

MOLECULAR BIOLOGY NEWSLETTER

Georg-August-Universität Göttingen · International Max Planck Research School



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2019

Welcome message

Dear alumni, students, friends and colleagues,

Welcome to the 10th edition of our annual Molbio newsletter, reviewing the events and activities of the past year, presenting contributions by current and former members of our graduate program, and honoring their achievements.

January 2019 marks the start of a new funding period for our International Max Planck Research School after our 18-plus proposal was successful. At the same time, the new DFG Cluster of Excellence “Multiscale Imaging: From Molecular Machines to Excitable Cells”, in which many of our faculty members participate, has been launched. Some of our Molbio faculty members serve also as fellows in the newly established Max Planck School “Matter to Life”, which is primarily hosted by the universities and Max Planck partners in Heidelberg, Göttingen and Munich. Beyond the continuous evaluation and readjustments of our curriculum, the dynamic research environment on the Göttingen Campus will be reflected in new scientific directions our IMPRS will explore in the near future.

A key measure of the new IMPRS funding period will be our new alumni mentoring program which is briefly introduced by our colleague Stefanie Klug on the back-cover (p. 36) of this newsletter. Along the same line, our annual PhD Career Forum, at which our alumni share their experiences and give career advice in presenta-

tions and round-table discussions, has become an integral and popular part of our annual Molbio retreats. The retreat in Bremen in summer 2018 was, once again, a great success and we are looking forward to our next retreat in Leipzig in April 2019.

In the year 2018, our Molecular Biology MSc and PhD programs successfully passed their third re-accreditation, a formal evaluation of the concept, structure and services provided. In addition, we enjoyed two celebrations: The 15th Anniversary of the



Molbio PhD Career Forum, Harnack Haus, Berlin

student-organized “Horizons in Molecular Biology” symposium (p. 32-33 of this newsletter) and the 10th Anniversary of the GGNB. The latter has recently been renamed “Göttingen Center for Neurosciences, Biophysics, and Molecular Biosciences” and became established as a permanent graduate center for international, campus-wide PhD programs in the life sciences under the umbrella of newly structured natural science graduate school GAUSS.

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As many of the readers will remember, our Molecular Biology Program started in 2000 together with its “twin program” and IMPRS in Neuroscience. Since 2005, the Neuroscience Program was coordinated by our dear colleague and respected faculty member Michael Hörner who sadly passed away after a prolonged battle with illness in October 2018 (p. 35 of this newsletter). Beyond the scientific coordination of the Neuroscience program and the close interaction with our activities, Michael was involved in teaching, headed the ELECTRAIN training lab at the ENI, and served as a speaker of the GGNB doctoral program “Molecular Physiology of the Brain”. We have greatest respect of his achievements and talented student mentoring and miss him very much as a colleague and dear friend.

P. Rehling, M. Rodnina, S. Burkhardt

Myc in stem cell polarity

Stem cell maintenance is dependent on a balance between stem cell self-renewal and production of differentiating daughter cells. Because disturbances in this balance can lead to tumorigenesis or stem cell loss, stem cell division needs to be tightly controlled. *Drosophila* neural stem cells, called neuroblasts, achieve this balance by dividing asymmetrically. Prior to division, the neuroblast establishes cortical polarity to regulate the inheritance of stem cell factors by the daughter stem cell, while the differentiating offspring cells receives factors inducing neural differentiation. One of the key regulators of neuroblast polarity is the Par-complex and its kinase subunit aPKC, which phosphorylates target proteins to achieve polarized localization to the apical or basal neuroblast side. Although the establishment of neuroblast polarity is well described, little is known about how polarity, cell division and proliferation rates are coordinated transcriptionally.

We identified the transcription factor Myc as an important regulator of neuroblast behavior. Interestingly, Myc cooperates with various components of the Tip60 chromatin remodeler complex,

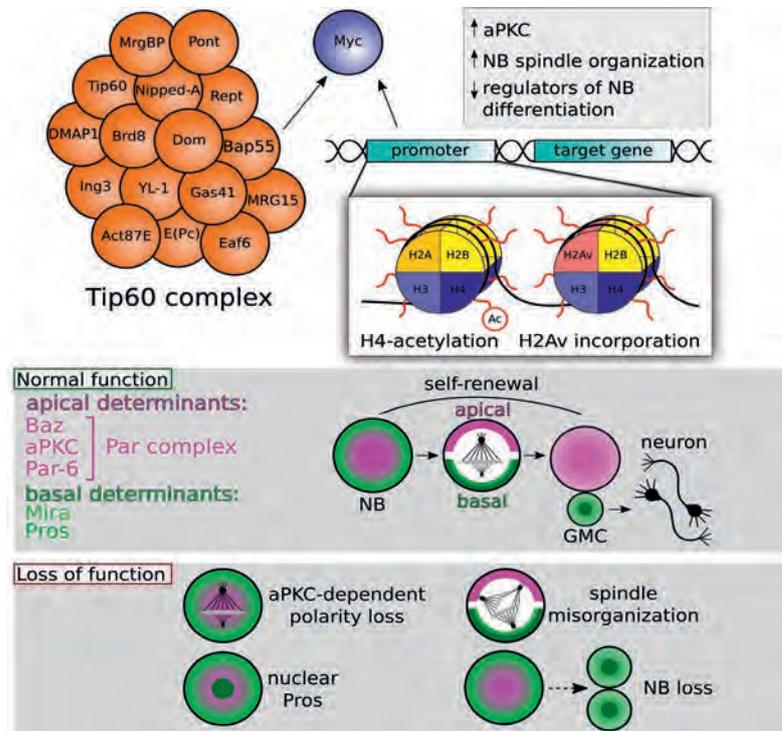


Fig. 1: Model for regulation of neuroblast division by Myc and the Tip60-complex. Myc interacts with the Tip60-complex to mediate histone acetylation and H2A variant incorporation to regulate neuroblast (NB) division. In the presence of Myc and the Tip60-complex, neuroblasts display apico-basal polarity and divide asymmetrically. Myc and the Tip60-complex ensure neuroblast polarity through induction of aPKC expression, the kinase subunit of the polarity regulating Par-complex. In addition and independent of aPKC, the Myc-Tip60 transcriptional network is required for spindle organization and prevents nuclear entry of the neural differentiation factor Pros, thus ensuring neuroblast maintenance. GMC = ganglion mother cell.

PhD-(and MSc-) related publications 2018 (PhD students of the Molecular Biology program in bold type)

Adio S, **Sharma H**, Senyushkina T, **Karki P**, Maracci C, Wohlgemuth I, Holtkamp W, Peske F, **Rodnina MV** (2018) Dynamics of ribosomes and release factors during translation termination in *E.coli*. *eLife* 7:e34252

Aksu M, **Pleiner T**, **Karaca S**, Kappert C, Dehne HJ, Seibel K, **Urlaub H**, **Bohnsack MT**, **Görllich D** (2018) Xpo7 is a broad-spectrum exportin and a nuclear import receptor. *J Cell Biol* 217(7):2329-2340

Andreeva I, Belardinelli R, **Rodnina MV** (2018) Translation initiation in bacterial polysomes through ribosome loading on a standby site on a highly translated mRNA. *Proc Natl Acad Sci USA* 115(17):4411-4416

Behler J, **Sharma K**, Reimann V, Wilde A, **Urlaub H**, Hess WR (2018) The host-encoded RNase E endonuclease as the crRNA maturation enzyme in a CRISPR-Cas subtype III-Bv system. *Nat Microbiol* 3(3):367-377

Boehning M, Dugast-Darzacq C, Rankovic M, Hansen AS, Yu T, Marie-Nelly H, McSwiggen DT, **Kokic G**, Dailey GM, **Cramer P**, Darzacq X, **Zweckstetter M** (2018) RNA polymerase II clustering through carboxy-terminal domain phase separation. *Nat Struct Mol Biol* 25(9):833-840

Böker KO, **Lemus-Diaz N**, Ferreira RR, Schiller L, Schneider S, **Gruber J** (2018) The Impact of the CD9 Tetraspanin on Lentivirus Infectivity and Exosome Secretion. *Mol Ther* 26(2):634-647

an interaction that is highly conserved in mammals, and required for maintenance of human embryonic stem cells. Like in mammals, *Drosophila* Myc recruits the Tip60-complex to target gene promoters, which acetylates histone H4 and exchanges the canonical histone H2A with the variant H2Av to induce gene expression.

By manipulating Myc and Tip60-complex components in *Drosophila* larval brain neuroblasts, we found that the Myc-Tip60 transcriptional network regulates various features of neuroblast division including apico-basal polarity, asymmetric cell division, proliferation rates and cell growth. In the absence of any components of the Myc-Tip60 transcriptional network, neuroblasts differentiate prematurely upon nuclear entry of the transcription factor Prospero, which induces neural differentiation.

Using RNA-sequencing we found that the Myc-Tip60 network regulates the expression of a large number of target genes, including the Par-complex kinase aPKC. A chromatin-immunoprecipitation assay confirmed aPKC as a direct target gene

of both Myc and Domino, a catalytic subunit of the Tip60-complex. Restoration of aPKC levels in the background of Myc or Tip60-complex loss of function fully rescued neuroblast polarity. However, live imaging of neuroblast divisions revealed that aPKC is not sufficient to restore asymmetric division. Instead, the Myc-Tip60 network regulates the expression of various components of the spindle apparatus.

Subsequent immunofluorescence staining and live imaging experiments identified abnormal spindle morphology and triple divisions upon Myc-Tip60 network knockdown as a likely cause. These results show that asymmetric division is not

solely dependent on regulators of apico-basal polarity but relies on the expression of spindle genes by Myc-Tip60.

In summary, our study has revealed a transcriptional network consisting of Myc and the Tip60 chromatin remodeling complex to regulate a variety of features of *Drosophila* neural stem cell division. This network therefore functions upstream in neuroblast transcriptional hierarchy. Since Myc-Tip60 is highly conserved in mammals and both Myc and Tip60-complex subunits have been associated with stem cell maintenance as well as tumor formation, our study adds valuable insight into functions of the Myc-Tip60 network.

Katja Rust completed her doctoral thesis in the group of Andreas Wodarz and defended her PhD thesis in November 2016. Currently she is a postdoctoral researcher at the University of California, San Francisco.

Results of this work were published in Rust K, Tiwari MD, Mishra VK, Grawe F, Wodarz A (2018) EMBO J 37, e98659



Brüning L, Hackert P, Martin R, Davila Gallesio J, **Aquino G**, **Urlaub H**, Sloan KE, **Bohnsack M** (2018) RNA helicases mediate structural transitions and compositional changes in pre-ribosomal complexes. Nat Commun 9:5383

Buddeweg A, **Sharma K**, **Urlaub H**, Schmitz RA (2018) sRNA₄₁ affects ribosome binding sites within polycistronic mRNAs in *Methanosarcina mazei* Gö1. Mol Microbiol 107(5):595-609

Buskin A, Zhu L, Chichagova V, Basu B, **Mozaffari-Jovin S**, Dolan D, Droop A, Collin J, Bronstein R, Mehrotra S, Farkas M, Hilgen G, White K, Pan KT, Treumann A, Hallam D, Bialas K, Chung G, Mellough C, Ding Y, Krasnogor N, Przyborski S, Zwolinski S, Al-Aama J, Alharthi S, Xu Y, Wheway G, Szymanska K, McKibbin M, Inglehearn CF, Elliott DJ, Lindsay S, Ali RR, Steel DH, Armstrong L, Sernagor E, **Urlaub H**, Pierce E, **Lührmann R**, Grellscheid SN, Johnson CA, Lako M (2018) Disrupted alternative splicing for genes implicated in splicing and ciliogenesis causes PRPF31 retinitis pigmentosa. Nat Commun 9(1):4234

Butkevich AN, Ta H, **Ratz M**, Stoldt S, **Jakobs S**, Belov VN, **Hell SW** (2018) Two-Color 810 nm STED Nanoscopy of Living Cells with Endogenous SNAP-Tagged Fusion Proteins. ACS Chem Biol 13(2):475-480

Cantuti-Castelvetri L, Fitzner D, Bosch-Queralt M, Weil MT, **Su MH**, Sen P, Ruhwedel T, Mitkovski M, Trendelenburg G, Lutjohann D, Möbius W, **Simons M** (2018) Defective cholesterol clearance limits remyelination in the aged central nervous system. Science 359(6376):684-688

X10 Expansion Microscopy

or: how to do super-resolution imaging with diapers

Biologists face a common problem: how do you visualize processes and structures within a cell? Fluorescence light microscopy provides an ideal tool for identifying multiple specific targets in parallel, and modern optics allow a magnification down to the nanoscale. Simply magnifying cells is not enough, however, as there is a limit to how close together two objects can be before they become indistinguishable in light microscopy. This so-called resolution limit, imposed by the wave-like nature of light, is ~250-300 nm. Imagine looking at a landscape but being unable to distinguish where a tree ends and where the birds sitting in it begin!

