IM FOKUS
Forschungsgruppe
Bioanalytische
Massenspektrometrie

NACHRICHTEN
Leibniz-Preis 2019
für Melina Schuh

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Neue Facility
Mikroskopie lebender Zellen
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IMPRESSUM

Titelbild: Einzelne Porteine lassen sich mittels cross-linking in Kombination mit Massenspektrometrie zur 3D-Struktur eines makromolekularen Komplexes anordnen. (Abbildung: Karl Bertram und David Haselbach / MPI-BPC)

Cover image: Individual proteins can be arranged within the 3D structure of a macromolecular assembly by cross-linking combined with mass spectrometry (Image: Karl Bertram and David Haselbach / MPI-BPC)

Hinweis: Obwohl aus Gründen der Lesbarkeit im Text die männliche Form gewählt wurde, beziehen sich die Angaben stets auf Angehörige beider Geschlechter.
**Protein cross-linking to support structure determination in electron cryo-microscopy of macromolecular complexes**

Henning Urlaub
Research Group Bioanalytical Mass Spectrometry

Cryo-electron microscopy (cryo-EM) can solve structures of highly dynamic macromolecular complexes. To characterize less well defined regions in cryo-EM images, cross-linking coupled with mass spectrometry (CXMS) provides valuable information on the arrangement of domains and amino acids. CXMS comprises covalent linkage of protein residues close to each other as well as identifying these connections by mass spectrometry. Here, we exemplify the advances of CXMS and its integration with cryo-EM for structural reconstruction.

Proteins are dynamic molecules, and they often join up with ligands and other proteins to form functional macromolecular complexes in the cell. Discovering the three-dimensional (3D) structures of such complexes is a huge challenge. Classical methods of structure determination, such as X-ray crystallography and nuclear magnetic resonance (NMR), are restricted by the size, the structural flexibility, and the heterogeneity of most macromolecular protein complexes.

Currently, cryo-EM is the method of choice for elucidating the structures of macromolecular complexes. In cryo-EM, 3D structures are reconstructed from 2D projections; to make this possible, the complex under investigation is embedded in amorphous ice, so that its structure is kept as close to the native state as possible. Thanks to technical improvements in electron microscopes and to the development of appropriate software, we can today reach impressive spatial resolution, often down to 3 Å or even below (1-4). Examples are structures of ribosomes, proteasomes, complexes involved in transcribing DNA to RNA, spliceosomes, nuclear pores, and structures of ribosomes, proteasomes, complexes involved in transcribing DNA to RNA, spliceosomes, nuclear pores, and complexes involved in protein translation. Nevertheless, this level of resolution has only been realized for a few of these structures. More than 90 % of the structures published so far have had a resolution of 3-5 Å or even less (https://pdbj.org/emnavi/stat.php). The most important reason for this is the freedom of movement of some protein components within the macromolecular complex, or of some regions within a protein. Moreover, the quality of the samples, the quality of the 2D images, and the statistical methods employed for reconstructing the 3D model all play a part. The major problem lies in the visibility of individual amino acid side chains, which cannot be seen when the resolution is poorer than 4 Å, rendering the location and the assignment of proteins in cryo-EM structures extremely difficult.

Here, the method of chemical protein cross-linking in combination with mass spectrometry (CXMS) comes to our help. CXMS makes it possible to find out which protein domains in macromolecular complexes are attached to one another, once they have been cross-linked chemically and the cross-linked protein regions have been identified and sequenced by mass spectrometry (6-8). Thus, CXMS is not an independent method for determining unknown structures, but it makes an enormous contribution to the interpretation of structures. This is especially the case in certain specific situations: (i) when no independent structural information about the arrangement of the proteins in a complex is to be had, (ii) when the proteins in the complex contain highly dynamic domains, the structures of which cannot be seen by crystallography or NMR and are invisible in cryo-EM, (iii) when the complex under study can only be investigated structurally in the presence of part of its normal protein complement, so that the positions of the missing proteins in the complex’s structure cannot be determined, or (iv) when a structural model for a protein or complex has been proposed and requires validation. Moreover, CXMS makes it possible to identify different conformations of an individual protein in a complex - for example, if the protein’s position changes when other proteins become bound to the complex, then this will affect its cross-linking pattern.

