moving with Muscleblind.
Nat. Cell Biol. 7, 1055-1056 (2005).

R.-P. Jansen and M. Kiebler.
Intracellular RNA sorting, transport and localization.
Nat. Struct. Mol. Biol. 12, 826-829 (2005).

M.A. Kiebler, **R.-P. Jansen**, R. Dahm, and P. Macchi.
A putative nuclear function for mammalian Staufen.
Trends Biochem. Sci. 30, 228-231 (2005).

2004

M. Lopez de Heredia and **R.-P. Jansen**.
RNA integrity as a quality indicator during the first steps of RNP purifications: A comparison of yeast lysis methods.
BMC Biochemistry 5, 14-19 (2004).

M. Lopez de Heredia and **R.-P. Jansen**.
mRNA localization and the cytoskeleton.
Curr. Opin. Cell. Biol. 16, 80-85 (2004).

C. Juschke, D. Ferring, **R.-P. Jansen**, M. Seedorf.
A novel transport pathway for a yeast plasma membrane protein encoded by a localized mRNA.
Curr. Biol. 14, 406-411 (2004).

INVITED LECTURES

2008

- Max-Delbrück Zentrum, Berlin
- SFB 423 Symposium, Göttingen
- Martin-Luther Universität, Halle/Saale
- Universität des Saarlands, Homburg/Saar
- Life Science Forum, Universität Tübingen
- Max-Planck-Institut für Entwicklungsbiologie, Tübingen
- Max-Planck-Institut für terrestrische Mikrobiologie, Marburg
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2007

- EMBL, Heidelberg
- Universität Bayreuth, Bayreuth
- EMBO/FASEB Conference on mRNA localization and translational control, Il Ciocco, Italy
- Quiagen, Düsseldorf
- Mini-Symposium DFG FOR 855, Würzburg
- Ringberg Meeting "Academia meets Industry", Ringberg/Tegernsee

2006

- Universität Bern, Switzerland
- Mini-Symposium DFG FOR 426, Schloss Rauischholzhausen, Giessen
- Georg-August Universität, Göttingen
- Wellcome Trust Centre for Cell Biology, Edinburgh, UK
- Graduate School Symposium, Heidelberg
- Gordon Conference on Molecular Biology of Fungi, Holderness, VT, USA
- Interfakultäres Institut für Biochemie, Universität Tübingen
- MNU Tagung, LMU Munich

2005

- Mini-Symposium DFG FOR 426, Schloss Rauischholzhausen, Giessen
- Workshop SystemsBiology, TUM, Munich
- FASEB Conference on mRNA localization and translational control, Tucson, AZ, USA

2004

- ELSO Conference, Nice, France

Claudia Petritsch
PUBLICATIONS

2008

Erben, V., Waldhuber, M, Langer, D., Fetka, I, Jansen, R. P., **Petritsch, C.**
Asymmetric localization of the adaptor protein Miranda is achieved by diffusion and sequential interaction of Myosin II and VI.
Journal of Cell Science (121), 1403-14, (2008).

Silber, J., Lim, D.A., **Petritsch, C.***, Maunakea, A. K.*, Persson, A.*, Yu, M., Vandenberg, S., Ginzinger, D. G., James, C. D., Costello, J. F., Weiss, W. A., Bergers, G., Alvarez-Buylla, A., Hodgson, G.
miR-124a and miR-137 inhibit proliferation of GBM cells and induce differentiation of tumor stem cells.
BioMedCentral Medicine (2008).

Du, R.*, Lu, K.*, **Petritsch, C.***, Liu, P., Ganss, R., Passague, E., Song, H., VandenBerg, S., Werb, Z., Bergers, G.
Hif1a induces the recruitment of bone marrow-derived vascular modulatory cells to regulate tumor angiogenesis and invasion.
*(*authors contributed equally), Cancer Cell (3), 206-20 (2008).*

Du, R., **Petritsch, C.***, Liu, P, Lu, K., Haller, A., Ganss, R., Song, H., Vandenberg, S., Bergers, G.
Matrix metalloproteinase 2 regulates tumor cell survival, invasion and vascular branching in GBM.
Neuro-oncology Mar 21 (2008).

2005

Waldhuber, M., Emoto, K. and **Petritsch, C**.
The Drosophila caspase DRONC is required for metamorphosis and cell death in response to irradiation and developmental signals.
Mech. Dev. 122 (7-8), 914-27 (2005).

2004

Ye B, **Petritsch C.***, Clark, I. E., Gavis, E. R., Jan LY. and Jan YN.
nanos and pumilio, two genes known for translational regulation of embryonic body patterning, are essential for proper dendrite morphogenesis in Drosophila peripheral neurons.
Current Biology, 14, 314-21 (2004).
**provided crucial reagents and data using transgenic, UAS-pumilio lines.*

INVITED LECTURES

2005

- "Vizualing asymmetric stem cell division in vivo". Symposium Wildbach Kreuth, Institute for Biochemistry, Gene Center Retreat, "Model organisms" and Poster session, Chair. Wildbad Kreuth, Germany.
- "Stem cell divisions in real-time". Institute for Zoology, LMU Munich, Martinsried, Germany.
- "Actomyosin-dependent regulation of asymmetric stem cell division". SFB 413 Symposium, Technical University Munich, Garching, Germany.
- "Asymmetric cell division of neural stem cells". SFB 646 Symposium, Großhadern, Germany.
- "Mechanism of asymmetric stem cell division in neural stem cells". Institute of Stem Cell Biology Gesellschaft für Strahlenforschung, GSF, Neuherberg, Germany.
- "Lessons from stem cell research in model organisms". Stem cell association. Medical Center of University of Munich, Großhadern

2004

- "Mechanism of asymmetric stem cell division in neural stem cells". University of Hohenheim, Stuttgart, Germany.
- "The motors that drive neural stem cell division". Max Planck Institute for Biochemistry, Martinsried, Germany.

Stefan Weiss
PUBLICATIONS

2008

Zuber, C., Mitteregger, G., Schuhmann, N., Rey, C., Knackmuss, S., Rupprecht, W., Reusch, U., Pace, C., Little, M., Kretzschmar, H.A., Hallek, M., Büning, H. and **Weiss, S.**
Delivery of single-chain antibodies scFvs directed against the 37 kDa/67 kDa laminin receptor into murine brain via recombinant Adeno-associated viral vectors for prion disease gene therapy.
J. Gen. Virol., 89, 2054-2060 (2008).

Nikles, D., Vana, K., Gauczynski, S., Knetsch, H., Ludewigs, H. and **Weiss, S.**
Subcellular localization of prion proteins and the 37 kDa/67 kDa laminin receptor fused to fluorescent proteins.
Biochimica Biophysica Acta – Molecular Basis of Disease, 1782, 335-340 (2008).

Zuber, C., Knackmuss, S., Zemora, G., Reusch, U., Vlasova, E., Diehl, D., Mick, V., Hofmann, K., Nikles, D., Fröhlich, T., Arnold, G., Brenig, B., Wolf, E., Lahm, H., Little, M. and **Weiss, S.**
Invasion of tumorigenic HT1080 cells is impeded by downregulating or blocking the 37kDa/67kDa laminin receptor.
J. of Molecular Biology, 378, 530-539, (2008).

Zuber, C., Knackmuss, S., Rey, C., Reusch, U., Röttgen, P., Fröhlich, T., Arnold, G.J., Pace, C., Mitteregger, G., Kretzschmar, H.A., Little, M. and **Weiss, S.**
Single chain Fv antibodies directed against the 37kDa/ 67kDa laminin receptor as therapeutic tools in prion diseases.
Molecular Immunology, 45, 144-151, (2008).

Heinemann, U., **Weiss, S.** and Zerr. I.
Therapeutische Ansätze zur Behandlung der Creutzfeldt-Jakob-Erkrankung.
Medizinische Monatsschrift für Pharmazeuten, 31 (10), 378-384, (2008).

2007

Zuber, C., Mitteregger, G., Pace, C., Zerr, I., Kretzschmar, H.A. and **Weiss, S.**
Anti-LRP/LR antibody W3 hampers peripheral PrPSc propagation in Scrapie infected mice.
Prion, 1 (3), 207-212, 2007.

Vana, K., Zuber, C., Nikles, D., **Weiss, S.**
Noval Aspects of Prions, their Receptor Molecules and innovative Approaches for TSE therapy.
Cellular and Molecular Neurobiology, 27 (1) 107-128, 2007.

Zuber, C., Ludewigs, H. and **Weiss. S.**
Therapeutic Approaches targeting the prion receptor LRP/LR.
Veterinary Microbiology, 123, 387-393, 2007.

Ludewigs, H., Zuber, C., Vana, K., Nikles, D., Zerr, I. and **Weiss, S.**
Therapeutic approaches for prion disorders.
Expert Review of Anti-infective Therapy, 5 (4), 613-630, 2007.

2006

Gauczynski, S., Nikles, D., El-Gogo, S., Papy-Garcia, D., Rey, C., Alban, S., Barritault, D., Lasmézas, C.I. and **Weiss, S.**
The 37 kDa/67 kDa laminin receptor acts as a receptor for infectious prions and is inhibited by polysulfated glycanes.
Journal of Infectious Diseases, 194, 702-709 (illustrated by the cover of this issue) 2006.

Vana, K. and **Weiss, S.**
A trans-dominant negative 37 kDa/67 kDa laminin receptor mutant impairs PrPSc propagation in scrapie-infected neuronal cells.
Journal of Molecular Biology, 358, 57-66 (Impact: 4.472). 2006.

Vana, K. and **Weiss, S.**
BSE - die gebannte Gefahr?
Epidemiologie, Therapie, Suszeptibilität und Übertragbarkeit bei Prionenerkrankungen.
BIOforum, 29 (1) 35-37, 2006.

Rey, C., Zuber, C. and **Weiss, S.**
Therapeutische Ansätze zur Behandlung von Prionerkrankungen.
Nova Acta Leopoldina, 94 (347) 129-144, 2006.