Until recently, we cheated our way around this resolution limit by tricking fluorophores into unlikely molecular states. Switching fluorophores on and off temporally separates their light emissions, allowing us to observe them separately and pinpoint their positions individually. This approach, such as practiced in STED

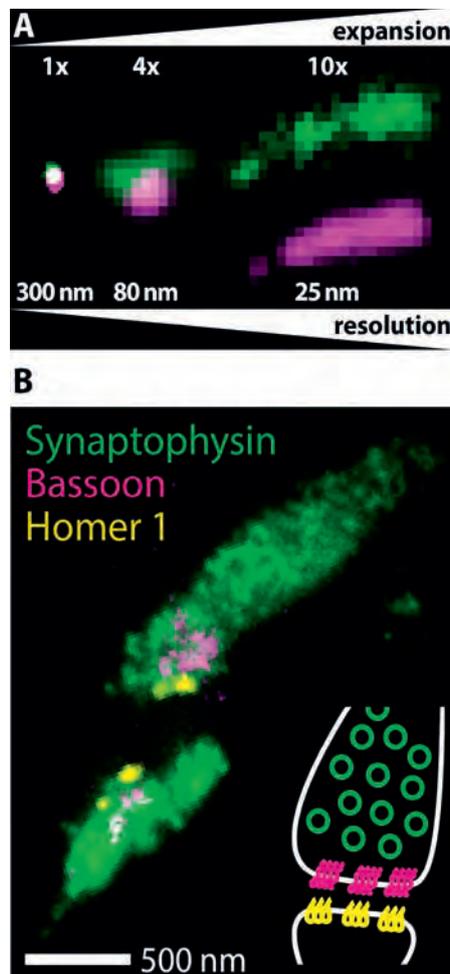


Fig. 1: X10 expansion microscopy allows multi-color imaging at 25 nm resolution on conventional microscopes. (A) In expansion microscopy, resolution directly corresponds to the expansion factor, as demonstrated here on a pre-synaptic protein (Bassoon, green) and a post-synaptic protein (Homer 1, magenta). This figure was reproduced from Truckenbrodt et al. (2018) EMBO Rep. **(B)** X10 allows the visualization of multiple sub-cellular structures in parallel, such as shown here for three synaptic markers: synaptic vesicles (Synaptophysin, green), the pre-synaptic active zone (Bassoon, magenta), and the post-synaptic density (Homer 1, yellow). This figure was adapted from Truckenbrodt et al. (2018) EMBO Rep.

and STORM microscopy, unfortunately requires large amounts of the most limited commodities of scientists: time and money. The demand of super-resolution microscopy on optics and fluorophores typically also limits imaging to one or two channels. Imagine photographing a landscape one

Choudhury P, Hackert P, **Memet I**, Sloan KE, **Bohnsack M** (2018) The human RNA helicase DHX37 is required for release of the U3 snoRNP from pre-ribosomal particles. *RNA Biology* 2018 Dec 24 [Epub ahead of print]

Cretu C, Agrawal AA, Cook A, Will CL, Fekkes P, Smith PG, **Lührmann R**, Larsen N, Buonamici S, **Pena V** (2018) Structural Basis of Splicing Modulation by Antitumor Macrolide Compounds. *Mol Cell* 70(2):265-273

de Moura TR, **Mozaffari-Jovin S**, Szabo CZK, Schmitzova J, **Dybkov O**, **Cretu C**, Kachala M, Svergun D, **Urlaub H**, **Lührmann R**, **Pena V** (2018) Prp19/Pso4 Is an Autoinhibited Ubiquitin Ligase Activated by Stepwise Assembly of Three Splicing Factors. *Mol Cell* 69(6):979-992.e6

Eckermann KN, Ahmed HMM, **KaramiNejadRanjbar M**, Dippel S, Ogaugwu CE, Kitzmann P, Isah MD, **Wimmer EA** (2018) Hyperactive piggyBac transposase improves transformation efficiency in diverse insect species. *Insect Biochem Mol Biol* 98:16-24

Farsi Z, Gowrisankaran S, **Kronic M**, Rammner B, Woehler A, Lafer EM, Mim C, **Jahn R**, Milosevic I (2018) Clathrin coat controls synaptic vesicle acidification by blocking vacuolar ATPase activity. *Elife* 7:e32569

Frey S, Rees R, Schunemann J, Ng SC, **Fünfgeld K**, Huyton T, **Görllich D** (2018) Surface Properties Determining Passage Rates of Proteins through Nuclear Pores. *Cell* 174(1):202-217

Harasimov K, **Schuh M** (2018) Actin Disassembly: How to Contract without Motors? *Curr Biol* 28(6):R275-R277

Science Spotlight 2018

feature at a time: first trees, then birds, then butterflies – you would never get an accurate picture!

A solution to these problems arose recently from an unlikely direction: baby diapers!

Superabsorbent hydrogels, like the ones found in baby diapers, can swell to many times their original volume when brought into contact with water. If we could expand a biological sample equally in all three dimensions, we would be able to resolve targets that previously were too close together, while still preserving the organization of the sample. The idea is strikingly simple: if cellular features are too close together to resolve – why can't we just spatially separate them?

In 2015, expansion microscopy was invented when the team of Ed Boyden at MIT found a way to couple biological samples into such hydrogels. They initially achieved 4-fold expansion, which separates features as close together as 70-80 nm before expansion far enough to push them beyond

the 250-nm limit – and thus resolving them! In the lab of Silvio Rizzoli, I further developed this idea and achieved 10-fold expansion in an approach we termed X10 microscopy. With X10, we can now resolve targets that originally were only 25 nm apart. Perhaps the best thing about it is that multi-color super-resolution imaging finally becomes easily achievable, almost trivial.

Since we can now do multi-color super-resolution microscopy on conventional microscopes, X10 also saves a lot of time and money. It is particularly important to me that this new approach makes super-resolution

microscopy available (and affordable!), not only to a few specialists, but to most biology laboratories. Various labs are now using X10 to investigate synapses, the cytoskeleton, protein trafficking, organelle organization, receptor signaling, and many more topics in all areas of biology. I hope that X10 is thus going to contribute to the on-going transformation of how we perceive biology through super-resolution imaging.

Sven Truckenbrodt completed his doctoral thesis in the lab of Silvio O. Rizzoli in October 2016. He is currently a post-doc in the lab of Johann G. Danzl at IST Austria.

These results were published in Truckenbrodt S, Maidorn M, Crzan D, Wildhagen H, Kabatas S, Rizzoli SO (2018) EMBO Rep e45836 and Truckenbrodt S, Sommer C, Rizzoli SO, Danzl JG (2019) Nat Protoc (in press)



Haselbach D, Komarov I, Agafonov DE, Hartmuth K, Graf B, **Dybkov O**, Urlaub H, Kastner B, Lührmann R, Stark H (2018) Structure and Conformational Dynamics of the Human Spliceosomal B-act Complex. Cell 172(3):454-464.e11

Hoffmann DB, Gruber J, Böker KO, Deppe D, Sehmisch S, Schilling AF, **Lemus-Diaz N**, Komrakova M, Schneider S (2018) Effects of RANKL Knockdown by Virus-like Particle-Mediated RNAi in a Rat Model of Osteoporosis. Molecular Therapy-Nucleic Acids 12:443-452

Jean P*, **Lopez de la Morena D***, Michanski S*, Jaime Tobón LM*, Chakrabarti R, Picher MM, Neef J, Jung S, Gültas M, Maxeiner S, Neef A, Wichmann C, Strenzke N, Grabner C, Moser T (2018). The synaptic ribbon is critical for sound encoding at high rates and with temporal precision. eLife:29275

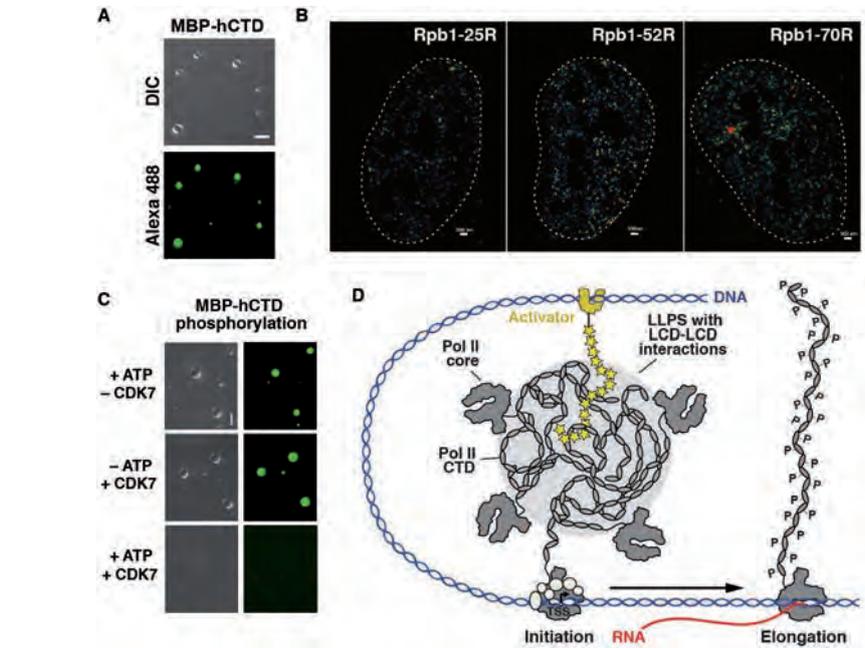
KaramiNejadRanjbar M, **Eckermann KN**, Ahmed HMM, Sanchez CHM, Dippel S, Marshall JM, Wimmer EA (2018) Consequences of resistance evolution in a Cas9-based sex conversion-suppression gene drive for insect pest management. Proc Natl Acad Sci USA 115(24):6189-6194

Keller B, Shoukier M, Schulz K, **Bhatt A**, Heine I, Strohmeier V, Speckmann C, Engels N, Warnatz K, Wienands J (2018) Germline deletion of CIN85 in humans with X chromosome-linked antibody deficiency. J Exp Med 215(5):1327-1336

Unstructural Biology of Gene Transcription

The vast number of biological functions that are exerted simultaneously in living cells requires a delicate coordination of biochemical processes in space and time. As a key organizational principle, eukaryotic cells use membranes to compartmentalize their biochemistry. Apart from membrane-bound compartmentalization, cells can further concentrate cellular components in so-called membraneless organelles. Accumulating evidence suggests that these biomolecular condensates are stabilized by multivalent low-affinity interactions between disordered low-complexity domains. Like oil droplets in water, with increasing protein concentration these interactions can lead to liquid demixing in a process called liquid-liquid phase separation (LLPS).

During the transcription of protein-coding genes, RNA polymerase (Pol) II clusters in short-lived nuclear condensates, but its underlying molecular basis has remained enigmatic. The largest Pol II subunit, Rpb1, possesses a disordered, C-terminal low-complexity domain (CTD) that is essential for pre-mRNA synthesis and co-transcriptional processing. The CTD forms a long, tail-like extensi-



on from the Pol II core and consists of multiple heptapeptide repeats with the consensus sequence $Y_1S_2P_3T_4S_5P_6S_7$. The human CTD (hCTD) is composed of 52 heptapeptide repeats, with an N-terminal half that contains mostly consensus repeats and closely resembles the 26-repeat *Saccharomyces cerevisiae* CTD (yCTD), and a C-terminal half with more diverging repeats.

Fig. 1: (A) DIC and fluorescence microscopy demonstrate the formation of phase separated MBP-hCTD droplets. Scalebar, 10 μ m. (B) Reconstructed PALM images of live human cells that express Pol II with different CTD lengths. (C) Phosphorylation by human CDK7 complex counteracts hCTD phase separation. Scalebar, 10 μ m. (D) Model for CTD-mediated phase separation in activated transcription

Keppeler D*, Martins Merino R*, Lopez de la Morena D*, Bali B, Huet AT, Gehrt A, Wrobel C, Subramanian S, Dombrowski T, Wolf F, Rankovic V, Neef A, Moser T (2018) Ultrafast optogenetic stimulation of the auditory pathway by targeting-optimized Chronos. EMBO J: e99649

Klusmann I, Wohlberedt K, Magerhans A, Teloni F, Korbelt JO, Altmeyer M, Dobbstein M (2018) Chromatin modifiers Mdm2 and RNF2 prevent RNA:DNA hybrids that impair DNA replication. Proc Natl Acad Sci USA 115(48):E11311-E11320

Komorowski K, Salditt A, Xu YH, Yavuz H, Brennich M, Jahn R, Salditt T (2018) Vesicle Adhesion and Fusion Studied by Small-Angle X-Ray Scattering. Biophys J 114(8):1908-1920

Kosinsky RL, Lorenz Chua R, Qui M, Saul D, Mehlich D, Ströbel P, Schildhaus H-U, Wegwitz F, Faubion WA, Johnsen SA (2018) Loss of RNF40 Decreases NF- κ B Activity in Colorectal Cancer Cells and Reduces Colitis Burden in Mice. Journal of Crohn's and Colitis, jcy165

Kretschmar FK, Mengel LA, Müller AO, Schmitt K, Bliersch KF, Valerius O, Braus GH, Ischebeck T (2018) PUX10 Is a Lipid Droplet-Localized Scaffold Protein That Interacts with CELL DIVISION CYCLE48 and Is Involved in the Degradation of Lipid Droplet Proteins. Plant Cell 30(9):2137-2160

We thus reasoned whether CTD-based LLPS could underlie Pol II clustering. To test this, we recombinantly expressed and purified human and yeast CTD. Indeed, human and yeast CTD self-associated to form micrometer-sized, phase-separated droplets in near-physiological buffer in the presence of dextran to mimic the crowded nuclear environment. Upon contact, two droplets fused into one that readily returned to spherical shape, underpinning the liquid-like nature of CTD droplets. Through a series of orthogonal experiments we could show additionally that phase separation strongly correlated with CTD length: As compared to hCTD, the shorter yCTD formed less stable droplets.