**Protein cross-linking**

To cross-link proteins, one generally uses chemical reagents that possess N-hydroxysuccinimide (NHS) ester or methionine residues. The most frequently used reagent disuccinimidylsulfate (DSS) links α-amino functions of lysines that are about 30 Å apart (strictly speaking; whose C-alpha atoms are 30 Å apart). Following chemical cross-linking, the proteins are digested by using endoproteases (usually trypsin) and the cross-linked peptides thus obtained are sequenced in the mass spectrometer. The peptides’ sequences allow the cross-linked amino acids to be identified and sequenced by mass spectrometry (LC-MS/MS). Thus, CXMS is not an independent method for determining unknown structures, but it makes an enormous contribution to the interpretation of structures. This is especially the case in certain specific situations: (i) when no independent structural information about the arrangement of the proteins in a complex is to be had, (ii) when the proteins in the complex contain highly dynamic domains, the structures of which cannot be seen by crystallography or NMR and are invisible in cryo-EM, (iii) when the complex under study can only be investigated structurally in the presence of part of its normal protein complement, so that the positions of the missing proteins in the complex’s structure cannot be determined, or (iv) when a structural model for a protein or complex has been proposed and requires validation. Moreover, CXMS makes it possible to identify different conformations of an individual protein in a complex - for example, if the protein’s position changes when other proteins become bound to the complex, then this will affect its cross-linking pattern.
Im Fokus: Forschungsgruppe Bioanalytische Massenspektrometrie

Cross-linking of complexes

Electron microscope

Mass spectrometry

Separation of cross-linked peptides

Docking of proteins

Reconstructed 3D volume

Docking of all protein structures in the 3D volume

Figure 2: Example of the procedures followed in structure determination of a macromolecular protein complex by CXMS and cryo-EM. For the CXMS (left), the purified macromolecular protein complex is treated with cross-linker and thereafter all its proteins are broken down into peptides with endoproteinases. The cross-linked peptides are separated from the non-cross-linked ones by gel filtration and sequenced in the mass spectrometer. If structural models of the proteins already exist, then the cross-linked protein regions can be matched up. For cryo-EM (right), protein complexes are embedded in amorphous ice and two-dimensional images of the complexes are produced. These are then processed in a multi-step procedure to give a three-dimensional image (“density volume”). This contains the protein structures; if the resolution is high enough these are visible, and if not then the CXMS results and any available structure models are used to place the individual proteins in the 3D volume. Figure from (5)

Bioanalytische Massenspektrometrie

Example of the procedures

Spliceosomes and pre-mRNA transcription complexes – prime examples of the use of CXMS in structure determination

The use of CXMS to determine the locations of proteins in 3D structures determined by cryo-EM is convincingly illustrated by the recently solved structure of the spliceosome (12-16) and Polyomavirus Il-dependent pre-mRNA transcription complexes (17-25) here at the MPI-BPC. The spliceosome is one of the most dynamic multifactorial nucleonucleoprotein complexes in eukaryotic cells. It catalyzes the excision of the introns and the ligation of the resulting exon ends of pre-mRNA to generate the mature mRNA. It consists of five small nuclear (sn) RNA molecules and up to 170 proteins. The spliceosome assemblies on the pre-mRNA to be spliced and passes through several functional stages, which differ substantially in both RNA-RNA interaction pattern and in protein compositions. The spliceosome's dynamics, the flexible nature of its proteins, and its massive molecular weight long impeded structural research into its functional states. However, in the past two years cryo-EM...
has brought to light impressive 3D structures of intact, functional spliceosomes. To locate proteins more precisely in the spliceosome’s various functional states, and to define their positions precisely, we use CXMS. Figure 3 illustrates a procedure of this kind, using the 3D volume model of the activated spliceosome, the B* complex (13) as obtained at a resolution of 5.8 Å (Fig. 3A). The structures of the individual proteins – those that were available – were fitted into the 3D volume of the spliceosome. Because of the limited resolution, the non-folded regions of the spliceosomal proteins Prp2, Bud13, Prp45, and Sp2 could not be assigned clearly enough. However, it is precisely these regions that are of greatest interest for understanding the spliceosome’s structure and function, as they interact sequentially with several other proteins. CXMS was used to assign these regions to their positions in the 3D structure of the B* complex. Figure 3B shows a part of the complex at higher magnification (not in 3D) and only those proteins that show defined elements of secondary structure. Figures 3C and 3D show these proteins as simple colored areas with correspondingly colored amino acids that were identified as cross-linking to the non-folded regions of the proteins Prp2, Bud13, Prp45, and Sp2. Figure 3E shows the corresponding amino acids and, schematically, the unfolded regions of the proteins Prp2, Bud13, Prp45, and Sp2, which were placed there on the basis of information derived from cross-linking. An extensive network of protein-protein interactions is revealed. This network is functionally important, as precisely these interactions are believed to “clamp” the non-folded regions of protein Prp2 so that it can exert its catalytic function and thus propel the B* complex into the next functional state of the spliceosome, the catalytically activated B* complex.