2005

Morel, E., Andrieu, T., Casagrande, F., Gauczynski, S., **Weiss, S.**, Grassi, J., Rousset, M., Dormont, D., Chambaz, J.
Bovine prion is endocytosed by human enterocytes via the 37 kDa/67 kDa laminin receptor.
American Journal of Pathology, 167 (4), 1033-1042, 2005.

Weiss, S.
Cellular Biochemistry: The Prion Protein receptor as a Target for Therapy in Prion Diseases.
Chemie an der LMU, VMK-Verlag, Monsheim, pp. 35-36, 2005.

2004

Leucht, C., Vana, K., Renner-Müller, I., Lasmézas, C.I., Wolf E. and **Weiss S.**
Knock-down of the 37-kDa/67-kDa laminin receptor in mouse brain by transgenic expression of specific antisense LRP RNA.
Transgenic Research, 13, 81-85, 2004.

Hundt, C. and **Weiss, S.**
The prion-like protein Doppel fails to interact with itself, the prion protein and the 37 kDa/67 kDa laminin receptor in the yeast two hybrid system (Rapid report).
Biochim Biophys Acta – Molecular Basis of Disease, 1689, 1-5, 2004.

Baloui, H., Von Boxberg, Y., Vinh, J., **Weiss, S.**, Rossier, J., Nothias, F. and Stettler, O.
Cellular prion protein/laminin receptor: Distribution in adult central nervous system and characterization of an isoform associated with a subtype of cortical neurons.
European Journal of Neuroscience, 20, 2605-2616, 2004.

INVITED LECTURES

2008

- The 37 kDa/67 kDa laminin receptor as a key player and therapeutic target for treatment of neurodegenerative diseases and cancer. Department of Neurologie, Georg-August-Universität Göttingen
- Anti-LRP/LR specific antibodies as therapeutics for the treatment of neurodegenerative diseases and cancer. Affimed Therapeutics AG, Heidelberg
- LRP/LR as a key player and molecular target for therapy in cancer and neurodegenerative diseases. Witwaters University, Johannesburg, South Africa, (via Video Conference)
- LRP/LR and PrPc as targets in TSE and cancer therapy. Satellite NoE-Neuroprion Joint Project Meeting, Prion 2008, Madrid, Spain, Auditorium Hotel
- Antibodies directed against the prion receptor LRP/LR provide alternative tools in prion diseases. Prion 2008, Auditorium Hotel, Madrid, Spain (Talk given by Dr. Chantal Zuber)
- The non-integrin laminin receptor LRP/LR as a key player and molecular target for therapy in neurodegenerative diseases and cancer. St George's, University of London, UK
- The 37 kDa/67 kDa laminin receptor as a key player in therapy of neurodegenerative diseases and cancer. Gene Center Retreat, Wildbad Kreuth
- Signal transduction and human diseases. University of Cape Town, Faculty of Human Health, South Africa
- The 37 kDa/67 kDa laminin receptor as a key player in therapy of cancer and neurodegenerative diseases. University of Cape Town, Faculty of Human Health, South Africa
- The 37 kDa/67 kDa laminin receptor as a target in Therapy of Neurodegenerative Diseases and Cancer. 24th Ringberg Meeting, Ringberg/Tegernsee

2007

- Therapeutic Approaches in Prion Diseases targeting the Prion Receptor LRP/LR. Neurologie, Georg-August-Universität Göttingen
- Funktion des 37 kDa/67 kDa Lamininrezeptors bei neurodegenerativen Erkrankungen. Physiologische Chemie,
- Johannes Gutenberg Universität Mainz
- The 37 kDa/67 kDa laminin receptor and the membrane bound PrPc as targets in TSE therapy. Satellite NoE-Neuroprion Joint Project
- Meeting, Prion 2007, Edinburgh, UK
- Therapeutic Approaches in prion diseases targeting the prion receptor LRP/LR. Bavarian Prion Research Foundation, ForPrion, LMU Munich
- The 37 kDa/67 kDa laminin receptor as a promising target for the treatment of prion diseases and cancer. Gene Center Retreat, Wildbad Kreuth
- The 37 kDa/67 kDa laminin receptor as a promising target for the treatment of prion diseases and cancer. 23rd Ringberg Meeting, Ringberg/Tegernsee

2006

- Innovative Strategies for the Treatment of Prion Diseases Arresting the Prion Receptor LRP/LR. Universitätsklinikum Göttingen. Göttingen
- Therapeutic Strategies for the treatment of TSEs targeting the 37 kDa/67 kDa laminin receptor. 6. Treffen der Nationalen TSE- Forschungsplattfom, Greifswald
- Therapeutic Strategies for the treatment of prion diseases targeting the prion receptor. Bavarian Prion Research Foundation, ForPrion,
- Arnold Sommerfeld Haus, Munich
- The Prion Receptor as a Target in TSE Therapy. Gene Center Retreat, Wildbad Kreuth

2005

- The 37 kDa/67 kDa laminin receptor as a promising target for therapy of prion diseases. Prion 2005. International Conference. Düsseldorf
- Der 37 kDa/67 kDa Laminin-Rezeptor als Target für die Therapie von Prionenerkrankungen. Symposium der Deutschen Akademie der Naturforscher Leopoldina. Vienna, Austria
- Virale und nicht-virale Delivery Systeme zum Ausschalten des Prionrezeptors als Therapieansatz zur Behandlung von Prion Erkrankungen. Ruhr Universität Bochum
- Der 37 kDa/67 kDa Lamininrezeptor als Target in der Therapie von Prionerkrankungen. Bavarian Prion Research Foundation, ForPrion, Schloss Hohenkammer
- The 37kDa/67 kDa Laminin Receptor as a Target in Therapy of Prion Diseases. Gene Center Retreat. Wildbad Kreuth
- Prion proteins and their receptor Molecules as Targets in TSE Therapy. 21st Ringberg Meeting, Ringberg/Tegernsee

2004

- Prion Protein and its Receptor Molecules. Deutsches Primaten Zentrum (DPZ), Göttingen
- The 37 kDa/67 kDa laminin receptor as a target in TSE therapy. NoE-Food-CT-2004-506579. First Annual Meeting, Gene Center Munich
- The 37kDa/67 kDa Laminin receptor as a target in therapy of prion diseases. Jahrestagung der deutschen TSE-Forschungsplattform, Düsseldorf
- Prion Receptors and Co-Receptors as promising targets in TSE Therapy. University of Applied Sciences Lausitz (U.A.S.L.), Senftenberg
- The 37 kDa/67 kDa Laminin Receptor as a Target in TSE Therapy, Bavarian Prion Research Foundation, ForPrion, Würzburg
- Role of Prion Proteins amd their receptor and Co-Receptor Molecules in the Prion life Cycle. First International Conference of the European Network of Excellence NeuroPrion: Prion 2004. Paris, France
- Role of Prion Proteins and their Receptor and Co-Receptor Molecules in the Life Cycle of Prions. Gene Center Retreat. Wildbad Kreuth
- Die Rolle des Prion Proteins und seiner Rezeptor- und Co-rezeptormoleküle im Lebenszyklus von Prionen. University of Bielefeld, Bielefeld
- Role of the 37 kDa/67 kDa laminin receptor in the life cycle of prions. MRC Prion Unit, UCL, Prion Seminar Series, Host: Prof. Dr. Charles Weissmann. London, UK
- The prion protein receptor as a target in diagnosis and therapy of TSEs. 20th Ringberg Meeting, Ringberg/Tegernsee

LAFUGA
PUBLICATIONS

2008

S. Baehs, A. Herbst, S. E. Thieme, C. Perschl, A. Behrens, S. Scheel, A. Jung, T. Brabletz, B. Goeke, **H. Blum**, and F. T. Kolligs.
Dickkopf-4 is frequently down-regulated and inhibits growth of colorectal cancer cells.
Cancer Letters [Epub ahead of print Dec. 2008]

S. Bauersachs, K. Mitko, S. E. Ulbrich, **H. Blum**, and **E. Wolf**.
Transcriptome studies of bovine endometrium reveal molecular profiles characteristic for specific stages of estrous cycle and early pregnancy.
Exp. Clin. Endocrinol. Diabetes 116, 371-384 (2008).

A. C. Crecelius, D. Helmstetter, J. Strangmann, G. Mitteregger, T. Fröhlich, **G. J. Arnold**, and H. A. Kretzschmar HA.
The brain proteome profile is highly conserved between Prnp-/- and Prnp+/+ mice.
Neuroreport 19, 1027-1031 (2008).

E. N. De Toni, S. E. Thieme, A. Herbst, A. Behrens, P. Stieber, A. Jung, **H. Blum**, B. Goke, and F. T. Kolligs.
OPG is regulated by beta-catenin and mediates resistance to TRAIL-induced apoptosis in colon cancer.
Clinical Cancer Research 14, 4713-8 (2008).

K. Mitko, S. E. Ulbrich, H. Wenigerkind, F. Sinowatz, **H. Blum**, **E. Wolf**, and S. Bauersachs.
Dynamic changes in messenger RNA profiles of bovine endometrium during the oestrous cycle.
Reproduction 135, 225-240 (2008).