Analogous to our results obtained *in vitro*, we next wanted to test the effect of CTD length on Pol II clustering in living human cells. We constructed three human cell lines encoding fluorescently labeled Pol II with different CTD lengths and analyzed Pol II clustering using three-dimensional photoactivated localization microscopy (PALM). Compared to wild-type cells, human cells containing a truncated, yeast-like CTD exhibited less Pol II

clustering. Further extension of the CTD, on the other hand, resulted in a more pronounced clustering signature. These results demonstrated that Pol II clustering in cells depends on the CTD and increases with increasing CTD length.

Assembly of the pre-initiation complex at Pol II promoters requires an unphosphorylated CTD and subsequent CTD phosphorylation by the cyclin-dependent kinase 7 (CDK7) in transcription factor IIH stimulates the transition of Pol II into active elongation. To investigate the impact of CTD phosphorylation on phase separation, we used recombinant CDK7 complex to phosphorylate hCTD and yCTD. In both cases CDK7-phosphorylation was incompatible with CTD phase separation.

Altogether, our results imply a simple model for CTD function during eukaryotic gene activation: Unphosphorylated Pol II clusters to form condensates, mediated by multivalent CTD-CTD interactions. Activation domains of transcription factors can form interactions with CTDs and further promote Pol II condensation. Condensates at promoters serve as reservoir of Pol II during activated transcription. Pol II incorporation into the pre-initiation complex and subsequent CTD phosphorylation by CDK7 ultimately releases single Pol II enzymes into active transcription elongation. These findings, together with other published results, provide the basis for analyzing the role of protein condensation for transcriptional regulation in the future.

Marc Böhning is a PhD student in the group of Patrick Cramer at the MPI for Biophysical Chemistry.

These results were published in Boehning M, Dugast-Darzacq C, Rankovic M, Hansen AS, Yu T, Marie-Nelly H, McSwiggen DT, Kokic G, Dailey GM, Cramer P, Darzacq X, Zweckstetter M (2018) Nat Struct Mol Biol 25:833-840



Lako M, Buskin A, Zhu LL, Chichagova V, Basu B, **Mozaffari-Jovin S**, Dolan D, Droop A, Collin J, Hilgen G, Armstrong L, Sernagor E, Lührmann R, Grellscheid SN, Johnson C (2018) Human iPSC-derived RPE and retinal organoids reveal impaired alternative splicing of genes involved in pre-mRNA splicing in PRPF31 autosomal dominant retinitis pigmentosa. Investigative Ophthalmology & Visual Science 59(9)

Li YZ, **Köpper F**, Dobbelstein M (2018) Inhibition of MAPKAPK2/MK2 facilitates DNA replication upon cancer cell treatment with gemcitabine but not cisplatin. Cancer Letters 428:45-54

Mager T*, **Lopez de la Morena D***, Senn V, Schlotte J, D'Errico A, Feldbauer K, Wrobel C, Jung S, Bodensiek K, Rankovic V, Browne L, Huet A, Jüttner J, Wood PG, Letzkus JJ, Moser T, Bamberg E (2018). High frequency neural spiking and auditory signaling by ultrafast red-shifted optogenetics. Nat Commun 9:1750

Maidorn M, Olichon A, Rizzoli SO, Opazo F (2018) Nanobodies reveal an extra-synaptic population of SNAP-25 and Syntaxin 1A in hippocampal neurons. MAbs DOI: 10.1080/19420862.2018.1551675

Maier LK, Stachler AE, Brendel J, Stoll B, Fischer S, Haas KA, Schwarz TS, Alkhnbashi OS, **Sharma K**, Urlaub H, Backofen R, Gophna U, Marchfelder A (2018) The nuts and bolts of the *Haloflex* CRISPR-Cas system I-B. RNA Biol 2018 May 21:1-12

Expanding the plant lipid droplet proteome

Lipid droplets (LDs) are ubiquitous but unique cellular compartments that have only recently been recognized as *de facto* organelles. Conserved throughout eukaryotes, they contain a phospholipid monolayer surrounding a core of neutral lipids - in contrast to other organelles, where a lipid bilayer surrounds an aqueous compartment. Consequently, a unique set of proteins is associated with this special membrane architecture of the LDs.

In plants, where LDs are of large economic value as they store the oil in major crops like oil seed rape or olives, not even a dozen protein families were proven to be LD-localized. The most prominent protein families are Oleosins, Caleosins and Sterleosins, which together account for more than 90% of the lipid droplet proteome in seeds. To further elucidate formation, function and degradation of the organelle, the discovery of new proteins is crucial.

To identify new LD proteins, we investigated a previously unstudied,

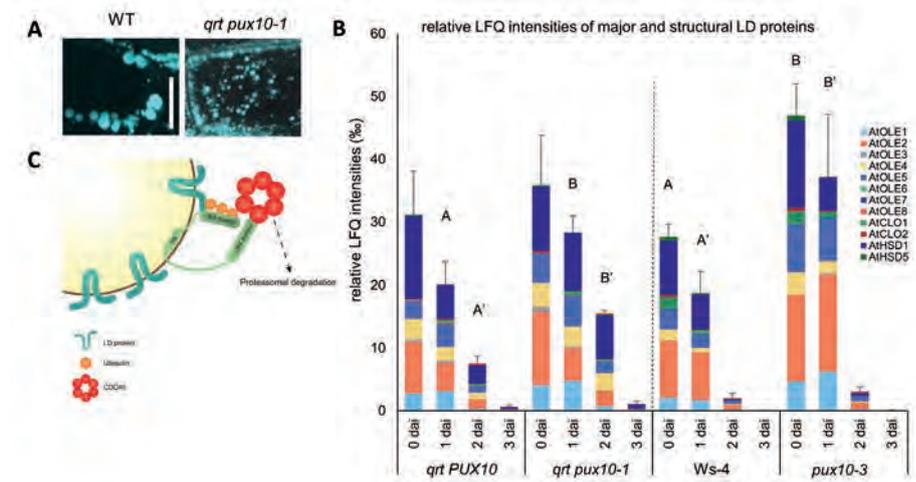


Fig. 1: (A) At 48 h of germination, LDs of the mutant are significantly smaller than the WT (Bar, 10 μ m). (B) In the mutants (*qrt pux10-1* and *pux10-3*), breakdown of LD proteins is delayed. (C) PUX10 is a scaffold protein functioning in the degradation of LD proteins

LD-rich organ: Tobacco (*Nicotiana tabacum*) pollen tubes. In a shotgun proteomics approach, we compared the proteome of LD-enriched fractions with the total and cytosolic fractions. Proteins that were both enriched in the LD fraction and of high abundance in that fraction were considered candidates qualifying for further investigation.

We confirmed the LD-localization of candidates by transiently expressing them in fusion with a fluorescent protein in tobacco pollen tubes. This way, we could confirm the LD-localization of three new proteins or protein families.

One of these newly identified LD proteins is a UBX-domain contain-

Mandad S, Rahman RU, Centeno TP, Vidal RO, Wildhagen H, Rammner B, Keihani S, Opazo F, Urban I, Ischebeck T, Kirli K, Benito E, Fischer A, Yousefi RY, Dennerlein S, Rehling P, Feussner I, Urlaub H, Bonn S, Rizzoli SO, Fornasiero EF (2018) The codon sequences predict protein lifetimes and other parameters of the protein life cycle in the mouse brain. *Sci Rep-UK* 8: 16913

Mentel M, Ionescu AE, Puscalau-Girtu I, Helm MS, Badea RA, Rizzoli SO, Szedlaczek SE (2018) WDR1 is a novel EYA3 substrate and its dephosphorylation induces modifications of the cellular actin cytoskeleton. *Sci Rep-UK* 8:2910

Papathanasiou P, Erdmann S, Leon-Sobrinho C, Sharma K, Urlaub H, Garrett RA, Peng X (2018) Stable maintenance of the rudivirus SIRV3 in a carrier state in *Sulfolobus islandicus* despite activation of the CRISPR-Cas immune response by a second virus SMV1. *RNA Biol* 2018 Sep 13:1-9

Pleiner T, Bates M, Görlich D (2018) toolbox of anti-mouse and anti-rabbit IgG secondary nanobodies. *J Cell Biol* 217(3):1143-1154

Richter F, Dennerlein S, Nikolov M, Jans D, Nataliia Naumenko N, Aich A, MacVicar T, Linden A, Jakobs S, Urlaub H, Langer T, Rehling P (2018) ROMO1 is a constituent of the human presequence translocase required for YME1L protease import. *J Cell Biol:jcb.201806093*

Richter KN, Wildhagen H, Helm MS, Ussling JE, Schikorski T, Rizzoli SO (2018) Comparative synaptosome imaging: a semi-quantitative method to obtain copy numbers for synaptic and neuronal proteins. *Sci Rep-UK* 8:14838

ing protein. This domain is conserved across eukaryotes. In yeast and humans, for example, proteins containing this domain play important roles in protein degradation like the ER-associated degradation (ERAD) pathway. The pathway for the degradation of plant LD proteins is largely unknown, and so we investigated whether this protein, PLANT UBX-DOMAIN CONTAINING PROTEIN 10 – PUX10, is involved in this process.

For this, we switched systems for tobacco to the model plant *Arabidopsis thaliana*, where the protein is conserved and can be easily studied through analyses of knockout mutants. The *pux10* mutants we acquired were not impaired in growth, however, we could observe a phenotype on cellular level: During germination, the LDs stored in the seeds are degraded to provide energy for the growth of the seedling before the start of photosynthesis.

This process is marked by a decrease in number of LDs in the cells, but an

increase in their size. In the *pux10* mutants, the LDs remained significantly smaller than in the Wild type (WT, Fig. 1A). This observation could correlate with a change of protein-to-oil ratio, so we investigated the abundance of LD proteins in the seedlings at different time points during germination by label-free proteomics. Indeed, in the mutants, the breakdown of known LD proteins like Oleosins and Steroleosins is significantly delayed, compared to the WT (Fig. 1B).

Additionally, we could also find ubiquitin accumulated on LDs isolated from mutant seedlings, and ubiquitination sites in some of the Oleosins

and Steroleosins. Taken together, our finding suggest that PUX10 is a LD-localized protein involved in the turnover of major LD proteins (Fig. 1C). However, the lack of PUX10 does not completely abolish the breakdown of LD proteins or LDs themselves, indicating redundant processes that still have to be determined.

Franziska Kretzschmar is a PhD student in the group of Till Ischebeck in the Department of Plant Biochemistry at the University of Göttingen.

These results were published in Kretzschmar FK, Mengel LA, Müller AO, Schmitt K, Blersch KF, Valerius O, Braus GH, Ischebeck T (2018) *Plant Cell* 30:2137-2160



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Sednev M, **Mykhailiuk V**, **Choudhury P**, Halang J, Sloan K, Bohnsack M, Höbartner C (2018) N⁶-Methyladenosine-Sensitive RNA-Cleaving Deoxyribozymes. *Angew Chem Int Ed Engl* 130 (46):15337-15341

Sednev MV, **Mykhailiuk V**, **Choudhury P**, Halang J, Sloan KE, Bohnsack MT, Höbartner C (2018) N⁶-Methyladenosine-Sensitive RNA-Cleaving Deoxyribozymes. *Angew Chem Int Ed Engl* 57(46):15117-15121

Zika Virus

Perspectives on a High Resolution Structure

Zika virus (ZIKV) is a mosquito-borne human pathogen and a member of *Flaviviridae* family, closely related to dengue virus (DENV), yellow fever virus (YFV), West Nile virus (WNV), Japanese encephalitis virus (JEV) and tick-borne encephalitis virus (TBEV). These viruses cause widespread morbidity and mortality every year. Amongst the major symptoms caused by these viruses are acute febrile illness with headache, myalgia, rash, encephalitis and severe neurological disorders.

ZIKV is one of the most widely studied flaviviruses as a result of a major epidemic in Brazil in 2015 with almost a million suspected cases. It can cause congenital Zika syndrome in infants and Guillain-Barré syndrome in adults. Development of an effective ZIKV vaccine and anti-viral therapeutics is necessary to combat any future mass epidemics. This can be enhanced by three-dimensional (3D) structure based functional analyses at atomic resolution.