Figure 4 illustrates further examples for the combination of CXMS and cryo-EM. Here, protein-protein cross-linking networks of Polymerase II-dependent pre-mRNA transcription complexes are shown with selected protein structures, which are placed in the corresponding 3D volumes of the complexes obtained by cryo-EM. In this manner, we were able to locate and orientate specific protein structures with the 3D structure of the corresponding pre-mRNA transcription complexes in a more precise manner, in particular within those parts of the 1D volume where the resolution of the corresponding complex is not sufficient to allow for unambiguous orientation of the proteins.

Figure 3: Modelling of non-folded protein regions of the spliceosomal proteins Prp2, Bud13, Prp45, and Sp2 within the activated spliceosome (B*) using information obtained by CXMS. (A) 3D structure of the B* spliceosome at a resolution of about 6 Å. With this resolution, the structures of spliceosomal proteins with defined protein domains can be located. However, proteins and domains with large non-folded regions remain invisible. (B) The region of the spliceosome without density volume, showing the structures of the spliceosomal proteins CWC22, Prp45, Prp2, and Brr2. (C) Here, the proteins are represented as colored areas and the amino acids that were found by mass spectrometry to be cross-linked are indicated (lysines, in colors corresponding to their proteins). (D) As (C), but without the structure models of the proteins. (E) Schematic representation of the unstructured regions of the proteins Cwc22, Prp45, Prp2, Sp2, and Bud1 in this region of the spliceosome.

Figure 4: Cross-linked protein networks and selected protein structures of the RNA Polymerase II Pre-initiator-Complex (PIC) (A) and paused Polymerase II elongation complexes (B and C). (A) EDC-derived inter-subunit cross-links between selected subunits in the PIC-cMed complex. Ribbon representation of Tfb1 and the surrounding domains of K93, K110, and Tfb4. BS3- and EDC-derived cross-links are depicted in red and black, respectively. The displayed cross-links aided modelling of the proteins and their anchor domains into the cryo-EM 3D volume. (B, C) Protein cross-linking network of paused and activated transcription elongation complexes with their specific proteins. NELF-A tentacle interaction with the Polymerase II is based on CXMS data (B) and the orientation of WDR61 relative to CTR9 (C) was possible because of the CXMS analyses of cross-linked amino acid residues of the respective proteins.
Polymerase II-dependent pre-mRNA transcription is the first essential step in eukaryotic gene expression by using double strand DNA as template for generating a pre-mature mRNA. Polymerase II consists of twelve different protein subunits. It cannot bind on its own to a promoter region for a protein-coding gene on the DNA to initiate transcription. It rather needs to be assembled with other protein factors (transcription factors) TFIIA, B, D, E, F, and H on the promoter, hence forming the pre-initiation complex (PIC). A so-called mediator complex (PIC-mediator) further stabilizes the interactions with DNA sequences upstream of the promoter region. Very recently, the group of Patrick Cramer solved the structure of the PIC-mediator including detailed structural information of TFIIH (23). In particular the spatial orientation of the essential TFIIH protein complex within the PIC-mediator has now been determined to the native nature of this complex. Here, we used cross-linking of the holoenzyme with EDC, which couples lysine and glutamate/aspartate residues. Importantly, EDC cross-linker connects residues that have a much smaller distance restrain as for example DSS so that TFIIH with its subunits can be more precisely located in the 3D volume of the holoenzyme. Figure 4A shows the EDC-derived cross-linking network of the PIC and highlights the cross-linking of the TFIIH proteins Rad3, Ssl1, Tfb1, and Tfb4.

After initiating, the transcription complex starts elongating the nascent RNA (that is, by forming a transcription elongation complex), but after a few nucleotides (25-150 base pairs) can stable pause in the promoter-proximal region. This step is used as an additional checkpoint to control gene expression of large assemblies of cross-links that are differentially isotopically labeled. Changes in the cross-link profiles between separately probed functional states may even yield semi-quantitative information on the abundances of the constituents’ different conformations. However, when complexes are analyzed by CXMS in parallel using cryo-EM, the entire mixture—with a certain heterogeneity (for example subcomplexes through disassembly, and various functional states, which could not be separated biologically)—will be cross-linked. Therefore, it is difficult to distinguish if a set of cross-links represents only the most abundent conformation, or rather results from a less abundantly present subcomplex or a different functional state. Conversely, cryo-EM offers this possibility through classification of collected images and can distinguish between various assembly and/or functional states in a single sample preparation. Improving quantitative cross-linking approaches can be expected to allow the description of entire sets of various conformational states even in macromolecular and heterogeneous complexes, while software development and improvements in structural dynamics of the RNA polymerase II-DSIF complex reveals a multidentate DNA-RNA clamp. 