T. E. Spencer, O. Sandra, and **E. Wolf**.
Genes involved in conceptus-

endometrial interactions in ruminants: insights from reductionism and thoughts on holistic approaches. *Reproduction 135, 165-179 (2008).*

C. Zuber, S. Knackmuss, G. Zemora, U. Reusch, E. Vlasova, D. Diehl, V. Mick, K. Hoffmann, D. Nikles, T. Fröhlich, **G. J. Arnold**, **E. Wolf**, H. Lahm, M. Little, and S. Weiss. Invasion of Tumorigenic HT1080 Cells Is Impeded by Blocking or Downregulating the 37-kDa/67-kDa Laminin Receptor. *Journal of Molecular Biology 378, 530-539 (2008).*

C. Zuber, S. Knackmuss, C. Rey, U. Reusch, P. Rottgen, T. Frohlich, **G. J. Arnold**, C. Pace, G. Mitteregger, H. A. Kretzschmar, M. Little, and S. Weiss. Single chain Fv antibodies directed against the 37 kDa/67 kDa laminin receptor as therapeutic tools in prion diseases. *Molecular Immunology 45, 144-151 (2008).*

2007

S. Bauersachs, K. Mitko, **H. Blum**, and **E. Wolf**. Technical note: Bovine oviduct and endometrium array version 1: a tailored tool for studying bovine endometrium biology and pathophysiology. *J. Dairy Sci. 90, 4420-4423 (2007).*

M. Helm, C. Luck, J. Prestele, G. Hierl, P. F. Huesgen, T. Froehlich, **G. J. Arnold**, I. Adamska, A. Gorg, F . Lottspeich, and C. Gietl. Dual specificities of the glyoxysomal/peroxisomal processing protease Deg15 in higher plants. *Proceedings of the National Academy of Sciences of the United States of America 104, 11501-11506 (2007).*

2006

S. Bauersachs, S. E. Ulbrich, K. Gross, S. E. Schmidt, H. H. Meyer, H. Wenigerkind, M. Vermehren, F. Sinowatz, **H. Blum**, and **E. Wolf**. Embryo-induced transcriptome changes in bovine endometrium reveal species-specific and common molecular markers of uterine receptivity. *Reproduction 132, 319-331 (2006).*

T. Frohlich, and **G. J. Arnold**. Proteome research based on modern liquid chromatography - tandem mass spectrometry: separation, identification and quantification. *Journal of Neural Transmission 113, 973-994 (2006).*

T. Fröhlich, D. Helmstetter, M. Zobawa, A. C. Crecelius, T. Arzberger, H. A. Kretzschmar, and **G. J. Arnold**. Analysis of the HUPO Brain Proteome reference samples using 2D DIGE and 2D LC-MS/MS. *Proteomics 6, 4950-4966 (2006).*

C. Klein, S. Bauersachs, S. E. Ulbrich, R. Einspanier, H. H. Meyer, S. E. Schmidt, H. D. Reichenbach, M. Vermehren, F. Sinowatz, **H. Blum**, and **E. Wolf**. Monozygotic twin model reveals novel embryo-induced transcriptome changes of bovine endometrium in the preattachment period. *Biol. Reprod. 74, 253-264 (2006).*

M. Donzeau, S. Bauersachs, **H. Blum**, P. Reichelt, T. Rohnisch, and W. Nagel. Purification of His-tagged hybrid phage antibody. *Analytical Biochemistry 352, 154-6 (2006)*

M. Hamacher, R. Apweiler, **G. Arnold**, A. Becker, M. Bluggel, O. Carrette, C. Colvis, M. J. Dunn, T. Frohlich, et al. HUPO Brain Proteome Project: summary of the pilot phase and introduction of a comprehensive data reprocessing strategy. *Proteomics 6, 4890-4898 (2006).*

E. Wolf, S. Hiendleder, S. Bauersachs, T. Frohlich, F. Sinowatz, **H. Blum**, and **G. J. Arnold**, "[Methods for transcriptome and proteome research: applications for studying the biology of reproduction in cattle]," Berl Munch. *Tierarztl. Wochenschr. 119, 7-16 (2006).*

2005

S. Bauersachs, S. E. Ulbrich, K. Gross, S. E. Schmidt, H. H. Meyer, R. Einspanier, H. Wenigerkind, M. Vermehren, **H. Blum**, F. Sinowatz, and **E. Wolf**. Gene expression profiling of bovine endometrium during the oestrous cycle: detection of molecular pathways involved in functional changes. *J. Mol. Endocrinol. 34, 889-908 (2005).*

F. J. Berendt, T. Frohlich, S. E. Schmidt, H. D. Reichenbach, **E. Wolf**, and **G. J. Arnold**. Holistic differential analysis of embryo-induced alterations in the proteome of bovine endometrium in the preattachment period. *Proteomics 5, 2551-2560 (2005).*

D. Diehl, H. Lahm, **E. Wolf**, and S. Bauersachs. Transcriptome analysis of a human colorectal cancer cell line shows molecular targets of insulin-like growth factor-binding protein-4 overexpression. *Int. J. Cancer 113, 588-599 (2005).*

S. Hiendleder, S. Bauersachs, A. Boulesteix, **H. Blum**, **G. J. Arnold**, T. Fröhlich, and **E. Wolf**. Functional genomics: tools for improving farm animal health and welfare. *Rev. Sci. Tech. 24, 355-377 (2005).*

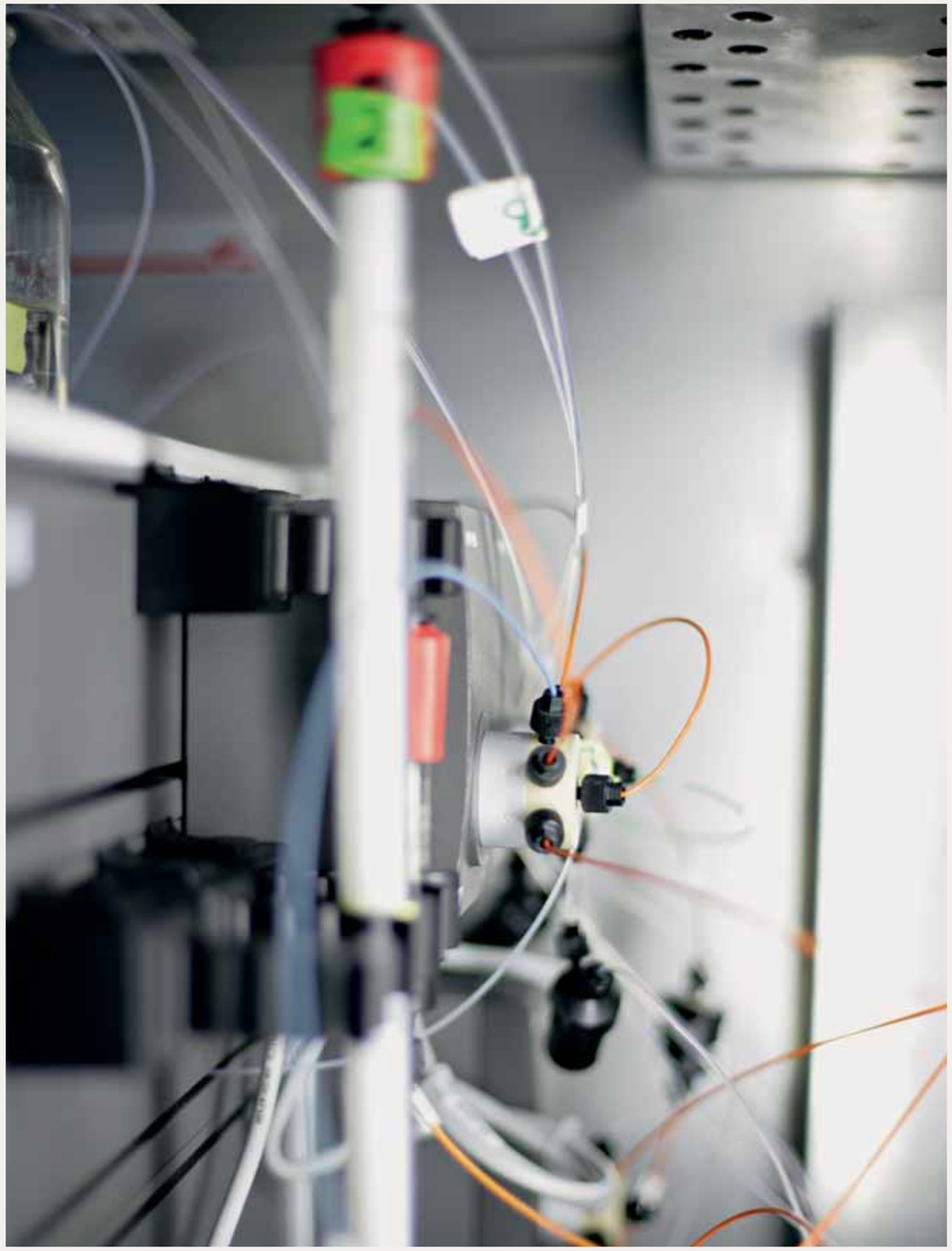
E. O. Hochleitner, B. Kastner, T. Fröhlich, A. Schmidt, R. Luhrmann, **G. Arnold**, and F. Lottspeich. Protein stoichiometry of a multiprotein complex, the human spliceosomal U1 small nuclear ribonucleoprotein - Absolute quantification using isotope-coded tags and mass spectrometry. *Journal of Biological Chemistry 280, 2536-2542 (2005).*

G. T. Bommer, C. J. Jager, E. M. Durr, S. Baehs, S. T. Eichhorst, T. Brabletz, G. Hu, T. Fröhlich, **G. J. Arnold**, D. C. Kress, B. Goke, E. R. Fearon, and F. T. Kolligs. DRO1, a gene down-regulated by oncogenes, mediates growth inhibition in colon and pancreatic cancer cells. *Journal of Biological Chemistry 280, 7962-7975 (2005).*

2004

S. Bauersachs, S. Rehfeld, S. E. Ulbrich, S. Mallok, K. Prelle, H. Wenigerkind, R. Einspanier, H. Blum, and **E. Wolf**. Monitoring gene expression changes in bovine oviduct epithelial cells during the oestrous cycle. *J. Mol. Endocrinol. 32, 449-466 (2004).*

J. Nicholls, P. Hahn, E. Kremmer, T. Fröhlich, **G. J. Arnold**, J. Sham, D. Kwong, and F. A. Grasser. Detection of wild type and deleted latent membrane protein 1 (LMP1) of Epstein-Barr virus in clinical biopsy material. *Journal of Virological Methods 116, 79-88 (2004).*