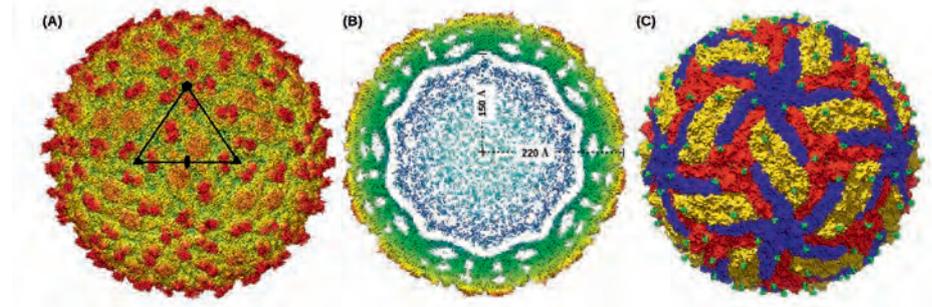


Fig. 1: Structure of ZIKV. (A) Cryo-EM map of ZIKV at a resolution of 3.1 Å viewed down an icosahedral 2-fold axis contoured at 3 σ . The icosahedral asymmetric unit is outlined by a black triangle. (B) Cross-section of the cryo-EM map showing the transmembrane regions and the envelope proteins. Coloring in (A) and (B) is radial with the shortest radius from the center being blue and the longest red. (C) Surface rendering of the envelope (E) proteins built into the cryo-EM map. The E-proteins are colored in yellow, red and blue. The glycan is shown in green.

We determined the 3D structure of mature ZIKV to an average resolution of 3.1 Å (Sevvana *et al.*, 2018) using cryo-Electron Microscopy (cryo-EM). Our paper describes the highest resolution structure yet reported for any lipid membrane-containing virus. In the past two decades, 3D structures of several flaviviruses and their com-

ponent proteins have been determined using cryo-EM, X-ray crystallography and NMR. Similar to other flaviviruses, ZIKV has an icosahedral symmetry with a diameter of about 500 Å enclosing a genome of about 11 Kb. The genome is packaged into a host-derived lipid membrane and encodes three structural proteins: en-

Stone OA, **El-Brolosy M**, Wilhelm K, Liu X, Romão A, Grillo E, Lai JKH, Günther S, Jeratsch S, Kuenne C, Lee I-C, Braun T, Santoro MM, Locasale JW, Potente M, Stainier DYR (2018) Loss of pyruvate kinase M2 limits growth and triggers innate immune signaling in endothelial cells. *Nature Commun* 9:4077

Truckenbrodt S, **Maidorn M**, Crzan D, Wildhagen H, Kabatas S, **Rizzoli SO** (2018) X10 expansion microscopy enables 25-nm resolution on conventional microscopes. *EMBO Rep* 19(9):e45836

Truckenbrodt S, Viplav A, Jahne S, Vogts A, **Denker A**, Wildhagen H, Fornasiero EF, **Rizzoli SO** (2018) Newly produced synaptic vesicle proteins are preferentially used in synaptic transmission. *EMBO J* 37(15): e98044

Vanshylla K, Bartsch C, **Hitzing C**, Krumpelmann L, **Wienands J**, Engels N (2018) Grb2 and GRAP connect the B cell antigen receptor to Erk MAP kinase activation in human B cells. *Sci Rep-UK* 8:4244

Vitali DG, Sinzel M, Bulthuis EP, Kolb A, Zabel S, Mehlhorn DG, Costa BF, **Farkas A**, Clancy A, Schuldiner M, Grefen C, **Schwappach B**, Borgese N, Rapaport D (2018) The GET pathway can increase the risk of mitochondrial outer membrane proteins to be mistargeted to the ER. *J Cell Sci* 131(10): jcs211110

velope (E), pre-membrane (prM) and capsid (C) and seven nonstructural proteins (Hasan *et al.*, 2018; Sirohi and Kuhn, 2017). The glycoprotein shell consists of membrane anchored E and M/prM proteins.

Flavivirus structural proteins, E and prM/M play a vital role in viral entry and receptor mediated endocytosis. They undergo large, pH-induced conformational changes during infection. During infection, the spiky, immature particles consisting of trimeric E:prM heterodimers change to smooth, mature particles consisting of dimeric E:M heterodimers (Hasan *et al.*, 2018; Sirohi and Kuhn, 2017). The mature particles subsequently become fusogenic and infectious in the low pH environment of endosomes. Although, the infection mechanism is similar in most flaviviruses, they show a vast variety of tissue tropism and manifest different disease symptoms. For example, WNV, TBEV, JEV and ZIKV are neurovirulent viruses.

We compared the high resolution structure of ZIKV both with an earlier

reported 3.8 Å resolution structure of mature Zika virus (Sirohi *et al.*, 2016) and with other published mosquito-borne flavivirus structures. We show that the biggest structural differences occur at sites that are relevant to the binding of specific cell surface molecules in potential hosts. Thus, small organic compounds designed to bind to these sites could block viral attachment. We also found that the differences in surface exposed residues among several flaviviruses might correspond to potential receptor attachment sites. Identification and subsequent mutational studies of the

surface exposed residues could be a strategy towards generating attenuated strains for successful vaccine design. In summary, we believe that our work could be a foundation to develop several mechanistic hypotheses in the field of flavivirus research and gives promise for the development of anti-flaviviral therapeutics.

Madhumati Sevana graduated from the Molecular Biology Program with an MSc in the group of George Sheldrick in 2003. After postdoc and scientific staff positions in Göttingen and Erlangen she continued in the Rossmann lab at Purdue University in 2016.



These results were published in Sevana M, Long F, Miller AS, Klose T, Buda G, Sun L, Kuhn RJ, Rossmann MG (2018) *Structure* 26, 1169-77

Vos SM, Farnung L, **Boehning M**, Wigge C, Linden A, Urlaub H, Cramer P (2018) Structure of activated transcription complex Pol II-DSIF-PAF-SPT6. *Nature* 560(7720):607-612

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Yavuz H, Kattan I, Hernandez JM, Hofnagel O, **Witkowska A**, Raunser S, Walla PJ, **Jahn R** (2018) Arrest of trans-SNARE zippering uncovers loosely and tightly docked intermediates in membrane fusion. *J Biol Chem* 293(22):8645-8655

Zinoviev A, **Goyal A**, Jindal S, LaCava J, Komar AA, **Rodnina MV**, Hellen CUT, Pestova TV (2018) Functions of unconventional mammalian translational GTPases GTPBP1 and GTPBP2. *Genes Dev* 32:1226-1241

Analysis of RNA helicases in human ribosome biogenesis

The production of ribosomes is an essential but highly complex and energy-consuming cellular process. During their maturation pre-ribosomes undergo various structural transitions before they achieve the final architecture present in mature ribosomal subunits. RNA helicases, which are best known for their functions in the NTP-dependent unwinding of RNA duplexes, have emerged as important regulators of pre-ribosome remodelling events.

In this study, we investigated the role of eukaryotic DEAH box helicase, DHX37, in ribosome biogenesis. Lack of DHX37 in pre-ribosomal complexes leads to pre-rRNA degradation indicating that the recruitment of the helicase is monitored by a surveillance pathway. Furthermore, our *in vivo* crosslinking

data reveal that DHX37 binds specifically to the U3 small nucleolar RNA (snoRNA). Importantly, U3 acts as a rRNA scaffold during early ribosome assembly and the timely release of this snoRNA is critical for the maturation of small ribosomal subunit. Our results reveal that the catalytic activity

of DHX37 is required for the release of U3 from pre-ribosomal complexes. We further identify UTP14A as a cofactor that can stimulate the ATPase activity of DHX37 and suggest that these proteins function together to promote dissociation of the U3 snoRNA from pre-ribosomes.

Priyanka Choudhury is a doctoral student in the group of Markus Bohnsack at the University Medical Center Göttingen.

These results were published in Choudhury P, Hackert P, Memet I, Sloan KE, Bohnsack M (2018) RNA Biology [Epub ahead of print]



The role of translation initiation in polysome formation

During translation, consecutive ribosomes load on an mRNA to form a polysome. The first ribosome docks at a single-stranded mRNA region before moving towards the start codon. The following ribosomes can select the start codon when the first ribosome has vacated the initiation site, but how exactly they bind to the mRNA is not known.

In the recent paper in PNAS, Andreeva et al. show that loading of the second ribosome on a natural 38-nt-long 5' untranslated region of *lpp* mRNA, which codes for the outer membrane lipoprotein from *Escherichia coli*, takes place even before the leading ribosome has moved away from the start codon. The rapid formation of this standby complex depends on the presence of ribosomal proteins S1/S2

in the leading ribosome. The early recruitment of the second ribosome to the standby site before translation by the leading ribosome and the tight coupling between translation elongation by the first ribosome and the accommodation of the second ribosome can contribute to high translational efficiency of the *lpp* mRNA.

In conclusion, these results not only indicate the role of the initiation standby site during the ribosome loading on a polysome, but also explain the high translation efficiency of a highly translated mRNA as well as suggesting a mechanism for translational control in polysomes.

Irena Andreeva completed her doctoral thesis in the group of Marina Rodnina at the MPI for Biophysical Chemistry and graduated in May 2016. Currently, she works as a Scientist, Process Development & Manufacturing at BioNTech RNA Pharmaceuticals in Mainz.

These results were published in Andreeva I, Belardinelli R, Rodnina MV (2018) Proc Natl Acad Sci USA 115:4411-4416



Replacing animal-derived secondary antibodies with nanobodies

Antibodies are widespread tools in both research and diagnostic laboratories to determine the amount or distribution of specific target molecules. Usually, a “primary” antibody, generated in mice or rabbits, is used to specifically recognize the molecule of interest. “Secondary” anti-mouse or anti-rabbit IgG antibodies are then used to detect the primary antibody and provide a measurable signal. The great demand for these versatile secondary antibodies requires the continuous immunization, bleeding and eventually killing of thousands of large animals, like goats and donkeys, worldwide.

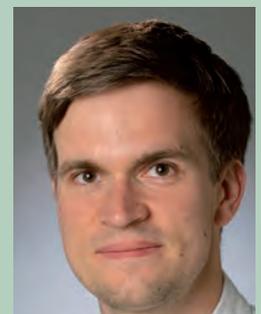
With a little help from our alpacas at the MPI-bpc, we have now generated a sustainable alternative: recombinant single-domain antibodies, called nanobodies. They can be produced on a

large scale in *E. coli* and in contrast to their animal-derived counterparts, their recombinant nature allows engineering them as fusion proteins with affinity tags or reporter enzymes. We demonstrated their superior performance in Western Blotting and showed that their site-specific labeling with multiple fluorophores creates small and bright imaging

reagents ideally suited for confocal and super-resolution microscopy. Since these nanobodies don't crosslink primary antibodies, they can be applied together in a one-step blotting or staining protocol. Moreover, they even allow multi-target localization with primary IgGs from the same species and of the same class.

Tino Pleiner completed his doctoral thesis in the group of Dirk Görlich at the MPI for Biophysical Chemistry and graduated in May 2016. Currently, he works as a postdoctoral scientist in the USA at Caltech, Pasadena, CA.

These results were published in Pleiner T, Bates M, Görlich D (2018) *J Cell Biol* 217:1143-1154



Grb2 and Grap pave the way for BCR-induced ERK activation in human B cells

The ERK MAP kinase signaling pathway is one of the main routes leading to B cell activation/proliferation via the B cell antigen cell antigen receptor (BCR). Our understanding of ERK activation has always been based on the analysis of mouse and chicken B cells, where it has been shown that ERK is dependent on Ras guanyl-releasing proteins (RasGRPs), which in turn require the activity of phospholipase C-gamma 2 (PLC γ 2). We present evidence that an alternative route to BCR-induced ERK activation is predominant in human B cells.

Our observation that inhibition of PLC γ 2 did not impede ERK activation indicated that the RasGRP pathway is dispensable in primary human B cells. This was further supported by

the lack of expression of essential Ras-GRP isoforms in human B cells. We could show that deletion of the adaptor proteins, Grb2 and Grap severely impaired ERK activation. These adaptors bind directly to the BCR-component Ig- α and are also recruited to the immunoglobulin tail tyrosine (ITT) motif in the cytoplasmic tail of mIgE isotype-switched

BCRs where they increase antigen sensitivity. Together, the data shows the importance of Grb2 and Grap for human B cells and also highlights differences in ERK activation mechanisms utilized by B cells from different species.

Kanika Vanshyla completed her doctoral thesis under the supervision of Jürgen Wienands und Niklas Engels at the University Medical Center Göttingen. Currently, she works as a postdoctoral fellow at the Laboratory for Experimental Immunology, Uniklinik Köln.