Acknowledgements
Patrick Cramer, Renhard Lührmann, Holger Stark, and Henning Urlaub, whose results are shown here, receive support from the DFG (SFK860 Integrative Structural Biology of Dynamic Macromolecular Assemblies). Karl Bertram, Olle Dykhov, Davide Zaccaria, Bethold Kastner, Christof Lenz, Sandra Schilbach, Alexandra Sütze, and Seychelle Voss helped in proofreading and finishing this article.

References
Der Schlaf ist alt, sehr alt. Vermutlich ist er vor über 500 Million Jahren entstanden, als die ersten Tiere ein Nervensystem entwickelten. Im Tierreich ist er entsprechend weit verbreitet – Säugetiere schlafen ebenso wie Fische und sogar Quallen. Schlaf scheint also eine unverzichtbare Funktion zu erfüllen.


„Wie wir herausgefunden haben, sind die Larven von C. elegans auf Schlaf angewiesen, um Hungerphasen zu überleben“, fasst Bringmann die Ergebnisse zusammen. „Dabei schlafen die Würmer offenbar nicht nur, um Energie zu sparen, sondern auch, um schädliche Alterungsprozesse aufzuhalten. Der Schlaf stellt für den Wurm unter diesen Bedingungen also eine Art Anti-Aging-Strategie dar.“

Die Göttinger Wissenschaftler hatten zunächst analysiert, inwieweit C. elegans überhaupt schlafen muss. Während Schlafentzug bei erwachsenen Würmern keine Auswirkung auf ihre Lebensdauer habe, würden schlaflose Larven sterben, erläutert Yin Wu, Doktorandin in Bringmanns Forschungsgruppe. „Wir wollten wissen, warum da so ist.“


Originalveröffentlichung


Wer ausreichend schläft, lebt gesünder – davon ist die Schlafmedizin heute überzeugt. Doch kann Schlaf auch verhindern, dass wir altern? Zumindest bei Fadenwürmern ist das der Fall, wie Wissenschaftler am MPI-BPC jetzt gezeigt haben: Der Fadenwurm Caenorhabditis elegans schläft ein, wenn er hungrig muss, und verlangsamt so das Altern seiner Zellen. Die Forscher weisen damit erstmals einen direkten Zusammenhang zwischen Schlaf und Altersprozessen nach, der so auch beim Menschen bestehen könnte. (Current Biology, 8. November 2018)

Mit einem Anruf rund eine Stunde vor der öffentlichen Verkündung der Preisträger hatte die DFG Melina Schuh die gute Nachricht übermittelt. "Die Auszeichnung hat mich völlig überrascht und ich freue mich sehr über diese große Ehre", berichtet die frisch gekürte Preisträgerin. "Ein Riesendank geht an meine bisherigen und jetzigen Mitarbeiterinnen und Mitarbeiter sowie die fantastischen Mentoren, die mich im Laufe meiner wissenschaftlichen Karriere unterstützt haben."

Die Deutsche Forschungsgemeinschaft (DFG) zeichnet die Biochemikerin am MPI-BPC damit für ihre wegweisenden Arbeiten zur Entwicklung befruchtungsfähiger Eizellen aus. Der wichtigste deutsche Forschungsförderpreis ist mit bis zu 2,5 Millionen Euro dotiert.

Leibniz-Preis 2019 für Melina Schuh

Kind mit chromosomalen Anomalien wie dem Down-Syndrom. Doch warum ist das so?


Eizellen nimmt ab, wenn Frauen älter werden


Wie solche Fehler bei der Halbierung des Chromosomens- satzes zustande kommen, erforscht die Biochemikerin in ih- rer Abteilung Meiose am MPI-BPC unter anderem mithilfe leistungsfächer Lichtmikroskope. So gelang es ihrem Team jetzt, den Prozess der Chromosomentrennung direkt live in unbebrüteten menschlichen Eizellen zu beobachten.
Leibniz Prize 2019 for Melina Schuh

The German Research Foundation (DFG) honors the biochemist at the MPI-BPC for her pioneering research on the development of fertilizable oocytes. The most important German research prize is endowed with up to 2.5 million euros.

I t is a great success for Melina Schuh that she has now been awarded the renowned Leibniz Prize for her groundbreaking research,” Managing Director Dirk Görlich congratulated the prizewinner. “We are extremely happy for our colleague! Her research on how fertilizable oocytes develop is scientifically extremely interesting and highly relevant to society! How does new life come into being? And what are the consequences if errors occur in egg cell development? Melina Schuh’s work has contributed significantly to our today’s understanding of how chromosomal abnormalities can lead, for example, to Down’s syndrome, miscarriages, and infertility.