Service and patents

Roland Beckmann

- Coordinator of the Collaborative Research Center (Sonderforschungsbereich) SFB594 "Molecular Machines in Protein Translocation and Folding" since 2008
- Member of the Cluster of Excellence "Center for Integrated Protein Science" (CIPSM) since 2006
- Board member of the LMU Munich Department of Chemistry and Biochemistry since 2006
- Member of the Cluster of Excellence "Nanoinitiative Munich" since 2006
- Board member of the Sonderforschungsbereich SFB646 "Regulatory networks in genome expression and maintenance" since 2005
- Board member of the Department of Chemistry and Biochemistry, LMU Munich 2005-2007
- Member of the Swiss Light Source (SLS) scientific advisory board 2004-2006
- Member of the faculty board (Fakultätsrat) of the Faculty of Chemistry and Pharmacy, LMU Munich
- Member of the board of the DFG research grant network Transregio 5 "Chromatin – Assembly and inheritance of functional states" 2004 - 2008

Karl-Klaus Conzelmann

- 2005- Editorial board member of Journal of Virology
- 2001- Editorial board member of Virus Research
- Founding member and executive board member of SFB 455 Virus Functions and Immune Modulation

Patrick Cramer

- Advisory editorial board member of The EMBO Journal
- Member of the scientific advisory board of the Max Planck Institute for Developmental Biology Tübingen
- Member of the review panel for the Taiwan Institute of Molecular Biology 2008
- Member of the scientific-technological advisory board of the Bavarian state government
- Member of the selection committee for the Heinz Maier Leibnitz-Preis of the DFG since 2008
- Coordinator of the Collaborative Research Center (Sonderforschungsbereich) SFB646 "Regulatory networks in genome expression and maintenance" since 2008
- Dean of the Faculty of Chemistry and Pharmacy of LMU Munich since 2007
- Member of the research board (Forschungsrat) of LMU Munich since 2007
- Founding member and executive board member of the Cluster of Excellence "Center for Integrated Protein Science" (CIPSM) since 2006

Klaus Förstemann

- Mentoring of students for international exchange (since 2007)
- Member of the steering committee („Leitungskollegium"), Department of Chemistry and Biochemistry, LMU Munich (2008-2010)

Ulrike Gaul

- Co-organizer of the Janelia Farm Conference "Visual Processing in Insects: From Anatomy to Behavior" (2007)
- Temporary member of the GCAT (Genomics, Computational Biology and Technology) study section, NIH (2006, 2007)
- Temporary member of the NDPR (Neurodifferentiation, Plasticity, and Regeneration) study section, NIH (2005)

Karl-Peter Hopfner

- Editorial board of Biophysical Chemistry
- Proposal reviewer for various funding agencies
- Reviewer for various scientific journals
- Co-Chair of the International Conference on Hybrid Methods, Lake Tahoe, USA (2006).
- Session Chair at The EMBO Conference 2009.

Ulrich Koszinowski

- Coordinator of Collaborative Research Center SFB 455 "Viral function and immune modulation" 1999-2010.
- Member of Leopoldina, Halle (since 1999)
- Board member of Gesellschaft für Virologie (since 2004)
- Member of Center of Advanced Studies[LMU] (since 2008)
- Member of the Faculty of Medicine Research Commission, LMU Munich (since 2006)
- Managing Director of Max von Pettenkofer Institute since 2008

PATENTS

- 2006 – Europ. Patent Nr. 996738: Recombinant Vector Containing Infectious, Viral Genome Seqences Greater Than 100 KB, Method For Producing Same and Use For The Mutagenesis Of The Viral Sequences.

Dierk Niessing

- Deputy Director of the Institute of Structural Biology (Director: Prof. Michael Sattler), Helmholtz Zentrum München, since 2008
- Commission Member of the Helmholtz Zentrum München to establish a concept for the support of young scientists, 2007.
- Organizer of the monthly Faculty Club at the Gene Center, since 2007.
- Representative of the Helmholtz Association at the Annual GAIN Initiative Meeting in Boston, USA, 2007
- Representative of the Helmholtz Association at the European Career Fair at MIT in Boston, USA, 2007
- Representative of the Tenure-Track group leaders of the Helmholtz Zentrum München, since 2006

Johannes Söding

- Frequent reviewer for Bioinformatics, BMC Bioinformatics, Nucleic Acids Research
- Occasional reviewer for BMC Genomics, BMC Struct. Biol., FEBS Letters, J Struct. Biology, PloS ONE, Proteins, Protein Science, Trends in Genetics
- Editorial board member for the ISMB 2006 in the Structural Biology and in the Sequence Analysis section
- Editorial board member for the ISMB 2007 in the Sequence Analysis section

Katja Sträßer

- Associated member of the Cluster of Excellence "Center for Integrated Protein Science" (CIPSM) and board member of its gender equality program since 2006
- Reviewer of publications submitted to Genes and Development, MCB, JBC, FEBS Letters, Biological Chemistry, FASEB
- Reviewer of EMBO long-term and short-term postdoctoral fellowship applications
- Reviewer of grant proposals to the German Research Foundation (DFG), the Swiss National Science Foundation (SNF), and the American National Science Foundation (NSF)

Achim Tresch

- Reviewer for Bioinformatics, PNAS, J. Comp. Biol.
- Chair of the working group "Statistical Methods in Bioinformatics" of the GMDS and German Section of the International Biometric Society
- Vice-Chair of the interdisciplinary working group "Bioinformatics" at Johannes Gutenberg University, Mainz

Daniel N. Wilson

- Member of the RNA Society
- Associate member of the Cluster of Excellence "Center for Integrated Protein Science" (CIPSM)
- Member of IMPRS
- Referee for Scientific Journals: NSMB, Mol. Cell, PNAS, EMBO J., NAR, RNA, JMB, JBC, AAC, etc

PATENTS

- (WO/2008/046584) LEPA AS A TARGET FOR ANTIBACTERIAL AGENTS
- (WO/2007/003410) USE OF LEPA FOR IMPROVING THE ACCURACY OF PROTEIN SYNTHESIS IN VITRO
- (WO/2006/059807) SCREENING METHOD FOR RIBOSOME RECYCLING INHIBITOR

Eckhard Wolf

- Dean for Research, Faculty of Veterinary Medicine, LMU Munich (since 2008)
- Co-ordinator of the BMBF-FUGATOplus Network REMEDY – Reproduction and metabolic problems of dairy cows (since 2008)
- Co-founder and Scientific Director of MWM Biomodels GmbH, Tiefenbach (since 2008)
- Board member of the Department of Veterinary Sciences, LMU Munich (since 2008)
- Scientific advisor of Minitüb GmbH (since 2007)
- Head of the scientific board for the BMBF program FUGATO (since 2003)
- Member of the DFG-Senatskommission „Grundsatzfragen der Gentechnik" (since 2006)
- Member of the DFG-Senatskommission „Stoffe und Ressourcen in der Landwirtschaft" (since 2006)
- Member of the DFG-Senatskommission „Tierexperimentelle Forschung" (since 2003)
- Board member of the Research Center Biomodels Austria, University of Veterinary Medicine, Vienna (since 2005)
- Member of the DFG-Fachkollegium 207 (since 2005)
- Deputy member of the coordination committee for German National Genome Research Network (NGFN) (2002-2007)
- Member of the Board of the Bavarian State Institute for Agriculture (since 2003)
- Scientific director of the Bavarian Research Center for Biology of Reproduction e.V. (since 2000)
- Co-ordinator of the BMBF-FUGATO Network FERTILINK – Functional genome research for the improvement of fertility (2005-2008)
- Speaker of the DFG Research Unit 478 "Mechanisms of embryo-maternal communication" (since 2003)
- Member of the faculty board (Fakultätsrat) of the Faculty of Veterinary Medicine, LMU Munich (since 2000)
- Coordinator (together with Martin Hrabé de Angelis) of the Munich ENU Mouse Mutagenesis Project (1999-2004)

PATENTS

- PCT/EP2008/007422 "De novo formation of artificial chromosomes in primary cells and their uses in xenotransplantation, cell and gene therapy" (filed 10.09.2008)
- EP 08 000 111.8 and US 61/019,001 "Transgenic pig with altered incretin function" (filed 05.01.2008)
- EP 07 017 102.0 "Method for categorizing samples containing spermatozoa by molecular profiling" (filed 31.08.2007)
- US 6,586,185 B2 "Use of polypeptides or nucleic acids for the diagnosis or treatment of skin disorders and wound healing and for the identification of pharmacologically active substances" (issued 01.07.2003)

Ralf-Peter Jansen

- Member of the Cluster of Excellence "Center for Integrated Protein Science" (CIPSM), 2006-2008
- Coordinator of the Sonderforschungsbereich SFB646 "Regulatory networks in genome expression and maintenance" 2004-2008
- Member of the board of the DFG research grant network FOR426 "Complex RNA-protein interactions in the maturation and function of eukaryotic mRNA", 2004-2007.

Claudia Petritsch

- Reviewer for various scientific journals

Stefan Weiss

- Member of the Editorial Board of the journal "Prion" (since 2008)
- Member of the Editorial Advisory Boards of the "Open Infectious Diseases Journal" (since 2008)
- Reviewer for scientific journals and funding agencies

PATENTS

- Little M, **Weiss, S.** (Applicants) (PCT patent application). WO/2005/035580; PCT/EP/2004/011268 103. Single Chain Antikörper gegen den 37 kDa/67 kDa Lamininrezeptor als Werkzeuge zur Diagnostik und Therapie von Prionerkrankungen und Krebs, deren Herstellung und Verwendung.
- Little M, Knackmuss S, Reusch U, Kipriyanov S, LeGall F, Mick V, Hoffmann K, Röttgen P, and **Weiss S.** EP 1709972 A1. Application No: 05007380.8; Use of an antibody against the laminin receptor or laminin receptor precursor for the treatment or diagnosis of several cancer types.