Vanshyla K, Bartsch C, Hitzing C, Krumpelmann L, Wienands J, Engels N (2018) *Sci Rep-UK* 8:4244



Students

Master's class 2018/19

Arjun Bhatta, Nepal
BSc, Sharda University, India

Margarita Chudenkova,
Russian Federation
BSc, Lomonosov Moscow State
University

Vladyslav Dembrowskyi, Ukraine
BSc, Taras Shevchenko National
University of Kyiv

Iga Grzadzielewska, Poland
BSc, Poznan University of
Medical Sciences

Aybeg Günenç, Turkey
BSc, Bogaziçi University

Kai-Lin Hong, Taiwan
MSc, National Taiwan University

Rohan Kapoor, India
BSc, Sri Venkateswara College,
University of Delhi

Selay Kaya, Turkey
BSc, Middle East Technical University,
Ankara

Nicole Kleiber, Germany
BSc, University of Munich,
University of São Paulo

Barbora Knotková, Czech Republic
MSc, The University of Manchester, UK

Hong-Yu Lee, Taiwan
BSc, National Taiwan University

Florian Mayr, Germany
BSc, University of Applied Sciences
Biberach

Mehar Monga, India
BSc, Sri Venkateswara College,
University of Delhi

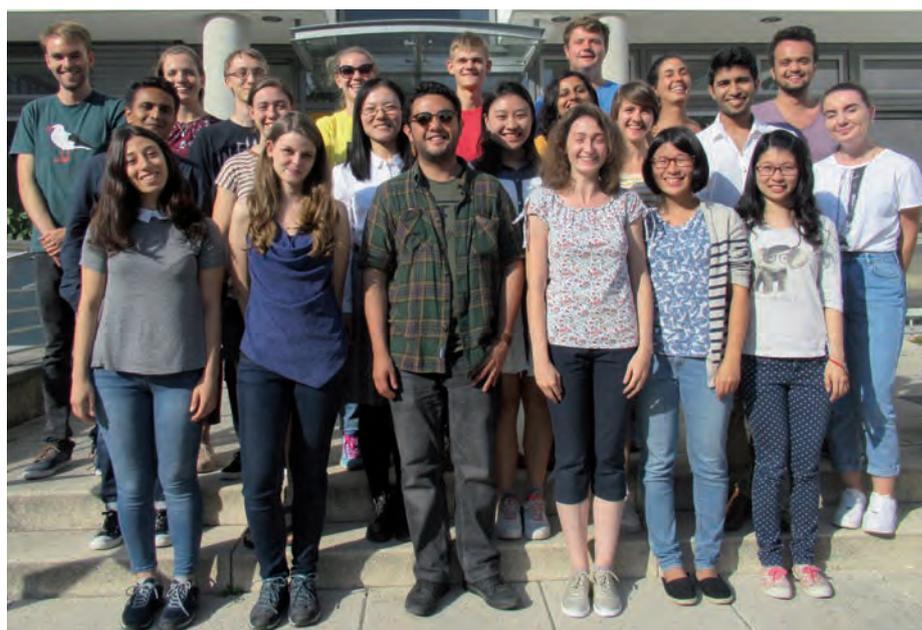
Vella Nikolova, Bulgaria
BSc, University of Sofia, Bulgaria

Alexander Rotsch, Germany
BSc, University of Göttingen

Jennifer Struck, Germany
BSc, University of Göttingen

Siqi Sun, China, P.R.
BSc, Shandong University, China,
Uppsala University, Sweden

Yuliia Tereshchenko, Ukraine
BSc, Taras Shevchenko National
University of Kyiv



Carlos Vanegas Torres, Mexico
BSc, University of Mexico

Marcel Werner, Germany
BSc, University of Göttingen

Yajie Zhu, China, P.R.
BSc, Tongji University, Shanghai

Evi Zhuleku, Albania
BSc, University of Bremen

Applications 2018

In 2018, 814 students from 74 countries applied.

Germany 24 / West Europe 19
East Europe 85
North America 22
Central/South America 24
North Africa 69
Central/South Africa 145
Asia, Near East 61 / Far East 365

PhD projects started in 2018

**Gerrit Altmepfen**

Development of methods to decrease aneuploidy in mammalian oocytes.

*Melina Schuh,
Ufuk Günesdogan,
Sarah Köster*

**Vitalii Mudryi**

Elongation factor P as a drug target.

*Marina Rodnina,
Alex Faesen,
Kai Tittmann*

**Anuruti Swarnkar**

Recognition of Deg1 degron by the ubiquitin ligase Doa10.

*Alexander Stein,
Dirk Görlich,
Peter Rehling*

**Gaurika Garg**

Structure-function studies of human pre-mRNA capping in promoter-proximal gene regulation.

*Patrick Cramer,
Alex Faesen,
Markus Zweckstetter*

**Dilantha Perera**

Nanobody libraries to screen for components of the nucleus which are critical for viral infection/propagation.

*Dirk Görlich,
Stefan Pöhlmann,
Markus Bohnsack*

**Cole Townsend**

High resolution cryo-EM of organellar supramolecular complexes.

*Holger Stark,
Henning Urlaub,
Alexander Stein*

**Ida Jentoft**

Analysis of the subcortical maternal complex in mammalian oocytes.

*Melina Schuh,
Peter Rehling,
Péter Lénárt*

**Panagiotis Poulis**

Ribosome dynamics upon frameshifting, monitored by single molecule Fluorescent Resonance Energy Transfer (smFRET).

*Marina Rodnina,
Jörg Enderlein,
Alex Faesen*

**Roya Yousefi**

Mitochondrial function and turnover in synapses.

*Peter Rehling,
Silvio Rizzoli,
Markus Bohnsack*

**Kseniia Lysakovskaia**

Mechanisms of enhancer synergy during transdifferentiation.

*Patrick Cramer,
Ufuk Günesdogan,
Gregor Eichele*

**Ninadini Sharma**

Mechanisms of the decline in female fertility with advancing maternal age.

*Melina Schuh,
Matthias Döbelstein,
Alex Faesen*

**Zhenwei Zhang**

High-resolution Cryo-EM of very large supramolecular complexes.

*Holger Stark,
Henning Urlaub,
Alexander Stein*

Students

Graduated

The Masters of 2018

Gerrit Altmeppen (*Melina Schuh*)
Development of methods for the artificial segregation of chromosomes in oocytes.

Oleksandr Dovgusha (*Patrick Cramer*)
Constrained multi-body approaches for map refinement in single particle analysis.

Jakob El Kholtei (*Shalev Itzkovitz, WIS*)
Spatial chronobiology of the mammalian liver.

Jose Lorenzo Ferrer (*Rotem Sorek, WIS*)
Systematic search for bacterial defense against conjugation and plasmid transformation.

Gaurika Garg (*Patrick Cramer*)
Structural Studies of Yeast Transcription Factor II H.

Alberto Hernandez Armendáriz (*Sara Cuylen*)
The chromosomal surfactant KI-67 during mitotic exit.

Ida Jentoft (*Melina Schuh*)
Mitochondrial organisation and dynamics during mouse oocyte meiosis.

Anubhav Kaphle (*Johannes Söding*)
Statistical method to discover *trans*-eQTLs for better prediction of gene expression from genotype data.

Kseniia Lysakovskaia (*Patrick Cramer*)
Tracking histone dynamics upon P-TEFb inhibition.

Vitalii Mudryi (*Marina Rodnina*)
Ribosome associated complex as a potential interactor of yeast elongation factor 3.

Dilantha Perera (*Roland Dosch*)
Towards the structure of the novel localization domain of an essential germ plasm assembly factor in Zebrafish embryos.

Panagiotis Poulis (*Marina Rodnina*)
Translocation on a slippery codon monitored by single molecular fluorescent resonance energy transfer (smFRET).

Martin Daniel Qui (*Jürgen Wienands*)
Analysis of B cell antigen receptor-dependent signaling complexes by auxin-inducible degron tagging.

Cole Townsend (*Holger Stark*)
Structural investigation of the human tri-snRNP and B²⁹⁷ spliceosomal complex by cryo-EM.

Taras Velychko (*Patrick Cramer*)
Role of cyclin-dependent kinase 12 (CDK12) in transcription regulation in human cells.



Damir Sakhapov (*Jacob Anglister*)
The interaction of CCR5 sulfated tyrosine residues with the RANTES/CCL5 protein.

Ninadini Sharma (*Melina Schuh*)
Development of methods to counteract chromosome dissociation due to maternal age effect.

Anuruti Swarnkar (*Alexander Stein*)
Recognition of the Deg1 degron by the ubiquitin ligase Doa10 investigated in a reconstituted system.

Liesel Tamon (*Steven Johnsen*)
Epigenetic regulation of ageing-related changes in bone.

Meike Wiegand (*Michael Meinecke*)
Assembly and characterization of the peroxisomal import pore.

Roya Yousefi (*Silvio Rizzoli*)
Evaluation of Protein Turnover in Different Subcellular Locations and Functional States Using SNAP-tag Fusion constructs.

Zhenwei Zhang (*Holger Stark*)
Structural investigation of human 17S U2 snRNP.

Valentyna Zinchenko (*Johannes Söding*)
Gene calling in metagenomics through deep learning of protein sequence features and evolutionary pressure information.

The Doctors of 2018

**Constantin Cretu**

Molecular architecture of SF3B and the structural basis of splicing modulation.

*Vladimir Pena,
Patrick Cramer,
Henning Urlaub*

**Stefan-Sebastian David**

Chromatin affinity purification coupled with mass spectrometry identifies novel histone ubiquitylation interactors.

*Wolfgang Fischle,
Patrick Cramer,
Claudia Höbartner*

**Ridhima Gomkale**

Insights into mitochondrial presequence and carrier import pathways.

*Peter Rehling,
Holger Stark,
Patrick Cramer*

**Tahere Kalantary Dehaghi**

Study of a kinesin adaptor in axonal transport and synapse formation.

*John Chua,
Dieter Klopfenstein,
Stefan Jakobs*

**Ina Klusmann**

The tumour suppressor p53 as a supporter of DNA replication.

*Matthias Dobbelstein,
Halyna Shcherbata,
Steven Johnsen*

**David López de la Morena**

Optogenetic stimulation of the cochlea.

*Tobias Moser,
Silvio Rizzoli,
Tim Gollisch*

**Indira Memet**

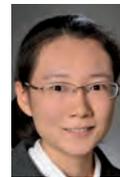
Insights into the regulation of RNA helicases by protein cofactors.

*Markus Bohnsack,
Marina Rodnina,
Peter Rehling*

**Frank Richter**

Investigating the role of ROMO1 in mitochondrial protein import and inner membrane morphology.

*Peter Rehling,
Stefan Jakobs,
Nils Brose*

**Minhui Su**

Microglia activation and regulation of remyelination in the central nervous system.

*Mikael Simons,
Blanche Schwappach,
Steven Johnsen*

**Oleksandr Yagensky**

Identifying stage-specific markers of Alzheimer's disease using quantitative proteomics.

*John Chua,
Dieter Klopfenstein,
Dirk Görlich*



My first year impressions as a PI

We are living in an era where antibiotic resistance is enormously growing and emerging viruses are threatening the human health. According to a recent estimate, yearly 700,000 people are dying due to superbugs. Therefore, we must understand the basic mechanisms that these superbugs use in order to develop better drugs. After years of fundamental research to understand basic molecular mechanisms of gene expression, my research took a new turn after moving to Würzburg.

Now based at the Helmholtz Institute for RNA based Infection Research (HIRI) I am working in a young and dynamic environment at the interface of basic and translational research to understand the role of RNA in infectious pathogens and the host. My research group focuses on non-standard gene expression strategies used by pathogens to tweak the protein synthesis machinery with the aim to translate hidden genes from alternative reading frames. We want to understand the mechanisms behind these non-standard translation events and use the potential of RNA as a drug target to fight infections.

In the beginning of 2018 I have started my lab and since then I still find myself trying to adapt to my new role as a junior professor and group leader. My position allows me to develop my own ideas, establish collaborations with researchers from diverse fields and build a large new network of scientists. A rewarding aspect of my career is the freedom it brings and I can see my ideas turning into knowledge. Being a researcher matches my personality well in that it allows me to try new approaches, be creative and develop solutions. Nowadays, I am mostly supporting my team rather than doing my own experiments, so I must admit

I really miss being at the bench. As a group leader, I am also responsible not only for my personal goals but also for my team's scientific goals and career development. Hence, it is very important for me to build an environment of trust and be approachable.



All HIRI group leaders enjoying the view, after a long hike during our retreat to the Alps

My first year as a PI in Würzburg was very much fun, but has been very challenging as well. Being in a very ambitious scientific environment, the expectations during the tenure track period are high. They include successful applying for prestigious grants, publishing high impact papers and increasing the visibility of our institute in the world. Therefore, I must plan very well and stick to these plans. I also learned how to take things easy, be patient and not get stressed when things take more time than planned. This way I can always find peace and focus on what really matters.

My day is very dynamic as I continuously attend meetings and juggle between my lab and office. I try to organize myself so that I can accomplish smaller tasks throughout the day, and reserve writing times in the early mornings. In the lab, we set

new goals every Friday for each team member and I assure they agree with the plan. In the beginning it was harder, as we had many technical issues and I was not able to estimate how long each team member may need for a given task. What I find helpful is that I give them enough time for reading and we discuss a lot in the beginning and they take off when they are ready. This way, although it takes more time, I believe my team members can be more creative and thinking will prevent errors throughout their projects.

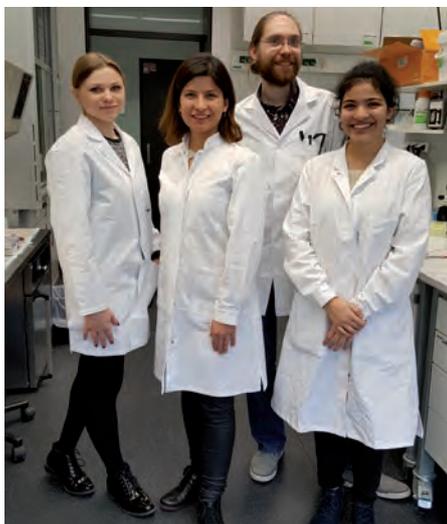
I was very lucky with my first recruitments and I am feeling blessed to work with a brilliant young team. I really wanted to work with people, who are truly curious about the scientific questions and like challenging tasks. I try to keep my team tight, well-connected and positive to make sure we can work solidly on our common goals.