Quality of eggs decreases as women get older

Sooner or later in a partnership the question arises whether to have children or not. In our society more and more couples decide to become parents later. However, this postponement is not free of risks. The quality of immature oocytes – which are already present in every woman from birth – decreases with the woman’s age. At the same time, the probability of miscarriages or a child with chromosomal abnormalities such as Down’s syndrome increases. But what are the reasons for this?

“The most common cause are errors that occur during the egg cell’s maturation, called meiosis, in which the egg halves the number of its chromosomes. Only one of the two sets of chromosomes remains in the mature egg, while the other is exported from the cell. Only then can the oocyte fuse with a sperm cell. Before the egg cell divides, related (homologous) chromosomes are first arranged in the cell center using so-called spindle fibers. There, they are separated and the spindle apparatus transports one copy each to the two cell poles.

Chromosomal aberrations due to errors in meiosis

The biochemist and her team were able to show that the chromosomes of immature oocytes belonging together are less stably attached to each other in women over 35 than in younger ones. She also found that chromosomes are often not correctly bound to the spindle apparatus. Both factors contribute to the susceptibility of meiosis to errors and lead to mature oocytes with a wrong number of chromosomes. “If such an egg is fertilized, the chromosomal aberration can have a negative effect on the course of pregnancy and the child’s health,” says the Max Planck Director.

In her Department of Meiosis at the MPI-BPC, the biochemist uses powerful light microscopes to investigate how such errors occur when the chromosome set is halved. Her team has now succeeded in observing the process of chromosome segregation live in unfertilized human oocytes. To understand the process of chromosome segregation in detail, Schuh and her group also developed a new method called Trim-Away which allows to remove defined proteins from the oocytes within a few minutes. By analyzing the resulting effects, the researchers can uncover the functions of the corresponding proteins during meiosis.

“Our findings contribute to a better understanding of how fertile eggs are produced and why children of older women suffer from chromosomal aberrations more often compared to younger ones. In the future, this knowledge could help women in their late 30s and early 40s to have children,” the Leibniz Prize winner hopes.

Together with Melina Schuh, nine other researchers were honored with this year’s Leibniz Prize, including the two female Max Planck Directors Ayelet Shachar of the MPI for the Study of Religious and Ethnic Diversity as well as Brenda Schulman of the MPI for Biochemistry. In total, 14 scientists who work or have worked at the MPI-BPC have so far received the renowned prize. (cr/translation fk)

Über den Leibniz-Preis


Melina Schuh

studierte Biochemie an der Universität Bayreuth und wurde 2008 nach mehrjährigen Arbeiten am European Laboratory of Molecular Biology (EMBL) in Heidelberg promoviert. Im Anschluss wechselte sie nach Cambridge (England), wo sie von 2009 bis Ende 2015 als Gruppenleiterin am renommierten MRC Laboratory of Molecular Biology forschte. Seit Januar 2016 ist sie Direktorin am MPI-BPC und leitet dort die Abteilung Meiose. Für ihre Arbeiten wurde sie bereits vielfach ausgezeichnet, zuletzt erhielt sie die EMBO Gold Medal.

The most important German research prize is endowed with up to 2.5 million euros.

16 Nachrichten

Nachrichten 17
To start with the most obvious question: What kind of services does the new facility offer?

Peter Lenart (PL): Here in the facility we cover the full range of light microscopy, with particular emphasis on imaging living cells. Our service includes help with sample preparation, planning experiments, image acquisition, image processing, and data analysis. Furthermore, we will provide regular training courses in light-microscopy and bio-image analysis.

How are you set up for these services?

PL: Antonio and I are an ideal combination in my view: I am a biologist by training and spent my whole PhD and beyond doing confocal microscopy and imaging live cells. Therefore, I have good expertise in sample preparation and assay development. Antonio complements this nicely because...

Antonio Politi (AP): ... I have a PhD in biophysics, much experience with microscope automation as well as image processing, and data analysis. Furthermore, we will provide regular training courses in light-microscopy and bio-image analysis.

Who can use the facility's services?

AP: Our facility is open to everyone at the MPI-BPC. If labs do not regularly use light microscopy but need this method for a specific project or experiment they can come to us and do their experiments here after a short introductory training. For more experienced users we are happy to provide project-related advice and tips for assay development. Resources permitting, we can also optimize assays and develop image analysis routines for users. Generally, we are happy to help in any way we can, for example, we can offer advice when groups would like to purchase a light microscope for their own lab.

How is the facility equipped?

PL: Our current rooms are sufficient to host eight microscopes in total. Two state-of-the-art confocal microscopes are already installed and in use, one of which is equipped for STED imaging invented by our Director Stefan Hell. One additional space is reserved for the iPAM microscope developed by Tom Jovin and Donna Arndt-Jovin here at the institute that will also be available to the facility’s users. The spaces left will be gradually equipped with microscopes to meet the demands at the institute. We purposely keep this flexible to offer our users the technology they need.