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PATENTS

- PCT/EP2008/007422 "De novo formation of artificial chromosomes in primary cells and their uses in xenotransplantation, cell and gene therapy" (filed 10.09.2008)
- EP 08 000 111.8 and US 61/019,001 "Transgenic pig with altered incretin function" (filed 05.01.2008)
- EP 07 017 102.0 "Method for categorizing samples containing spermatozoa by molecular profiling" (filed 31.08.2007)
- US 6,586,185 B2 "Use of polypeptides or nucleic acids for the diagnosis or treatment of skin disorders and wound healing and for the identification of pharmacologically active substances" (issued 01.07.2003)

Seminars

Name		Institute	Title	Date
2008				
Neugebauer	**Carla**	MPI-CBG Dresden	Making snRNPs: essential regulatory roles for RNA polymerase II and Cajal bodies	14.01.08
Najmanovitch	**Ramon**	EBI Cambridge	Towards a systems level understanding of molecular recognition	15.01.08
Manke	**Thomas**	MPI for Molecular Genetics, Berlin	Quantitative models of regulatory interactions and molecular networks	15.01.08
Müller	**Dirk**	ETH Zürich	Control Mechanisms in the Synthesis of Molecular Machines	15.01.08
Beissbart	**Tim**	DKFZ Heidelberg	Use of statistical data modeling to uncover biological pathways	15.01.08
Lehmann	**Maik**	Universität Heidelberg	Systems Surfology: Exploring the fascinating world of surfing viruses	15.01.08
Lindquist	**Jonathan**	Universität Magdeburg	Modeling T-cell Activation	15.01.08
Korbel	**Jan**	Yale University	Mapping Genome Structural Variation Using Novel Functional Genomics Approaches	15.01.08
Tresch	**Achim**	Universität Mainz	Probabilistic Models that uncover the hidden Information Flow in Signalling Networks	15.01.08
Sigrist	**Stephan**	Bio-Imaging Center Würzburg	Shedding light in assembly of synapse structure and function	21.01.08
Walter	**Tobias**	MPI für Biochemie, Martinsried	Making fat cells? The cell biology of lipid storage	28.01.08
Antequera	**Francisco**	Universidad Salamanca	DNA replication initiation at human promoter regions	18.02.08
Gerber	**André**	ETH Zürich	Global analysis of RNA-protein interactions	25.02.08
Gasser	**Susan**	Friedrich Mischer Institute for Biomedical Research, Basel	Spatial concerns as part of an epigenetic program: lessons from worms and yeast	17.03.08
Jossinet	**Fabrice**	Université Louis Pasteur, Strasbourg	PARADISE: a bioinformatics framework to study and construct RNA architectures	07.04.08
Kunkel	**Thomas**	NIEHS	Division of labor at the eukaryotic replication fork	14.04.08
Yang	**Wei**	NIDDK	Stop-action movie of UvrD helicase unwinding DNA 1 base pair per step	05.05.08
Wente	**Susan**	Vanderbilt University Medical Center	Regulation of nucleocytoplasmic transport	19.05.08
Famulok	**Michael**	Universität Bonn	Exploring chemical space with aptamers	16.06.08
Gaul	**Ulrike**	Rockefeller University, New York	The role of glia in nervous system development	30.06.08
Voit	**Eberhard**	Georgia Tech and Emory University	Mathematical modeling of combined genomic and metabolic systems	07.07.08
Vassylyev	**Dimitry**	University of Alabama at Birmingham	Structural studies of bacterial RNA polymerase	14.07.08
Gross	**David**	Louisiana State University Health Sciences Center	Protein complexes that dynamically regulate heat shock gene transcription in yeast	24.07.08
Schroeder	**Gunnar**	Stanford University School of Medicine	Towards high resolution structure from low resolution data	19.09.08
Verma	**Prof. Inder**	Salk Institute, La Jolla, California, USA	Cancer: a malady of genes	22.09.08
Cravatt	**Benjamin F.**	The Scripps Research Institute, La Jolla, USA	Mapping dysregulated biochemical pathways in human disease by activity-based proteomics	13.10.08
Neher	**Erwin**	Max-Planck-Institut für biophysikalische Chemie, Göttingen	Multiple Roles of Calcium Ions in the Regulation of Neurotransmitter Release	15.10.08
Grosse	**Frank**	Leibniz Institut für Altersforschung	Cdc45 and TopBP1 at the initiation step of DNA replication	20.10.08
Tainer	**John**	The Scripps Research Institute, La Jolla, USA	XPD and Mrell/Rad50/Nbs1 Complexes: Structural insights into the cancer and aging phenotypes from mutations of these genome guardians	27.10.08
Westhof	**Eric**	Université Louis Pasteur, Strasbourg	The elementary modules of RNA architecture	10.11.08
Danner	**Stefan**	Maiwald Patentanwalts GmbH	Patenting of biotech inventions – strategies and pitfalls	18.11.08
Römling	**Ute**	Karolinska Institut, Stockholm	Characterisation of c-di-GMP signalling in Salmonella typhimurin	24.11.08
Kuhn	**Andreas**	Universität Hohenheim	Membrane protein insertion in bacteria	01.12.08
2007				
Labib	**Karim**	Paterson Institute for Cancer Research, University of Manchester	Studying the cell cycle by functional proteomics	22.01.07
Llorca	**Oska**	Centro de Investigaciones Biològicas, Madrid	Repair of DNA damage by large macromolecular complexes visualized in 3D using Electron microscopy	29.01.07
Tora	**Laszlo**	IGBMC, Strasbourg	Regulation of RNA polymerase II transcription at the minimal promoter level	05.02.07
Topf	**Maya**	University of California, San Francisco	Refinement of protein structures by combining comparative modeling and cryoEM density fitting	12.02.07
Sinning	**Irmgard**	Universität Heidelberg	Regulation of protein transport by the SRP systems: are three components enough?	26.02.07
Görlich	**Dirk**	Universität Heidelberg	Transport through nuclear pore complexes	05.03.07
Yuyupov	**Marat**	IGBMC Illkirch	X-ray study of mRNA movement on the ribosome	02.04.07
Hahn	**Steven**	The Fred Hutchinson Cancer Research Center	Mechanisms of RNA polymerase transcription initiation and activation	16.04.07
Fried	**Michael**	University of Kentucky	06 Alkylguanine-DNA Alkyltransferase: new functions from a guardian of the genome	23.04.07
Frey	**Erwin**	LMU Munich	Modeling of stochastic processes in biology: intracellular transport, cell motility and biodiversity	07.05.07
Djabali	**Karima**	Columbia University, College of Physicians & Surgeons	Hutchinson-Gilford progeria lamin A-biomarker for aging	04.06.07
Vassylyev	**Dmitry**	University of Alabama at Birmingham	Structural studies of prokaryotic transcription intermediates	11.06.07
Auble	**David**	University of Virginia	Regulation of transcription preinitation complex assembly and dynamics	25.06.07
Blobel	**Günter**	Rockefeller University, New York	Traffic through the nuclear pore complex	10.07.07
Hoijmakers	**Jan**	Erasmus University Rotterdam	Impact of DNA damage and repair on cancer, aging and life span extension	12.10.07
Livneh	**Zvi**	Weizmann Institute Rehovot	Regulation and mechanism of translesion DNA synthesis (error-prone repair) in mammalian cells	12.10.07
Wigley	**Dale**	Imperial College London	Structure and Mechanism of RecBCD	12.10.07
Lamond	**Angus**	Wellcome Trust Center Dundee	A dual imaging & proteomics strategy for studying protein organisation and dynamics in mammalian nucleoli	12.10.07
Tschochner	**Herbert**	Universität Regensburg	Aspects on eukaryotic ribosome biogenesis	12.10.07
Brickner	**Jason**	Northwestern University, Evanston, USA	Epigenetic regulation of gene expression through subnuclear localization	12.10.07
Mellor	**Jane**	Oxford University	A signal transduction pathway controlling dynamic H3K4me3 on active genes	12.10.07
Thoma	**Fritz**	ETH Zürich	Shining light on chromatin structure and dynamics in yeast	12.10.07
Maquat	**Lynne**	Rochester University	In mammalian cells, the pioneer translation initiation complex is poised for nonsense-mediated mRNA decay	12.10.07
Steinmetz	**Lars**	EMBL Heidelberg	Comparing transcriptome maps in yeast	12.10.07
Harvey	**Jagger**	Norwich University	The butterfly's storm: small RNAs as network initiators and modulators	12.10.07
Hentze	**Matthias**	EMBL Heidelberg	Control of protein synthesis by miRNAs and regulatory RNA-binding proteins	12.10.07
Singer	**Robert**	Rockefeller University, New York, USA	Modeling the synthesis and behavior of mRNA	12.10.07
Pieler	**Thomas**	Universität Göttingen	Structural and functional aspects of vegetal localization complexes in Xenopus oocytes and embryos	12.10.07
Wahle	**Elmar**	Universität Halle	Post-transcriptional gene regulation in Drosophila: hsp70 and nanos mRNAs	12.10.07
Jessberger	**Rolf**	TU Dresden	Mammalian cohesins, meiosis and aneuploidies	05.11.07
Gaul	**Ulrike**	The Rockefeller University New York	Decoding regulatory networks: transcription and translation control in Drosophila	12.11.07
Locher	**Kaspar**	ETH Zürich	Structure and mechanism of ABC transporters facilitating bacterial nutrient uptake or multidrug extrusion	19.11.07
Micura	**Ronad**	Leopold Franzens University Innsbruck	Chemical synthesis for RNA structural biology	03.12.07
Melchior	**Frauke**	Universität Göttingen	Mechanism, function and regulation of SUMOylation	10.12.07
Grubmüller	**Helmut**	MPI for Biophysical Chemistry, Göttingen	Molecular dynamics simulations of biological nanomaschines: May the force be with you	17.12.07