My goal is to stay positive during this period as an early-stage group leader as it greatly influences my interaction with my two kids. Things were not always as great as I went through very hard times. Still I feel pain when I remember how much I let my work to drain my energy

My first year impressions as a PI (continued)

and affect my family in the past. As a junior scientist and mother I always felt under pressure and constantly insecure. After having a kid, I was advised by seniors to look for industry jobs near my husband, who was working as a group leader at TU-Braunschweig. However, I still wanted to stay in academia and at the same time have a family.

My career path was cleared by my husband's support and his commitment. Being a successful automotive engineer with a PhD in Germany, he was getting attractive job offers on a regular basis. However, he knew the chances of me finding a good job were slimmer as a foreigner, woman and mother in life sciences. Therefore, he insisted to prioritize my academic career and my dreams over his.



Research Group REMI: Tatyana, Neva, Matthias and Anuja (from left to right)

When I luckily got the offer from Würzburg, we decided to move with the family, although we knew Würzburg was not the ideal place for him. He quit his group leader position in academia, but miraculously found a manager position in a leading auto-



Neva with her husband, her daughter Alya and her son Aren

motive company only 30 min drive from Würzburg.

Here, I am surrounded by great minds, very supportive mentors and a group of all young group leaders in HIRI. We are in touch with each other about new recruitments, teaching and administrative matters. Being the first recruitments of HIRI, we also have close bonds with the lab managers and the IT people. All this makes my everyday life much easier and also much more fun.

Würzburg is also a very charming city, with its chilled people and its unusually warm climate. Therefore, it feels very Mediterranean in the spring and summer. Since we moved here with my family, we really enjoy the city and are amazed how easy it was to build a social network. Here, I stand 11 years from the first day I moved to Germany on a very rainy day with a single suitcase, now having a family with two kids and more than 50 boxes to pack in the next month to move to our new flat. 10 years ago, I was really not imagining Germany could become my new home and a country that I would

love as much as Turkey, where I am originally coming from.

While my journey continues, I am curious to see where I will be in 10 years. I am also curious to read about your stories and perhaps one day we will meet to have a glass of Frankonian wine on the old bridge in Würzburg.

Neva Caliskan completed her doctoral thesis under the supervision of Marina Rodnina and graduated from the Molecular Biology Program in May 2013. She continued her research in the Department of Physical Biochemistry at the MPI for Biophysical Chemistry as a postdoctoral fellow and project leader until 2017. Neva is now Junior Professor at the Helmholtz Institute for RNA based Infection Research (HIRI) in Würzburg, heading the Research Group *Recoding Mechanisms in Infections* (REMI).

From protein biochemistry to human genetics

After completing my PhD, while I was sending out job applications, I realized that I actually did not wish to continue working in academia. As every good student, I kept putting decision making off. Did I want to become a postdoc in a respectable lab or sell my soul to the pharmaceutical industry and earn lots of money? I thought my chances should be high finding an R&D protein biochemist position at a company. So I found myself sending applications for scientist openings in European companies. I made the decision subconsciously: not a postdoc and not on another continent. However, as I kept applying for wet lab positions in industry, I could not proceed further than telephone interviews. One day, I asked myself what else could I do other than purifying and characterizing proteins? I could speak Turkish! So I searched for job openings entering 'Turkish and biochemistry'. There was one hit. The rare disease company Centogene was looking for a clinical scientist who could write molecular diagnostics reports in Turkish. This is how I started working in the field of human genetics. After consulting Steffen Burkhardt and Katharina Hoff, one of the Molbio alumni living in Mecklenburg-Vorpommern, I moved to Rostock.

My work in Göttingen mostly involved worrying about protein-protein interactions. In Rostock, I became part of a team of scientists whose job was to analyze genomic data and prepare diagnostics reports. Initially, I had to learn a lot on human genetics: different testing methods, mode of inheritance, complex pedigrees, variant classification and very importantly how to pronounce the word "consanguineous". I used to wake up from bad dreams as I imagined having made copy-paste mistakes on my reports! But luckily this phase ended rather quickly as I realized

that our understanding on disease mechanisms of rare inherited disorders is nothing different than our understanding on mechanisms of protein-protein interactions. Centogene receives samples from about 90 countries and develops its own mutation database, which meant that I had access to valuable resources to study novel gene/phenotype relations. So in the two years I spent there, I have been involved in publishing two of such discoveries. I also could travel to my home country and present some of our findings at a breast cancer congress in Istanbul.

Apart from my scientific interests in Centogene, I would like to emphasize



Halenur Yavuz in Rostock

that this was still a very corporate setting. Everything was about developing/maintaining efficient workflows. A big part of my daily work was to help automate diagnostic reporting. As the software developer happened to be my partner, the new topic of our dinner discussions became how to define requirements, program/test new software, train colleagues and troubleshoot their feedback. I have to say, as much as a scientist who does not have experience in coding, I enjoyed software development quite a lot! So much that by the time my partner decided to take a new position in Mannheim, I accepted a position as a requirement scientist in Bio.logis GIM. This is a Frankfurt-based IT

company that develops software customized for molecular diagnostics laboratories.

In the brief five months I spent commuting between Mannheim and Frankfurt, I got the chance to observe interdisciplinary interactions between teams of biologists and software developers. I was mostly involved in bringing the two worlds together. Although I was rather curious to see what kind of products these two teams would go on to develop, I decided to jump back to diagnostics and assumed my current clinical scientist position in the center of human genetics (SYNLAB MVZ Humangenetik Mannheim). Here in Mannheim, I continue my work in molecular diagnostics and enjoy playing with big genomic data. This time a new challenge awaits me: preparing diagnostic reports in German! I guess now I have no choice but to finally improve my German to a professional level. But by now, I see no harm in taking up challenges my work brings me. On the contrary, my unexpected transition from protein biochemistry to molecular diagnostics (with a brief detour to software development) proved me once how valuable it is to keep an open mind.

Halenur Yavuz-Kienle

completed her PhD research with Reinhard Jahn at the MPI for Biophysical Chemistry and graduated in 2014. Following a short postdoc phase, she worked as a scientist for Centogene AG in Rostock from 2016 to 2018. After a transitional period at bio.logis Genetic Information Management GmbH in Frankfurt, Halenur joined SYNLAB MVZ Humangenetik Mannheim.

A Seven Nation Army for healthcare

When Business, Medicine and Artificial Intelligence synergize to tackle the bottleneck in healthcare

Still inspired by the rock music I used to play in Göttingen, I could not think of a better description of IQVIA's Analytics Center of Excellence (ACOE) team in Germany. Seven professionals, different countries and backgrounds, but one common goal: pushing healthcare forward by enabling clinical trials.

Up to almost 90% of clinical trials fail to reach their recruitment targets within their specified time periods, causing as much as 20% of the trials to be closed or terminated early. In simple words, most of the new medicines and medical devices do not reach the patients in need and most of the potential from the medical R&D sector is actually wasted because of the failure of clinical trials.

Indeed, finding the right patients for trials is not an easy task, but the multidisciplinary ACOE team has been recently established at IQVIA to work on this issue. Our job as consultants requires data-driven understanding of different markets in healthcare (diseases), knowing the significant developments in each of them, and analyzing possible resources and opportunities to find the best solutions. However, treating diseases solely as regular markets is a fatal mistake and it would have taken several pages to explain why, and this is where the medical and pharmaceutical knowledge becomes important: to help in understanding what the business data mean in clinical terms and, therefore, provide clinically precise recommendations to our clients. Besides business and medicine, the potential of IQVIA's truly unparalleled data is tremendously expanded by the use of Artificial Intelligence (AI), which enables the transformation of data patterns into predictions of substantial information that are not directly covered in it.

On joining the team in March 2018, the most important thing for me was to have a steep learning curve. Since then, I have been developing business skills and increasing my knowledge in different fields on a daily basis. For instance, I learnt a handful of analytical tools and methodologies and I have gained knowledge on the pharmaceutical market and its newest trends. Additionally, I have got closer to the big data world and I have learnt to code in more than one programming language. Besides, I was trained on soft skills, such as creating commercial presentations and communicating results to our clients.



Six out of the seven members of IQVIA's ACOE team in Germany (Ahmed Warda on the right)

Since I was recruited as the 'medical guy' in the team, I had the privilege to use my knowledge as a pharmacist and my experience from my MSc and PhD in molecular life sciences in my own projects as well as in supporting others'. This responsibility requires maintaining my medical knowledge up-to-date. So, from time to time during work I read papers on the molecular pathogenesis of diseases and I am very happy to have the freedom to do so.

One more change for me, and probably one of the striking differences between academia and industry, is having much freedom to develop my skills in whichever area I find myself into. For example, I am free to take time learning a new coding language, new data sources, or increasing my business or medical knowledge, whichever I see fitting best my needs. One has the freedom to learn something new and apply it to the business as long as it helps the team.

In the end, I would like to thank my manager Steffen Brehmer and each one of the team members very much for supporting me every day, especially during my onboarding time. The environment is lovely -and generally in IQVIA we are becoming more of a family than only colleagues. I am very lucky to be learning from my team mates and to be working side by side with such humble Consulting and Artificial Intelligence gurus.

Ahmed Warda completed his doctoral research in the group of Markus Bohnsack at the University Medical Center Göttingen and graduated in November 2017. In March 2018 he joined IQVIA in Frankfurt as analyst/consultant.

Becoming an entrepreneur

Or how to start a company in three months

Last summer, few weeks after my PhD thesis defense, I was innocently sitting at my desk in the lab analyzing data from my last experiments. I went on to check my email and found a very odd letter with the title “Meeting with Jack”. Who is Jack? Why anyone wants me to meet him? I quickly skimmed through the email. It turns out there is a program in Berlin called Entrepreneur First, they are recruiting and that my profile stood out as similar to people who have participated in the program in the past. Sounded like a typical spam. But it was a program for people to build their own startups. Hmm... I always wanted to start a company at some point in life. What if it is a real thing? I decided to reply...

I do not remember what happened next, but on the first of October last year I arrived in Berlin. I met fifty other participants who all looked like me: partially excited and partially confused about what was going to happen next. The idea behind Entrepreneur First program is to bring together smart people with technical or business backgrounds and let them meet each other, form teams and grow them into successful businesses. If organizers believe in the team and their idea, they are going to invest and hope that the company will make it big in the future so they can multiply their money. In some cases, it worked out very well. For example, one of their portfolio companies with a sophisticated name “Magic Pony” was sold to Tweeter for more than 100 million British pounds. Not bad as for as for a company that was formed by two complete strangers just three years back.

But it all has to start somewhere. Our first mission was to find a co-founder

and an idea we can work on together. This was by far the most intense networking experience I have ever had in my life. Fifty exceptional people representing all possible professional backgrounds, nationalities and ages. I have met a person who raised millions of Euros to build the first hyperloop proto-



Networking session at the Entrepreneur First Program

type in Europe, Siemens’s lead engineer on autonomous driving, expert on hydrogen sensors and many other brilliant people. It felt intimidating. I had to build a team with one of them. Although all these people were amazing individuals, I could not find a co-founder with whom I could leverage my knowledge of molecular biology.

By the end of the first week, I was out of ideas and out of my voice. I have spoken to so many people about some many different things but there was no sight of a team on the horizon. I set down for a cup of tea with a fellow cohort member called Balendu, a biophysicist who had the exact same problem. He told me about his idea of using a specific biopolymer for cybersecurity application. As he was explaining it, something has just clicked in my head. Why not to use this polymer in molecular diagnostics? Just apply the same concept for signal amplification in standard biochemical assays. It made sense. We spent an en-

tire day discussing science and prototyping on the white board. The next day, we formed a team. Three months later, we started our company Fast Biotechnologies.

So many things have happened in these three months. We pivoted multiple times. We became disillusioned about our original assumptions and then inspired by other potential applications of the method. We have learned that understanding the customer is a key to any successful business and that technological solution always has to follow and not come first. For most of the time, I felt out of my comfort zone doing things I had no idea about and learning on the spot. Perhaps in the end, doing business is not that much different from PhD.

Where it will all go? Now, we are developing our technology for quick diagnosis of sepsis and are looking for investors to grow our startup. It is exciting, it is challenging and it certainly feels crazy to start a company right after PhD. All I know is that the journey is worth it.

It has been almost 6 months since I have received that invitation email. Now I know who is Jack and I am happy I did reply.

Oleksandr Yagensky

completed his doctoral research with John Chua in the Department of Neurobiology (Reinhard Jahn) at the MPI for Biophysical Chemistry. After his graduation in June 2016 and four months of postdoctoral research in the same group, he joined Entrepreneur First in Berlin as a cohort member.

Working in the humanitarian sector

A one-year mission as an epidemiologist in Maputo, Mozambique for Médecins sans Frontières

After finishing my PhD, I decided I would like to switch my career from academia to public health and non-governmental organizations. I wanted to do something more applied, where I can see the impact of my work. Given that my PhD was in bioinformatics, the easiest switch seemed to be towards epidemiology. The first step into that world was via an internship in Geneva with Médecins sans Frontières (MSF), a medical humanitarian organization. I was analyzing medical data collected in different projects around the world. Surprisingly for me, I ended up having a job very similar to my PhD; I was analyzing data, summarizing the results and presenting them at scientific conferences. The part, which is more applied compared to my PhD was that the analysis had impact on the projects of MSF as well as it was used for advocacy.