In addition, we have a cell culture lab to prepare live samples for imaging. Not least, we also provide lab space for sample preparation.

As you can see here, all our rooms are brand-new. The architect, the institute’s building service, and the workshops really did a great job! In addition, the IT Service helped us a lot in putting up the IT infrastructure and virtual machines. So we had fantastic support all the way from administration to management in setting up this facility and very much thank all of them for their help!

Who is already using the facility?

AP: We have regular users from Melina Schuh’s team, from Dirk Görlich’s group, as well as from Gregor Eichele’s department, and we got contacted by several more people from all over the institute after our official opening event in early December. One of our current favorites are the brain preparations from Eichele’s team: It is a real imaging challenge, and it is simply fascinating to watch the coordinated beating of cilia in the ventricles.

Once people have acquired the images, how can these be processed?

PL: We have central servers for image processing which we maintain together with the IT Service. We use virtual machine technology to run image processing software that can be accessed from remote computers. Thus, users can come to our image analysis terminals in the facility, but if they prefer, they can access all services and software from any computer at the institute or even from home. (Interview: fk/cr)
Einweihung der Facility Mikroskopie lebender Zellen


Lab warming of the Facility for Live-cell Imaging

T here was almost no getting through in the spacious new Facility for Live-cell Imaging when Peter Lenart welcomed the guests to the lab warming in the afternoon of December 3. “Our new coffee machine arrived just in time, so we were really lucky,” the facility head happily released. Operational manager Antonio Politi had selected this one personally and prepared one coffee after the other in high-throughput for their guests. “Users who come to us on a frequent basis can also be introduced to operating this great espresso machine in addition to the microscopes,” he offered smiling. The new microscopes, which Lenart and Politi presented to the visitors in small groups with the support of technical assistant Jasmin Jakobi, also attracted a lot of attention. Currently, the microscopes are strongly frequented by employees from the Departments of Gene and Behavior, Meiosis, and Cellular Logistics. Further systems are to be purchased gradually, in line with the needs of the institute’s staff. We wish the facility a good start and many happy microscopy enthusiasts! (cr)

Thomas Burg appointed professor at the Technical University Darmstadt

The head of the Max Planck Research Group Biological Micro- and Nanotechnology assumed his new position on September 1, 2018.

Which experiences and memories will you keep from your time at the MPI-BPC?

The MPI-BPC is unique in its scientific diversity, and the collaborative spirit here at the institute is exceptional. Furthermore, from the start I was impressed by the excellent service and support. Everyone, not only the scientists, but also the staff at the administration, central services, and facilities share an enthusiasm for a joint mission – this is something you do not see like that in many other places.

What convinced you to accept the offer from the TU Darmstadt?

In Darmstadt, I have the opportunity to work on research projects with a long-term perspective. The TU Darmstadt is an outstanding university with great students in my field, so I also look forward to teaching and having contact with students at all levels. It was therefore an easy decision for me to accept the offer.

What are your goals in the next years?

While the lab is gradually migrating to Darmstadt, we will expand our research on microsystems to connect live-cell imaging, cryo-light microscopy, and cryo-electron microscopy. Associated with this are many intriguing challenges that will keep us busy for the next few years. For example, we want to better understand the physical principles that govern the limits of vitrification (ice crystal-free freezing) in cells and tissues of different size and composition. In parallel, we will explore the many opportunities in superresolution light microscopy that emerge from the high stability of fluorescent molecules at cryogenic temperature. Darmstadt is perfect for this type of research due to the interaction between engineering and natural sciences within the Rhein-Main-region. And, of course, I look forward to continuing our many fruitful collaborations in Goettingen and especially at the MPI-BPC, which has been a fantastic home for our group over the past nine years.

Did you want to stay in Germany? Would you have moved abroad?

I am very happy that I received the offer from the TU Darmstadt, but if it had not worked out I would have applied abroad, as well. However, for my family staying in Germany was definitely the first choice. (Interview: fk)

What do you like most about your work as a scientist?

It is great that I can work together with young people with whom I share the same interest. It is always a thrill to conceive something and then make it work in the lab. This more than compensates for the inevitable failures you are bound to experience from time to time.

Thomas Burg studied physics at the ETH Zurich (Switzerland) and received his PhD from the Massachusetts Institute of Technology (MIT) in Cambridge (United States) in 2005. He has been heading the Max Planck Research Group Biological Micro- and Nanotechnology at the MPI-BPC since 2009.