Name		Institute	Title	Date
2006				
Kräusslich	**Hans-Georg**	Universität Heidelberg	Assembly and inhibition of human immunodeficiency virus	09.01.06
Nissen	**Poul**	Aarhus University	Structure and function of the calcium pum	23.01.06
Carmo-Fonseca	**Maria**	IMM, University of Lisbon	Imaging spliceosome dynamics in live cells	30.01.06
Braun	**Thomas**	MPI for Heart and Lung Research, Kerckhoff-Institute, Bad Nauheim	Molecular determinants of mammalian stem cell differentiation and maintenance	06.02.06
Griesinger	**Christian**	MPI Göttingen, Karl-Friedrich Bonhoeffer-Institut	Parkinson disease in NMR spectroscopic view	13.02.06
Wilson	**Daniel**	MPI for Molecular Genetics, Berlin	Understanding the structure and function of the universal translator, the ribosome	20.02.06
Hell	**Stefan**	MPI Göttingen	Fluorescence nanoscopy: breaking the diffraction barrier by the RESOLFT concept	06.03.06
Paro	**Renato**	ZMBH Heidelberg	Epigenetics of tissue regeneration and remodelling	13.03.06
Hinnebusch	**Alan**	NIH Bethesda, USA	Mechanisms of coactivator recruitment in transcriptional activation by GCN4	20.03.06
Holstege	**Frank**	UMC Utrecht	Genome-wide transcription regulation and Mediator	03.04.06
Valcarel	**Juan**	ICREA and Centre de Regulacio Genomica, Barcelona	Mechanisms of alternative splicing regulation	10.04.06
Wedlich-Söldner	**Roland**	MPI für Biochemie, Martinsried	Novel insight into the actin organization of budding yeast	08.05.06
Roeder	**Bob**	Rockefeller University, New York	The role of diverse coactivators in transcriptional regulation in animal cells	21.06.06
Nickelsen	**Jörg**	Ruhr Universität Bochum	Regulatory networks in chloroplast gene expression	03.07.06
Forest	**Katarina**	UW-Madison, Dept. of Bacteriology, Wisconsin	Structural and functional biology of the pilus retraction motor PilT	24.07.06
Famulok	**Michael**	Universität Bonn	Exploring chemical space with aptamers	09.10.06
Nehrbass	**Ulf**	Institut Pasteur, Korea	Regulatory networks in genome expression and maintenance	16.10.06
Plückthuhn	**Andreas**	Universität Zürich	Repeat proteins as tailor-made binding reagents	30.10.06
Zweckstätter	**Markus**	MPI für Biophysikalische Chemie, Göttingen	High-resolution views of protein misfolding and of a membrane protein-inhibitor complex	06.11.06
Jensen	**Torben**	Aarhus University	Quality control of mRNP formation	20.11.06
Driessen	**Arnold**	Universität Groningen	The bacterial Sec translocase, a remarkable machine	27.11.06
Rospert	**Sabine**	Universität Freiburg	Ribosome-associated chaperones – dynamics at the tunnel exit of eukaryotic ribosomes	04.12.06
Kapanidis	**Achillefs**	University of Oxford	Dissecting transcription mechanisms using single-molecule fluorescence	11.12.06
Darzacq	**Xavier**	Ecole Normale Supérieure, Paris	Observing transcriptional events in live cells	18.12.06
Klipp	**Edda**	MPI for Molecular Genetics, Berlin	Computational analysis of cellular stress response	20.12.06
Stark	**Alexander**	MIT, Cambridge, USA	Comparative genomics of 12 Drosophila genomes	20.12.06
Devos	**Damien**	EMBL Heidelberg	Structural characterization of protein complexes	20.12.06
Söding	**Johannes**	MPI for Developmental Biology, Tübingen	New methods for protein structure and function prediction	20.12.06
2005				
Stojkovivc	**Miodrag**	University of Newcastle	Human embryonic stem cells: from bench to bedside	31.01.05
Posern	**Guido**	MPI Martinsried	Connecting the cytoskeleton to transcriptional control: The RHO-Actin-SRF signalling pathway	07.02.05
Kühlbrandt	**Werner**	MPI Frankfurt	Molecular mechanisms of photoprotection in the plant Light complex LHC-II	14.02.05
Egly	**Jean-Marc**	IGBMC Strasbourg	TFIIH dysfunctions originate genetic discorders due to both DNA repair and transcription defects	21.02.05
Behrens	**Axel**	London Research Institute	Transcriptional control by MAP kinases in neurons and T cells	28.02.05
Mann	**Matthias**	University of Southern Denmark, Odense	State of the art mass spectrometric technologies applied to organellar and signalling proteomics	14.03.05
Kretzschmar	**Hans**	LMU Munich	New finding on the function of PrP and the therapy of prion diseases	11.04.05
Gaub	**Hermann**	LMU Munich	Nano-manipulation: the art of touching molecules	18.04.05
Proudfoot	**Nick**	Sir William Dunn School of Pathology, University of Oxford	Connecting transcription to RNA processing in eukaryotes	25.04.05
Hernandez	**Nouria**	Universitè de Lausanne	Mechanisms of basal and regulated human RNA polymerase II and III transcription	02.05.05
Mapp	**Anna**	University of Michigan	Small molecule replacements of transcriptional activation domains	30.05.05

Name		Institute	Title	Date
Schröder	**Renée**	University of Vienna	RNA folding and proteins with RNA chaperone activity	20.06.05
Libri	**Domenico**	C.N.R.S	Spurious transcription and nuclear degradation: a Penelope's strategy?	27.06.05
Ha	**Taekjip**	University of Illinois	Single-molecule views of nature's nano-machines	11.07.05
Schramke	**Vera**	CNRS-IBSM, Marseilles	RNAi-directed chromatin modification coupled to RNA polymerase II transcription in fission yeast	25.07.05
Steitz	**Thomas**	Yale University, USA	Motion in macromolecular machines	14.09.05
Vindigni	**Alessandro**	ICGEB Trieste, Italy	Biochemical and structural characterization of the human RECQ1 helicase	19.09.05
Kanaar	**Roland**	Erasmus University Rotterdam	Dynamics of genome maintenance processes	14.10.05
Gasser	**Susan**	FMI Basel	Chromatin and long-range chromosomal structure in the nucleus	14.10.05
Buratowski	**Steven**	Harvard Medical School, Boston, USA	Connecting transcription with mRNA processing	14.10.05
Hurt	**Ed**	Universität Heidelberg	Connections between transcription and nuclear transport	14.10.05
Tollervey	**David**	Wellcome Trust Center Edinburgh	The tail of A-degrading activity	14.10.05
Teichmann	**Sarah**	EBI Hinxton	Regulating the regulators	14.10.05
Allain	**Frederic**	University of Zürich	Studying alternative splicing using NMR	14.10.05
Beckmann	**Roland**	Charite Berlin	Structural basis of protein sorting	14.10.05
Ellenberg	**Jan**	EMBL Heidelberg	Dynamic and function of SMC complexes	14.10.05
Herr	**Winship**	ISREC Lausanne	Regulating the human chromosome cycle	14.10.05
Brückner	**Katja**	Harvard Medical School, Boston	Drosophila models for cancer development	24.10.05
Ficner	**Ralf**	Universität Göttingen	Structural basis for the m3G-cap mediated nuclear Import of spliceosomal snRNPs	14.11.05
Grothe	**Benedikt**	LMU Munich	Temporal processing in the mammalian auditory system – new roles for synaptic inhibition	21.11.05
Meister	**Gunter**	MPI für Biochemie, Martinsried	Biochemical dissection of human RNA silencing pathways	05.12.05
2004				
Haas	**Christian**	Adolf-Butenand-Institut, Munich	The 100-year anniversary of Alzheimers's disease research: The secret of secretases	19.01.04
Werten	**Sebastian**	IGBMC Strasbourg	The structural biology of RNA polymerase II coactivators	26.01.04
Treisman	**Richard**	Cancer Research UK London	Regulation of transcription by MAP kinease Cascades and actin dynamics	16.02.04
Buerstedde	**Jean-Marie**	GSF München	The beauty contest of immunoglobin gene diversification	23.02.04
Uhlmann	**Frank**	London Research Institute	The mechanisms of sister chromatid cohesion and segregation	27.02.04
Dittmer	**Wendy**	LMU Munich	Functional DNA-based nanomachines	08.03.04
Spahn	**Christian**	Humboldt Universität, Berlin	Hijacking of the translational machinery by viral IRES RNAs - structural investigations using cryo-EM	13.03.04
Laufs	**Jürgen**	Ingenium Pharmaceuticals AG Munich	ENU mutagenesis in forward and reverse genetics: fast generation of genetic variants for functional analysis and target identification in mice and rats.	29.03.04
Musacchio	**Andrea**	University of Milan	A mechanism of signal propagation in the spindle checkpoint based on the MAD2 conformational switch	19.04.04
Ulrich	**Helle**	MPI Marburg	Control of genome stability by ubiquitin and SUMO	26.04.04
Mayer	**Thomas**	MPI für Biochemie, Munich	Small molecules: Versatile probes to study the functions of kinesins in mitosis	03.05.04
Thomm	**Michael**	Universität Regensburg	Mechanism and regulation of transcription in the hyperthermophilic archaeon Pyrococcus furios	24.05.04
Edenhofer	**Frank**	Universität Bonn	Engineering stem cells by protein transducrion	07.06.04
Stemman	**Olaf**	MPI für Biochemie, Munich	Novel regulation of sister chromatid separation and mitotic exit in vertebrates	21.06.04
Lehner	**Christian**	Universität Bayreuth	Controlling progression through mitotic and meiotic divisions	02.08.04
Winterhager	**Elke**	Universität Duisburg-Essen	Connexins play an obligate role during placental development	04.10.04
McAllister	**William**	Morse Institute of Molecular Genetics, New York	Structural aspects of transcription by T7 RNA polymerase	11.10.04
Jung	**Kirsten**	LMU Munich	Molecular mechanisms of stimulus perception by Escherichia coli and modular analysis of the signal transduction network	08.11.04
Goody	**Roger**	MPI for Molecular Physiology, Dortmund	Structural and mechanistic investigations on the regulation of intracellular vesicular transport	15.11.04
Czaplinski	**Kevin**	EMBL Heidelberg	"40-Lo VE is required for localization of the XenopusTGF-Beta (VG1) mRNA during oogenesis	22.11.04
Nickel	**Walter**	Universität Heidelberg	Unconventional mechanisms of eukaryotic protein secretion	06.12.04
Aloy	**Patrick**	EMBL Heidelberg	The third dimension for protein interactions and complexes	20.12.04