After one year of the internship I was recruited to go on my first mission with MSF. It was a one-year assignment as an epidemiologist to work in Maputo, Mozambique. So, first of all I have to clarify I was not in the middle of the bush having to cross a river full of crocodiles every day like many of my friends imagined it (however some of my colleagues do work in remote villages). I was based in a project in the capital where MSF was working together with the Ministry of Health on HIV, drug-resistant tuberculosis and hepatitis C. I was in charge of monitoring and evaluating the project. What does that mean? In every project, MSF collects data on the medical activities and the objective is to analyze this data to: i) monitor each activity done in the project, ii) evaluate how successful each intervention is, especially, if the new medical strategies are implemented

(always in collaboration with Ministry of Health), as well as using these evaluation results in case the new strategies are successful to advocate changes in national health policies, iii) have the cumulative numbers and statistics, which are published in annual MSF reports that are publicly available and provide transparency to all the donors.



Iris Finci (second from the left): The first week in her new office in Maputo

Generally, in MSF, we summarize the results of analyses in either reports that can be internally shared, with the Ministry of Health when we want to advocate for a new approach, or we also publish scientific articles where we can share our experiences with the wider scientific audience and influence policy changes on a larger scale.

Compared to academia, priorities are different when it comes to analyzing data and sharing the results. Definitely, there is increasing tendency towards publishing the experiences in scientific journals but it is not the main motivator. The main goal is to have evidence-based decision making, i.e. analyze the existing interventions, evaluate their impact, identify parts that need improvement, and subsequently implement changes.

Finally, I remember how we talked a lot about intercultural communication in Göttingen. For me, that was the first encounter with such a concept. But working with MSF brought this to a whole new level. I was immersed in a completely new and different culture and I had to adapt. Of course, there were challenges but at the same time there

were so many enriching aspects: I met so many amazing people, I learned a lot from them about their culture and their view on life. Also, this experience in a way opened my mind more.

Iris Finci completed her Master's thesis with Ivo Feußner (Plant Biochemistry) in the Molecular Biology Program in March 2010. In 2016 she received her PhD degree from the University of Lausanne. In November 2016, she joined Médecins Sans Frontières as a data analyst (epidemiology), before she worked as an Epidemiological Activity Manager in Maputo, Mozambique.

Is there a right way?

From time to time, I find myself in situations where I am thinking about my life as a graduate student in Göttingen. The most recent one was a few weeks ago, when I was teaching a minicourse for a week, which meant that I had to be in the class every morning at 8 am. As I had to walk to work in the dark every morning, I had flashbacks of the times I biked during cold and dark winter mornings to get to the Molbio classes. And then immediately I thought: not sure how I did it every morning and how these students are doing it today... Maybe I am getting old!

Thinking about it, I can't believe nearly 14 years have passed since the day I arrived in Göttingen to join the Molbio program. I never thought this journey would impact my life so much through all the people I've met, all the places I've travelled to and all the things I've learned. It seems as if it all happened very recently and the memories from those days are still fresh in my mind.

Throughout that journey and all the ones I have made afterwards, I have been lucky to have a great companion. Sohail and I met as undergrads at Tehran University. Though seemingly impossible at times, we have always found a way around our two-body problem in science. From the time we both got accepted to the same graduate program to the day we both ended up in the same lab for our postdoctoral training, to today that we run a lab together, we have always tried not to let science take us apart.

To achieve this, we have made many compromises and many hard choices that we don't regret. My rationale: life is too short to be spent the way we don't like it!

Being together has been even more important for us than before since September 2016, when our son Nickan was born. This was when Sohail and I were both ready to wrap up our postdoctoral work and go on the job market. Between all the experiments that needed



to get done, all the deadlines that needed to be met, and all the goals that were set to be achieved, having a kid seemed like the most important plan! Obviously, when the time seemed right for this, it was perhaps the worst time. With six weeks of maternity leave and



Homa, her husband Sohail and their son Nickan

a lot waiting for me in the lab, I asked my parents for help. Having been lucky to have their full support for all my life, this event wasn't going to be an exception. When informed, they volunteered

to take care of our son for the first few months of his life. All I needed to do was to arrange my experiments so that I could come home twice during the day to nurse him and be ready to jump out of the bed as needed during the night. This seemingly straightforward plan had its own very many challenges ranging from getting an extended visa for my parents to dealing with all the job application deadlines and the long experiments that had no understanding for a crying baby (and *vice versa*).

When the time came for my parents to leave and the plan A at the daycare failed miserably, we decided to hire a nanny to take care of our son at home. By talking to the people at work, we identified the right person who happened to have a PhD in Physics and had taken a year of paternal leave (Yes! 1 year!) from his academic position in Europe to take care of his own son while his wife was finishing her postdoctoral training. This was a good short-time resolution until we moved

Homa Ghalei was a PhD student in the group of Markus Wahl at the MPI for Biophysical Chemistry. After her graduation in November 2010 she continued in the same group as a postdoctoral research fellow before she joined the Scripps Research Institute on the Jupiter Campus in Florida as a research associate in April 2012. Since October 2017, Homa is Assistant Professor in the Department of Biochemistry at Emory University School of Medicine in Atlanta, Georgia, USA.

Is there a right way? (continued)

to Atlanta in September 2017, where we had to figure out everything again. Finding a place to live, crawling up the waitlist of the campus daycare to avoid the maddening traffic of Atlanta and dealing with our two-body problem at work were just a few of the problems we faced right away. In the end, we had to move twice in four months, sent

Nickan to a daycare that was far away from our working place for half a year, and made a big compromise at work to continue to live all together.

Was there a better way? Were there easier solutions to all these problems? Did we make the right choices at every step? Are we good parents? These are all questions that I ask myself every

now and then and which will perhaps always remain unanswered. The sparkly eyes of Nickan, the joy of victory when we brainstorm and find out something together with Sohail at work, and the very many happy moments we all have together as a family tell me that we might be on the right track for now.

Honors and Awards

Faculty Members (current and former)

Bertram Brenig has been awarded the Honorary Professorship of the Moscow State Academy for Veterinary Medicine and Biotechnology.

Dirk Görlich has been awarded the Animal Welfare Prize of the Federal Ministry of Food and Agriculture (BMEL) together with Tino Pleiner.

Reinhard Jahn has been awarded an ERC Advanced Grant.

Marina Rodnina has been awarded an ERC Advanced Grant.

Johannes Soeding was awarded a 550 k€ grant by the German Ministry for Education and Research (BMBF) in their computational life sciences framework.

Melina Schuh has been awarded the Leibniz Prize 2019 of the DFG, the EMBO Gold Medal, and the Colworth Medal of the Biochemical Society.

Students (current and former)

Mohamed El Brolosy has been awarded the Best Poster Prize at the Lindau Nobel Laureate Meeting 2018.

Hadil El Sammak has been awarded a PhD fellowship of the Boehringer Ingelheim Fonds.

Simone Mayer received the NARSAD Young Investigator Award of the Brain and Behavior Research Foundation.

Tino Pleiner has been awarded the Animal Welfare Prize of the Federal Ministry of Food and Agriculture (BMEL) together with Dirk Görlich.

Salma Sohrabi-Jahromi received the „RNA Society Junior Researcher Poster Award“ for the best poster presentation at the EMBL symposium on „Complex Life of RNA and the first poster prize at the „Horizons in Molecular Biology“ 2018 meeting.

Minhui Su received the „Munich Cluster for Systems Neurology“ (SyNergy) Award for female PhD students.

Sven Truckenbrodt has been awarded an EMBO Long-Term Fellowship and the ISTplus fellowship from the Marie Skłodowska-Curie program under the European Union's Horizon 2020 research and innovation initiative.

Ahmed Warda received 2018 PhD Award of the Göttingen Center for Molecular Biosciences (GZMB).

Summa cum laude distinctions for outstanding PhD theses have been awarded in 2018 to **Constantin Cretu**, **Ina Klusmann** and **David López de la Morena**. Congratulations!

Science, Sushi and Salsa in SoCal

A journey with obstacles to the beauty of Southern California

I always wanted to live in America. No matter how crazy it might appear sometimes, you have got to admit that most game-changing ideas that affect our daily lives are coming out of this country! Los Angeles with its astounding cultural and social diversity, undoubtedly epitomizes all of what I thought would be uniquely American. My journey here, however, was everything but straightforward.

My PhD time was a lot of fun and I was very grateful to have been given the unique opportunity to build up an alpaca farm at the MPI bpc to generate and engineer so-called nanobodies. At the end of my PhD, however, I felt overwhelmed with deciding what I am most likely going to study for the rest of my career. I knew I had to choose an important biological question.

After a lot of reading, I discovered that my curiosity continuously drove me to one central question: How does a cell quality-control its countless building parts to ensure smooth operation of the myriad of parallel processes?

I had arranged for a few postdoc interviews with labs at MIT, UCSF and Caltech via skype. I was most intrigued by talking to Raymond Deshaies, an HHMI professor at Caltech, and his sharp sense for uncovering the mechanisms of cellular protein quality control. He was happy to learn that I

would be visiting San Francisco for a conference and offered to fly me into L.A. for an interview. It was a rainy and cold December day in San Francisco. Not exactly what I thought living in California would be like. Surprisingly, it just took a one hour flight down south to change this first impression. I still have very vivid memories of the day I first visited Caltech. It felt like entering a small paradise. In contrast to SF,

stated and had to start all over again. Luckily, Ray connected me to a new aspiring group leader who was planning to work on a very similar project that Ray and I had discussed. Rebecca Voorhees had been offered positions at Harvard, MIT and Yale, but decided to join Caltech, where she was offered a generous endowment and plenty of lab space. For my interview with her, I had to give a public talk at the LMB in Cambridge, UK, and

met plenty of the faculty there! We immediately connected and found our mutual interest in studying membrane protein quality control; in particular what basic principles govern the assembly of important membrane protein complexes like receptors, ion channels and transporters at the endoplasmic reticulum.



The author posing for a photo after a strenuous high-altitude hike in the Sierra Nevada Mountains

it was a hot winter in L.A. and many people were enjoying their lunch outside. The campus was overwhelmingly beautiful and people seemed suspiciously relaxed. I am talking about outdoor Tai Chi and meditation classes on campus! The interview went great and I happily accepted the position I was offered.

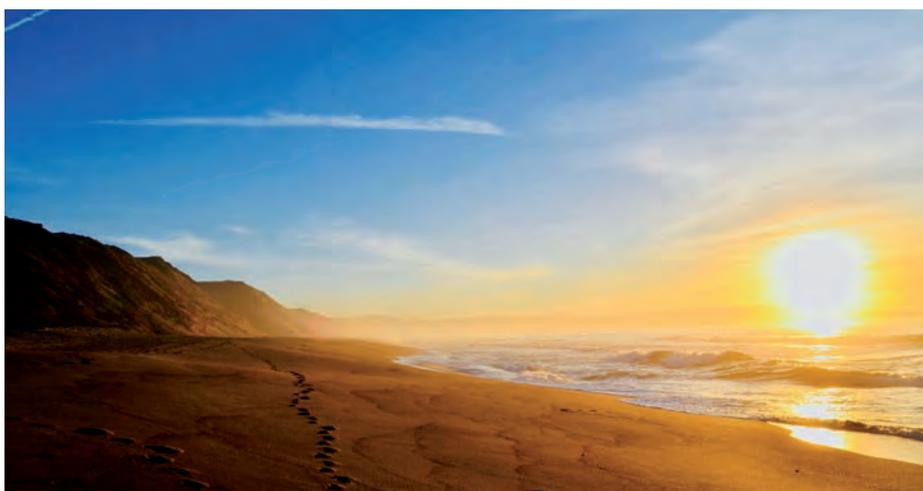
Only a month later I received an email from Ray with the subject line 'Departure'. Ray had decided to shut down his lab at Caltech to become a high-ranking director at Amgen. I was deva-

My first weeks in L.A. made up for all the stress I had been going through that year. Our lab manager, a 40 year-old quirky Filipino-American, offered that I could live with him for free for basically as long as I wanted until I found a place of my own. He grew up loving L.A. and quickly made it his mission to show me his favorite spots! Being a foodie, like many Angelenos, he introduced me to the culinary diversity of L.A. and often stubbornly insisted on inviting me to dinner. After three weeks I found a room in a beautiful house located just a two minute

Science, Sushi and Salsa in SoCal (continued)



A little oasis in the otherwise desert-like Joshua Tree National Park



Sunset over the pacific coast along California's famous Highway No. 1

walk away from work. My two roommates proved to be the most pleasant people I have ever lived with and we rapidly became friends. They even invited me to their Mexican wedding in Bacalar, a dreamy town located on the 'Lagoon of Seven Colors'.

I couldn't help but falling in love with the beauty of Mexico. Rapidly, I changed my vacation plans and returned a month later for a road trip through Yucatan. California itself has a lot of beauty to offer. The rough pacific coast along Highway 1, the sheer

mind-blowing vastness of Yosemite Valley or the surreal desert-like Joshua Tree national park are all within easy reach. I also developed a serious Sushi addiction and inspired by all the Latin culture around me started to learn Salsa.