Thomas Burg

20 Neues aus dem Institut

21 Neues aus dem Institut
New Campus Seminar series – an experiment to foster multidisciplinary conversation

Research groups and individual scientists sometimes tend to work in isolation. With its innovative concept, the new Campus Seminar series at the Göttingen Max Planck Campus is designed to overcome this isolation and to promote exchange between the scientific disciplines at the institute. The series is organized by eight research group leaders of the MPI-BPC and the MPI for Dynamics and Self-Organization. Three of them – Alex Faesen, Stefan Glöggler, and Juliane Liepe – were interviewed by the representatives of our institute’s PhD/Postdoc Community.

Have you attended a seminar in a different field that enhanced your work or made you land in a new job?

Alex Faesen (AF): I did my PhD in a famous cancer institute, but my background was not biology and I had never heard of p53, an extremely well-studied cancer gene. My PhD laboratory worked only tangentially on cancer. So the only way for me to get a good understanding of cancer research was to attend student and postdoc seminars. I am glad I had that foresight, as having a broad conceptual understanding of scientific fields other than your own is invaluable in later stages of your career. Diversity matters, on many levels.

Stefan Glöggler (SG): I was trained as a chemist and was very much exposed to investigating catalysts and materials during my studies. During talks and seminars of students and postdocs from different departments and research institutions, I discovered my interest in connecting what I have learned as a chemist with questions related to biochemistry and biology. This combination of interests has become a strong drive that motivates my research.

Juliane Liepe (JL): I was initially trained in biochemistry. During the first years of my degree I attended seminars in theoretical physics. To be totally honest, this was not completely voluntary as we had to visit seminars from unrelated fields to be admitted to the exams. During those seminars I realized, however, that there is a different way of thinking specific to every field. In those seminars I was confronted with different approaches and tools. This surely triggered in me the interest to combine approaches from different fields in my later research and it became decisive for my scientific career so far.

How will the audience benefit from this new Campus Seminar series with a mix of two topics in an hour?

AF: The science in our institute is very diverse, so this will introduce an extra challenge when presenting your work. Compared to your normal group meeting or specialized conference, the speaker will have to distill the presentation down to the concepts and principles. Details will be less important. This is an incredible skill to learn, and one that does take time and energy in preparing a non-expert talk, who has to introduce your research question could heavily benefit.

JL: Working in a highly interdisciplinary field, I cannot stress enough how important it is to be able to communicate with experts from different fields despite we all use different languages. With the Campus Seminar we hope to provide a platform to practice both, understanding talks from a different discipline as well as communicating your research to non-experts.

Is there a chance that some audience will leave after the first talk?

AF: We are all busy people, so it is understandable that sometimes you only have time for that one talk that you really want to see, and we (and the speaker) would be very happy that you did decide to come, despite that the order of speakers will only be decided on the spot. In order to help everyone in their planning, we aim to be relatively strict with the time. However, since you can have lunch while listening to the talks, you potentially do not lose time at all.

We will not police people, but will encourage people to stay by providing an important service and forum to the PhD/Postdoc Community. In the end, we hope that people will see the value of staying and spend that little extra time. Do you really want to be that person that walks out of that room for all (including the next speaker) to see?

JL: Or, would you like to be the second speaker, who spent time and energy in preparing a non-expert talk, who has to introduce your research question could heavily benefit.

What is the best thing that you foresee this initiative will bring?

AF: Our main motivation is to invest into the PhD/Postdoc Community. For me, meetings like these were often the highlight of my week. If you feel inspired, if you have learned something new or even got ideas you can employ in your own research: That would be the best reward.

JL: Those seminars forced me to really master my topic and to combine approaches from different fields in my later research; the campus seminar organizers appreciated your feedback and constructive criticism on this initiative. Kindly contact: Alex Faesen (afaesen@mpibpc.mpg.de) Stefan Glöggler (stefan.glaegger@mpibpc.mpg.de) Juliane Liepe (juliane.liepe@mpibpc.mpg.de)
Göttinger Nacht des Wissens 2019


Unser Institut wird gemeinsam mit dem MPI für Experimentelle Medizin sowie dem MPI für Dynamik und Selbstorganisation erneut im MPI für Sonnensystemforschung seine Aktionen präsentieren. Unser herzlicher Dank geht schon einmal an unsere dortige Gastgeber, die uns immer so nett aufnehmen – und an unsere Abteilungen und Forschungsgruppen, die sich bei der Nacht des Wissens mit großem Engagement engagieren!


Eine Übersicht aller Angebote bei der 4. Nacht des Wissens finden Sie auf www.ndw.uni-goettingen.de (cr)

Göttingen Science Night 2019

will again present their research at the MPI for Solar System Research. Our heartfelt thanks go to our wonderful hosts there – and to our departments and research groups who participate in the upcoming Science Night!