Gene Center in the media

ROLAND BECKMANN

Date	Title	Source
2007	„Wie Proteine fertig gemacht werden“	Einsichten LMU Munich
29 October 2006	“New Details about the Molecular Post Room in Cells“.	Max Planck Society
24 August 2006	„Aller guten Dinge sind drei, Mysteriöses Molekül der Proteinsynthese in Hefe entschlüsselt“.	LMU Munich
12 May 2006	“The Molecular Post Office Inside the Cell“.	Max Planck Society
04 May 2006	„Auf den Spuren der zellulären Sortiermaschine, LMU-Professor erzielt Durchbruch in Proteinforschung“.	LMU Munich
July 2005	„Funktion folgt Form – Aufklärung der Proteinsortierung mit Schockgefrorenem“.	Laborjournal

KARL-KLAUS CONZELMANN

12 October 2006	Molekulare „Unterschrift“ schützt Zellen vor Viren - Forscher enträtseln Mechanismus der Immunabwehr	LMU Munich

PATRICK CRAMER

13 October 2008	„Beobachtung der RNA-Entstehung verfeinert: Positionierungssystem liefert verlässliche Fehlerabschätzung“.	LMU Munich
06 October 2008	„Patrick Cramer erhält Forschungspreis der Bayer Science & Education Foundation“.	LMU Munich
02 October 2008	„Familie-Hansen-Preis 2009 geht an Prof. Dr. Patrick Cramer“.	Presse-Information, Bayer AG
28 December 2007	„Nachschub für die Massenproduktion – Zentraler Apparat des Zellwachstums sichtbar gemacht“.	LMU Munich
28 December 2007	„Pfad der RNA enthüllt - Satelliten-Navigation für Biomoleküle“.	LMU Munich
14 November 2007	„Vom Ursprung der biologischen Evolution – Blick in die Zelle zeigt frühes Protein aus der RNA-Welt“.	LMU Munich
09 February 2007	„Warten auf den Reparaturdienst der Zelle – Wie gefährliche DNA-Schäden gefunden werden“.	LMU Munich
16 January 2007	„Vom Quantensimulator bis zum neuen „Homo Oeconomicus“. Vier zukunftsweisende Forschungsprojekte mit dem Forschungspreis der Philip Morris Stiftung ausgezeichnet“.	LMU Munich
16 January 2007	„Philip Morris Forschungspreis 2007 für LMU-Professor – Biochemiker Patrick Cramer untersucht Übersetzung der Gene“.	LMU Munich
05 October 2006	„Chemie Nobelpreis für Genforscher Kornberg – LMU Wissenschaftler Cramer maßgeblich an Arbeit beteiligt“.	LMU Munich
02 December 2005	„Leibniz-Preis für LMU-Professoren Cramer und Krausz“.	LMU Munich
29 October 2004	„Zwei Forschungspreise gehen an LMU-Forscher – Genzentrum nimmt international Spitzenstellung ein“.	LMU Munich
08 July 2004	„Partnerwechsel wie am Fliessband - Enzymdomäne verknüpft Prozesse im Zellkern“.	LMU Munich
May 2008	„Struktur von RNA-Polymerasen – Lost in Transcription“.	Laborjournal
December 2007	„Forschungsprofessur in LMUexzellent - Vorstoß zu den Geheimnissen der Gene“.	Münchner Uni Magazin
15 November 2007	“Allowing an élite“.	Nature
25 October 2007	„Die Denker der Zukunft“.	Capital

Date	Title	Source
13 July 2007	„Tiefer Blick in die Gene – das Rätsel der DNA-Schrift“.	Bayerische Staatszeitung
2007	„Großes Kino aus der Zelle“.	Artikel der Philip-Morris-Stiftung
17 January 2007	„Der Abräumer – LMU-Professor Patrick Cramer (37) wird mit Philip-Morris-Forschungspreis ausgezeichnet“.	Die Welt
05 October 2006	„Sprachrohr des Erbguts“.	Süddeutsche Zeitung
05 October 2006	„Nobelpreis fürs Kopieren”.	Der Tagesspiegel
05 October 2006	„Geheimnisvolle Kopiermachine”.	Die Welt
05 October 2006	„12 Köpfe für Münchens Zukunkf”.	Münchner Abendzeitung
04 October 2006	„Chemie-Nobelpreis an Roger Kornberg für Eukaryotische Transkription – Münchner LMU-Forscher war der Erstautor der gewürdigten Arbeit”.	vdbiol, Verband deutscher Biologen und biowissenschaftlicher Fachgesellschaften e.V.
04 October 2006	„Charismatischer Forscher mit Weitblick”.	Deutschlandfunk
July 2006	„Genzentrum München – Brain Drain einmal umgekehrt”.	BIOspektrum
2006	„Der Pol-Forscher”.	Einsichten LMU München

ULRIKE GAUL

18 November 2008	„Alexander von Humboldt-Professur: Pressekonferenz mit Preisträgern in Berlin“	Alexander von Humboldt-Stiftung
15 October 2008	„Alexander von Humboldt Professuren vergeben“	Bundesministerium für Bildung und Forschung; Alexander von Humboldt-Stiftung
15 October 2008	„Zwei der erstmals vergebenen Alexander von Humboldt-Professuren gehen an die LMU“	LMU Munich
17 October 2005	„Specialized ‘GPCR‘ proteins are the key to protecting the fly brain”	Rockefeller University
05 July 2005	“Size doesn’t matter – Rockefeller scientists show that microRNAs play an essential role in the development of the fruit fly”	Rockefeller University
03 December 2008	„Die Wechsel-Wirkung – Systembiologin Ulrike Gaul kommt von der Rockefeller University an das Genzentrum der LMU“	Süddeutsche Zeitung
03 December 2008	„Ulrike Gaul: Die pragmatische Abenteurerin“	biotechnologie.de
01 December 2008	„Man spürt Aufbruchstimmung”	Focus Magazin
01 December 2008	Bericht in der „Abendschau”	Bayerisches Fernsehen
28 November 2008	„Ich bin keine Quotenfrau”	die tageszeitung
27 November 2008	„Molekularbiologin: Deutschland ist ein attraktiver Forschungsstandort“ – Interview für “Informationen am Morgen”	Deutschlandfunk
16 October 2008	„Auf Exzellenz-Shoppingtour”	Focus online
15 October 2008	„Humboldt für fünf Millionen“	Frankfurter Rundschau; dpa
01 May 2008	“Bring out your dead cells – Support cells in the fruit fly brain moonlight as undertakers”	ScienceNews

KARL-PETER HOPFNER

25 April 2008	Blinder Passagier mit Potenzial Neues Molekül und neue Enzymfunktion für das Erkennen von DNS-Brüchen in Bakterien entdeckt	LMU Munich
14 February 08	Flexibel in Form für die DNA Bindungsmodell eines Enzyms aufgeklärt	LMU Munich
01 February 2008	Kampf den Freibeutern – Wie der Körper virale Moleküle erkennt	LMU Munich
09 November 2007	Resistenz bei Chemotherapie: Wie sich Tumoren gegen den Wirkstoff Cisplatin wehren	LMU Munich
11 June 2007	Neue Erkenntnisse zur Erbgut-Verdoppelung: LMU-Forscher analysieren Helikasen-Struktur	LMU Munich
2006	„Die Zelle und ihr Publikum“	Einsichten LMU Munich
May 2005	Wie DNA entkleidet und HIV geholfen wird – Zwei LMU-Publikationen aus der Strukturforschung	LMU Munich

Date	Title	Source
08 October 2004	Molekularer Klebstoff für das Erbmaterial – Ringförmige Proteinkomplexe halten DNA-Strukturen	LMU Munich
09 November 07	Hartnäckiger Krebs: Warum Chemotherapie manchmal wirkungslos ist	Süddeutsche Zeitung (Wissen)
08 November 2007	Resistenz bei Chemotherapie geklärt	Wiener Zeitung
08 November 2007	Forscher klären Resistenz gegen Chemotherapie	Frankfurter Neue Presse
08 November 2007	Resistenz bei Chemotherapie – Ursachen gefunden	n-TV
08 November 2007	Warum Chemotherapie manchmal nicht hilft	Welt Online
08 November 2007	Forscher klären Resistenz gegen Chemotherapie	Handelsblatt
08 November 2007	Forscher klären Resistenz gegen Chemotherapie	Schwäbische Zeitung online
01 February 2008	Wie sich Tumoren gegen den Wirkstoff Cisplatin wehren	Deutsche Zeitschrift für klinische Forschung

DIERK NIESSING

05 December 2007	Zellulärer Frachtverkehr – Die Ladung hilft beim Bau der Lokomotive	LMU Munich & GSF – Nationales Forschungszentrum für Umwelt und Gesundheit
02 June 2005	Transportproteine vernetzen GSF und LMU. Neue Helmholtz-Nachwuchsgruppeuntersucht den Güterverkehr in der Zelle	LMU Munich & GSF – Nationales Forschungszentrum für Umwelt und Gesundheit
24 March 2005	Brain Gain: Recruiting and keeping excellent young scientists	Helmholtz Gemeinschaft
January 2007	Rückkehr aus dem gelobten Land – vom Brain Drain zum Brain Gain	Münchner UniMagazin
30 August 2006	Akademische Migrationsbewegung – Forschung braucht flache Hierarchien	Süddeutsche Zeitung
May 2006	Beschäftigungsperspektiven in Deutschland – Deutscher Wissenschaftsnachwuchs tagt in Boston	GSF - Aktuell
February 2006	Brain Gain in Boston – Helmholtz Gemeinschaft auf der European Career Fair	GSF - Aktuell
February 2006	Eine Chance für junge Wissenschafter	GSF - Aktuell
16 October 2005	Kampf um die besten Köpfe	Welt am Sonntag
07 October 2005	Von den Guten die Besten	FAZ.NET
08 June 2005	Ein Modell für den Informationsfluss: Molekularbiologe Niessing untersucht den Erbgut-Transport in der Zelle – mit einer Forschergruppe, bei der Universität und GSF kooperieren.	Süddeutsche Zeitung