At the booth of the Department of Theoretical and Computational Biophysics you may dive into the world of proteins and at the Department of Genes and Behavior you can find out whether you are an early riser, a night owl, or neither. But why do we have to sleep at all? Answers may be found in the hands-on activities of the Research Group Sleep and Waking. Experiments of the Department of Meiosis, on the other hand, follow the motto: In the beginning there was the egg! Here, adults as well as the youngest can explore the secrets of the egg cell. And if you want to learn more about what happens in our body, join Jens Frahm’s lecture MRI movies in realtime – following movements in our body live at 7 pm (lecture in German).

You may find an overview of all events at the 4th Science Night at www.ndw.uni-goettingen.de (cr)

Horizons turns 15: Looking back at the scientific fiesta of 2018

Over 250 researchers from 30 countries together with renowned scientists joined us at the MPI-BPC for the special 15th anniversary Horizons in Molecular Biology symposium.

Fifteen years ago, Horizons in Molecular Biology was conceived by the students of the IMPRS in Molecular Biology to widen their own horizons beyond the rut of classes and lab work. The symposium has since grown from a humble idea to one of the most sought-after events in Göttingen. It aims to bridge the gap between young researchers and experienced scientists by providing them a platform for interaction. The four-day long event included a career fair, scientific talks, poster sessions, panel discussions, speed dating, and career workshops. The social events in the evenings offered time to relax and network in informal settings. It was great fun to hear one’s favorite scientist’s talk in the morning and share the dance floor with them in the evening.

The eclectic career fair had speakers from academia, industry, science communication, consulting, and even modeling. Their unique stories inspired and reassured the audience that there is more than meets the eye for one’s future. Daisy Robinton, a scientist as well as a fitness and lifestyle model, gave an inspiring talk on the state of modern fitness in the morning. Her story is one of overcoming adversity and finding true self-worth. Her dedication to fitness and body image advocacy is truly inspiring.

The scientific talks were just as impressive. Barry Marshall, a Nobel laureate in Physiology or Medicine, gave a talk on the discovery of the role of Helicobacter pylori in stomach ulcers. His talk was educational and inspiring, providing insight into the potential for disease prevention and treatment. Keynotes included orientation talks about the biology of the body and the brain, the role of the immune system in disease, and the importance of sleep in the body.

The symposium was not just about the science. The event also included a number of social activities, such as a welcome reception at the University of Göttingen’s central hall and a farewell dinner at a local restaurant. These events provided opportunities for networking and informal discussions.

Looking back at the scientific fiesta of 2018, it is clear that the Horizons symposium has become an important event for young researchers and established scientists alike. The symposium provides a platform for discussion and networking, and it has helped to foster collaborations and new friendships.

Ninadini Sharma on behalf of the Horizons organizing committee
Samba-Server gehören schon seit mehr als 20 Jahren zum festen Bestand bei der GWDG, haben sich im Einsatz bewährt und sind bis auf Weiteres unverzichtbar. Sie stellen für den Göttingen Campus die zentralen Druckdienste und einen Zugang zu den persönlichen UNIX-Speicherbereichen für Arbeitsplatzrechner bereit, wobei die Nutzung überwiegend unter Windows, aber auch unter macOS oder FreeBSD/Linux erfolgen kann.

Am 23. August 2018 fand das diesjährige, von der GWDG veranstaltete Treffen der Institutsadministratoren auf dem Max-Planck-Campus in Göttingen statt. Themenschwerpunkt waren die weitreichenden Änderungen im Bereich Massenspeicher in den vergangenen Monaten.


Thomas Otto

Influential Max Planck authors

76 Max Planck scientists are among the most highly cited researchers 2018. The list also includes 17 Nobel Laureates. One of them is Stefan Hell, Director at the MPI-BPC.

The Clarivate Analytics citation analysis, now in its fifth year, provides information about researchers who have published the most highly cited publications in recent years. In addition to the research areas, the corresponding institutions are also listed. With a total of 356 successful scientists, Germany ranks fourth among the scientific locations after the United States, Great Britain, and China. Among the research organizations, the Max Planck Society ranks fifth behind Harvard University (United States), the National Institutes of Health (United States), Stanford University (United States), and the Chinese Academy of Science.

The methodology that determines the who’s who of high-impact researchers draws on the data and analysis performed by bibliometric experts from the Institute of Scientific Information at Clarivate Analytics. The publication and citation data come from the Web of Science, a web-based database for scientific and commercial purposes containing the scientific literature of over 30,000 journal titles.

Modified from a press release of the Max Planck Society

Science hotspots: The most successful scientists work in North America, Europe, and China. Australia is catching up. (Image: Clarivate Analytics)