KATJA STRÄSSER

01 June 2007	Eine Kinase mit zwei Arbeitsplätzen – LMU-Forscherinnen erweitern Wissen um Translation	LMU Munich
01 August 2008	LMU-Biologin erhält eine Million Euro EU-Förderung	LMU Munich
06 August 2008	LMU Biologist Receives EU Grant of One Million Euros	LMU Munich
May 2008	„Wege in die Biotechnologie“	BMBF brochure
July 2008	“The Path to ERC Grants: Researchers in Germany Excel“	DFG brochure
04 August 2008	Eine Million für Münchner Forscherin	Münchner Merkur
13/14 September 2008	„Exzellente Forschungslandschaft“ – Molekularbiologin erhält hochdotiertes Stipendium	Münchner Merkur
02 October 2008	Katja Sträßer: Den Weg vom Gen zum Eiweiß im Visier	BMBF

DANIEL N. WILSON

20 August 2008	„Im Kampf gegen multiresistente Keime: Wie ein Antibiotikum gegen Krankenhauskeime wirkt“	LMU Munich
18 August 2008	„Wie Notfall-Antibiotika Bakterien lahm legen”	Goethe University, Frankfurt
11 April 2008	„Störung der Proteinfabrik”	Goethe University, Frankfurt
09 November 2007	“New Study illuminates ability of hot-water bacteria to survive cold shock“	RIKEN, Japan
25 September 2006	„Struktur eines Ribosom-Antibiotikum-Komplexes aufgeklärt”	Max Planck Institute for Molecular Genetics, Berlin

Date	Title	Source
29 April 2005	„Baumeister des Lebens“	Max Planck Institute for Molecular Genetics, Berlin
12 April 2004	„Unverzichtbare Rolle der dritten tRNA-Bindungsstelle des Ribosoms für fehlerfreie Übersetzung der Erbinformation nachgewiesen“	Max Planck Institute for Molecular Genetics, Berlin
24 September 2008	„Mensch gegen Mikrobe”	Süddeutsche Zeitung
05 September 2008	“Translation Translocations”	Science
20 June 2008	“Antibiotics Flip a Switch”	ACS Chemical biology
19 May 2008	“Ribosomal peptide-bond formation”	Chemistry and Biology
20 February 2007	“Ribosomal translocation: LepA does it backwards”	Chemistry and Biology
November 2006	“Ribosom-Antibiotikum-Komplex Aufgeklärt”	ChemiePlus
October 2006	“Antibiotic blocks mRNA path on the ribosome”	Nature Structural and Molecular Biology
20 November 2005	“The ins and outs of protein synthesis”	Chemistry and Biology
January 2005	“Ribosome Recycling & Termination of Protein Synthesis”	Photo Science (HasyLab)
March 2005	“X-ray crystallography study on ribosome recycling: the mechanism of binding and action of RRF on the 50S ribosomal subunit.”	PSI

ECKHARD WOLF

28 May 2008	Über 700.000 Euro Startkapital für LMU-Spin-offs: BioStemTec und Nanostove erhalten EXIST-Förderung	LMU Munich
19 March 2008	Nachwuchsforscher der LMU-Tiermedizin erhalten 1,7 Millionen Euro Fördermittel durch das BMBF	LMU Munich
25 October 2007	Zitationsvergleich 2001 bis 2004: Reproduktionsbiologie	Veterinary Faculty of LMU Munich
29 July 2005	Genetisch veränderte Schweineorgane für Transplantation	LMU Munich
31 March 2005	Tierschutzkongress am 1./2. April: Landwirtschaft soll wieder tierfreundlicher werden	Freie Universität Berlin
20 December 2004	„Laborjournal”: LMU-Tierärzte werden am meisten zitiert	LMU Munich
November 2008	Klonkuh Uschi und ihre schmackhaften Erben	Bild der Wissenschaft
27 September 2008	Pharming: Wie Landwirtschaft für Medikamente eingespannt wird	Deutsche Welle
September 2008	REMEDY: Wie hängen Stoffwechselstörungen und Fruchtbarkeitsprobleme bei der Milchkuh zusammen?	GenomExpress
20 August 2008	Klonen – Sicherheitskopie vom Vieh	Süddeutsche Zeitung
10 July 2008	Biopharming – Medikamente aus der Landwirtschaft	Bayerischer Rundfunk Bayern 2
05 July 2008	Happy Birthday Dolly	radioeins
May 2008	Transgene Schweinemodelle für translationale Forschung in der Medizin	Journal für Verbraucherschutz und Lebensmittelsicherheit
10 April 2008	Geklont für die medizinische Forschung	Hamburger Abendblatt
March 2008	Dollys Erben	brand eins
01 February 2008	USA lassen Vermarktung von Klonfleisch zu	VDI nachrichten
December 2007	Betazell-Fehlfunktion und Diabetesmellitus bei Mäusen mit einer C95S Mutation im Insulin 2 Gen	GenomExpress
03 November 2007	Die Menschenkloner können wir nicht aufhalten	Tagesanzeiger Zürich
21 October 2007	Report aus der Klonfabrik	Deutschlandfunk
October 2007	Zitationsvergleich 2001 bis 2004: Reproduktionsbiologie (E.W. Nr. 1)	Laborjournal
10 August 2007	Klonfamilie bekommt Nachwuchs	FOCUS
July 2007	Organspende aus dem Schweinestall	Technology Review
07 May 2008	Schöne neue Nahrungswelt - Was werden wir in Zukunft essen?	hr fernsehen
October 2007	Transgene Versuchstiere	Nova Acta Leopoldina NF 95, Nr. 353, 37-54
January 2007	Wie macht sich ein früher Embryo bei seiner Mutter bemerkbar?	BIOspektrum
13 June 2006	Genmanipulierte Schweine beleben einen alten Traum neu – die Transplantation von Tierorganen auf den Menschen	Süddeutsche Zeitung
February 2006	Betacellulin: Ein Wachstumsfaktor für pankreatische Zellen	MedReport
12 January 2006	Organe von Schweinen sollen Kranken helfen	Süddeutsche Zeitung

APPENDICES: GENE CENTER IN THE MEDIA

Date	Title	Source
January 2006	FERTILINK - Funktionale Genomforschung zur Verbesserung der Fruchtbarkeit von Nutztieren	GenomExpress
2006	Perspektiven des Klonens in der Tierzucht und in der biomedizinischen Forschung	LEOPOLDINA (R. 3) 51, 407-414
2006	Biologie und Biotechnologie der Reproduktion	Hülsenberger Gespräche 2006, Schriftenreihe der H. Wilhelm Schaumann Stiftung, Hamburg, pp 19-26
2006	Biotechnologische Ansätze zur Klärung der physiologischen Bedeutung des bovinen Prionproteins und seiner Rolle in der Pathogenese von BSE	Nova Acta Leopoldina NF 94, 237-247
23 November 2005	Klon-Karrieren: Vom Frosch zum Schaf	Hessischer Rundfunk
27 September 2005	Schweine als Organspender	Süddeutsche Zeitung
September 2005	Funktionelle Genomanalyse im tierischen Organismus – FUGATO schließt den Reigen im Nationalen Genomforschungsnetzwerk	GenomExpress
01 August 2005	Genetisch veränderte Schweine als Organlieferanten? Protein soll vor Abstoßungsreaktion bei Transplantation schützen	SCINEXX Das Wissensmagazin
15 March 2005	„Klonen von Menschen wäre mit Inzest vergleichbar"	Ärztezeitung
11 February 2005	Der Disput mit dem Zauberlehrling	Süddeutsche Zeitung
2005	Genetische Prädispositionen für erhöhte Blutcholesterinwerte im Mausmodell	Biologie in unserer Zeit 35, 14-15
December 2004	Zitationsvergleich 1999 bis 2001: Tiermedizin (E.W. Nr. 1)	Laborjournal
October 2004	Der Doktor und sein liebes Vieh	LMU Einsichten
January 2004	Revolution im Schweinestall	Technology Review
2004	Von Klon-Kühen und Fluoreszenz-Ferkeln	Zukunft im Brennpunkt. abayfor (Hrsg), Band 3, pp 51-54

RALF-PETER JANSEN

05 December 2007	„Zellulärer Frachtverkehr: die Ladung hilft beim Bau der Lokomotive"	Helmholtz Zentrum München - Deutsches Forschungszentrum für Gesundheit und Umwelt
09 August 2006	„Ein Botenmolekül auf Reisen – Neuartiger RNA-Transport garantiert gezielte Proteinverteilung"	LMU Munich
2006	„Die Zelle und ihr Publikum"	Einsichten LMU Munich
09 June 2005	„Transportproteine vernetzen GSF und LMU – Neue Helmholtz-Nachwuchsgruppe untersucht den Güterverkehr in der Zelle"	Helmholtz Zentrum München - Deutsches Forschungszentrum für Gesundheit und Umwelt
02 June 2005	„Transportproteine vernetzen GSF und LMU. Neue Helmholtz-Nachwuchsgruppe untersucht den Güterverkehr in der Zelle"	LMU Munich
18 April 2005	„Wie DNA entkleidet und HIV geholfen wird – Zwei LMU-Publikationen aus der Strukturforschung"	LMU Munich
21 January 2005	GSF an neuem SFB beteiligt: "Netzwerke in Expression und Erhalt des Genoms"	Helmholtz Zentrum München - Deutsches Forschungszentrum für Gesundheit und Umwelt
17 December 2004	„Neuer SFB an der LMU nimmt seine Arbeit auf – Netzwerke in Expression und Erhalt des Genoms"	LMU Munich
19 November 2004	„DFG richtet sieben neue Sonderforschungsbereiche ein"	Deutsche Forschungs-gemeinschaft (DFG)

STEFAN WEISS

04 September 2006	Creutzfeldt-Jakob: heilende Zuckermoleküle?	FOCUS, 36, page 113 (2006)
19 May 2008	Metastatic target in the basement.	BioCentury, The Bernstein Report on BioBusiness, 16 (22) page A8 (2008)

Campus Grosshadern-Martinsried

Contact:
Gene Center Munich
Ludwig-Maximilians-Universität (LMU) Munich
Feodor-Lynen-Strasse 25
81377 Munich
Germany

Phone: +49 89 2180 - 769 65
Fax: +49 89 2180 - 769 99

Email: genecenter@lmb.uni-muenchen.de
Internet: www.lmb.uni-muenchen.de