Although the transition from a well-organized German lab to a completely new lab was challenging in the beginning, I am now enjoying the experience of seeing it grow and thrive. Caltech is a fascinating place to do science! From walking robots,

the search for life on exoplanets or the Nobel Prize for my PhD topic, protein engineering, there is always something exciting happening on campus. My first year abroad has been a tremendous professional and personal enrichment and I am looking forward to all the challenges and experiences the coming years are about to bring my way!

Tino Pleiner completed his doctoral thesis with Dirk Görlich in the Department of Cellular Logistics at the MPI for Biophysical Chemistry. He graduated from the Molecular Biology Program in May 2016. After a postdoc year in the same group, Tino joined the California Institute of Technology (Caltech) in Pasadena as a postdoctoral scientist in November 2017.

Peerview 2018: Science and Society

Most career fairs for molecular biology PhD students have two categories: academic and non-academic. That is the dichotomy presented to those of us who fret about the next step: the canonical path, or the “alternative career”. However, as recent statistics show, only 0.5% of PhD students worldwide will eventually occupy a permanent position in academic research. This begs the question: when 99.5% of us are not in academia, is that still “alternative”?

Diving deeper into the options presented as “alternative” career paths, they are with few exceptions jobs in the pharmaceutical industry, consulting, or scientific publishing. While these are all very interesting pursuits, it is difficult to imagine that all 99.5% of us share the same passion for these three fields. Therein lies the idea that evolved into the inaugural Peerview meeting which took place in September 2018.

IMPRS MolBio PhD students Kai-Hsin Chan and Marija Liutkute organized Peerview: Science and Society on September 24-15th, 2018. As the title suggests, the meeting explored the interfaces of science and society, not only through pharma, but also through social entrepreneurship, science communication, and science policy.

Nacht des Wissens organizer Dr. Benjamin Bühring spoke about the need for true dialog between scientists and the general public: only if a relationship is built on trust can communication be effective, he said. ReAct scientific officer Dr. Maria Pránting presented the initiatives her organization spearheads to combat antibiotic resistance in a non-governmental capacity, highlighting the detrimental effect of the language we use to describe antibiotic use in developing countries. RAND corporation



analyst Dr. Sarah Parks gave insight into how nonprofit consultancies systematically evaluate the impact of scientific research. Max Planck Innovation officer Dr. Mareike Göritz laid out the many different ways basic research finds its way onto the market.

Francis Crick Institute PhD student and cofounder of SixFold Bioscience Anna Perdrix Rosell shared, in an impromptu breakfast roundtable, her adventures at a recent San Francisco startup incubator, giving participants a glimpse of what it is like to pull together a million pounds of funding for an idea. Last but not least, Seeding Labs founder and CEO Dr. Nina Dudnik spoke about her journey from a PhD candidate to head of a company supplying academic labs in developing countries with entire shipping containers' worth of second hand lab equipment. “Your skills are very valuable.” She told the audience, exhorting us to look beyond the “rarified environments” we occupy and realize our own potential to make a difference in the world.

Last but not least, Prof. Reinhard Jahn gave a talk on the evolving policy of the Max Planck Society towards its young scientists, and Prof. Stefan Hell regaled participants with the story of his winding path towards the STED microscope. At the end of the meeting, participants put the communication skills they learned into a “sketch your science” competition, where they used only pen and paper to describe their projects within two minutes.

This audience was made up of IMPRS PhD students from Berlin, Dortmund, Dresden, and Munich. By focusing on fellow IMPRS students, the organizers hoped to build a network of like-minded young scientists, and strengthen the relationships between the IMPRS on the student level. Representatives from Munich left promising to organize an edition of Peerview in 2019, so this hope could very well be on its way to fruition. In the meantime, the organizers would like to thank Dr. Steffen Burkhardt and Dr. Stefanie Klug for the support and absolute trust he showed throughout the planning.

Kai-Hsin Chan

Kai-Hsin Chan and **Marija Liutkute** are both PhD students of the Molecular Biology Program in the Department for Physical Biochemistry of Marina Rodnina at the Max Planck Institute for Biophysical Chemistry.

AACR 2018: Cancer Research Central

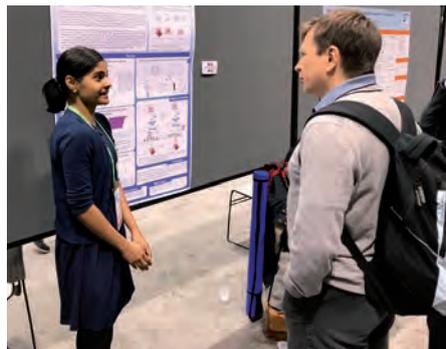
During my PhD on epigenetic regulation in cancer, one of my favorite experiences has been attending conferences. Through generous travel grants the IMPRS programs provide wonderful opportunities to attend international conferences and last year we found the best way to use this. A group from Steve Johnsen's lab attended the annual meeting of the American Association for Cancer Research (AACR) in Chicago in April 2018.

On an extensive and comprehensive scale this meeting brings together the cutting edge of every aspect of cancer research from the basic understanding of mechanisms driving these pathologies to the therapeutics currently tested in clinical trials to policies that will help implement these. Over 20,000 academics, clinicians, industry scientists and many more were present at the meeting with this year's theme 'Driving Innovative Cancer Science to Patient Care', which was covered in all aspects. For someone interested in the development and progression of cancer it was the perfect place to broaden my horizons.

The scientific sessions offered something for everyone, from developments in techniques to medical research. There was a focus on immunotherapy, which was fittingly also the field in which the Nobel Prize for Medicine was awarded later in 2018. For me the poster session was one of the highlights. Due to the sheer number of people it was different from other conferences as each poster drew a larger audience than usual and this allowed many animated discussions with a wide spectrum of people. It was here that someone enquired about the antibody I had used for an experiment that I struggled with for two years. It turns out he had developed the antibody that I finally used, which was a happy



The Johnsen group in downtown Chicago during AACR 2018



Madhobi Sen at her poster



Steve Johnsen, Xin Wang, Madhobi Sen and Oliver Hahn at the 5K Runners for Research event to raise awareness and funds for cancer research

coincidence. While many talks were interesting, for me the highlight was the plenary session by Cigall Kadoch, an inspiring young female scientist, carrying out some fascinating research.

This meeting also organized a 5K run for cancer, which encourages people participating to raise money for cancer research. During the run, Chicago truly was a windy city and our strength was tested in just staying upright against it. As we get involved in the details of our research it is sometimes hard to imagine how it could benefit our ultimate goal of 'curing' cancer. Participating in the run gave us a different experience of being involved in the same cause. In fact, Steve raised one of the highest amounts of donations and won a medal for it!

Conferences are a great way to get to know a new place. With its presence in pop culture, American culture was not new to us. Nonetheless, walking through the Chicago downtown was a spectacular experience. It was also in Chicago's Chinatown that along with our Chinese colleague Xin, we explored Chinese culture. Okay I'm lying, we explored Chinese food, extensively, and it was great.

After a week of intense discussions and general merriment we came back having learnt new things, with new ideas and memories that we will remember forever. For anyone looking for an amazing learning experience in cancer research I would highly recommend using the IMPRS travel grant to attend the AACR annual meeting.

Madhobi Sen was a PhD student in the Tumor Epigenetics Group of Steven Johnsen at the University Medical Center Göttingen. She successfully defended her thesis in January 2019

Feeling the Lindau spirit

68th Lindau Nobel Laureate Meeting, 24th-29th June 2018 #LINO2018

At almost all scientific meetings you will get a chance to hear about good science. What is special about the Lindau Nobel Laureate Meeting is that you also get a chance to learn how to be a good scientist. First, you need to be curious (make no mistake, hard work is an essential part of curiosity). Then, you will need to have one amazing idea that is going to make you famous. Or do you? Michael Rosbash, giving a new spin to Sydney Brenner's original quote, has different advice for you: "Ideas are cheap, and most of them are wrong. Unless they are based on some new experimental discovery. Progress in science depends on new techniques, new discoveries and new ideas, probably in that order." So don't be afraid to embrace new technologies, or to invent some yourself. Don't work for the impact factor, as it does not reflect the quality of your research, suggests Randy Schekman. And most importantly, your work was paid by society, so share it. Science is for everyone, not just for scientists.

Katarina Harasimov

My time at the Lindau meeting was really an amazing experience. Besides talking to Nobel laureates, it was equally rewarding to meet so many other young, diverse scientists. Many of them already had ideas for their own start-ups or other ways to make a difference in the world. Besides lectures and exchanges, another format was the panel discussions. In a very heated debate about open access and the publishing industry, Nobel laureate Randy Schekman (Editor-in-chief of eLife) clashed with Daniel Ropers, CEO at Springer Nature. What I took away was that you should find something you love doing but at the same time keep in mind that we have a responsibility to contribute to society. Many of the Nobel laureates turned away from flashy science that would get



Molbio group photo in Lindau: Katarina Harasimov, Madobi Sen, Oleh Rymarenko, Frank Richter, Vindhya Pillai, Shama Sograte Idrissi, Mohamed El Brolosy (from left to right)



Göttingen young scientists of the Molbio program and other GGNB programs together with Stefan Hell

them a lot of funding and turned towards health needs in less developed parts of the world. The small sessions with Nobel laureates really facilitated to listen to their experiences and points of view and they were surprisingly open to discuss personal questions as well.

Frank Richter

Cancellation of the direct train from Göttingen to Lindau was the only disappointment that awaited me on this trip. The meeting itself featured everything a young scientist could wish for. It was an incredible opportunity to meet hundreds of aspiring young scientists and healthcare professionals from all over the world

Feeling the Lindau spirit (continued)

as well as some of the most accomplished scientists in their field. It is this combination that, in my opinion, makes the meeting truly wonderful. The lectures by Nobel laureates varied from presenting the cutting-edge research (e.g. Robert Lefkowitz and Randy Schekman), nostalgic and touching stories of their scientific paths (e.g. Ada Yonath and Torsten Wiesel) to comprehensive conversations about the urgent problems of modern scientific community (e.g. Aaron Ciechanover and Michael Levitt). Numerous interactive events like open exchanges and panel discussions as well as nicely organized social events gave plenty of opportunity for networking. To its participants (including me) the Lindau meeting provides a strong inspirational and motivational boost, which is so important for early career scientists. It was one of the major highlights of my year 2018.

Oleh Rymarenko

LINO2018 was a very enriching experience. As Oleh writes, it was a combination of science, and discussions on current issues in the community. Furthermore, in agreement with Frank, this single week taught me that doing what one loves is as important as extending one's role towards the matters of society. On similar theme, Rolex sponsored a breakfast session titled "Excellence in science for society", in which I had the opportunity to participate as a student panelist. The discussion highlighted Dr. Andrew Bastawrous's (an ophthalmologist and Assistant Professor at the London School of Hygiene & Tropical Medicine) journey of eradicating preventable blindness using smart phone technology. The discussion was riveting on how the combination of technology and existing knowledge can generate pocket friendly advancements in healthcare. In similar file of events, organized in LINO2018,



the spirit of science caught up with all its participants and led to a very thought-promoting and interactive meeting.

Vindhya Pillai

For me the Lindau Nobel Laureate Meeting was in the true sense of the word an inspiring experience. I was completely astounded by the range of topics that were discussed at this meeting. The most striking aspect for me was to observe how many of these scientists have used the voice that they had gained as a result of winning the Nobel Prize to contribute in very positive ways to society. Whether it was Steven Chu's advocacy for climate change research, Peter Doherty's advice on the importance of communicating science to the public or their joint panel discussion on the role of scientific knowledge in today's 'post-factual' climate. Another highlight for me was the science walk with Michael Young where he in his quiet way told us about the fascinating circadian rhythms and what makes a good scientific question. Similarly, I was very encouraged by the humility of some of the greatest scientists in the world. Overall, we were urged to think about how we could communicate science more meaningfully and not just in the narrow scientific bubbles that we often exist in.

Madhobi Sen

Current and former Molbio students at the 68th Lindau Nobel Laureate Meeting

Mohamed El Brolosy is a PhD student in the group of Didier Stainier at the MPI for Lung and Heart Research in Bad Nauheim, where he did his external Molbio Master's thesis.

Katarina Harasimov is a PhD student in the group of Melina Schuh at the MPI for Biophysical Chemistry.

Vindhya Pillai was a PhD student in the group of Alexander Stein at the MPI for Biophysical Chemistry.

Frank Richter completed his PhD research in the group of Peter Rehling at the University Medical Center in September 2018.

Oleh Rymarenko is a PhD student in the group of Dirk Görllich at the MPI for Biophysical Chemistry.

Shama Sograte Idrissi is a PhD student in the group of Silvio Rizzoli at the University Medical Center Göttingen.

Madhobi Sen completed her PhD research in the group of Steven Johnsen at the University Medical Center Göttingen in January 2019.

15th Anniversary of Horizons in Molecular Biology

For the 15th time students of the IMPRS for Molecular Biology program had brought together hundreds of young scientists for an exciting week of science at the Horizons in Molecular Biology student symposium. This year more than 250 participants from 21 countries came to Göttingen during 10-13 September to attend the anniversary edition of the meeting. Consistent with previous Horizons, it was a fruitful meeting full of scientific discussions, networking opportunities and social events.

The symposium started with the 11th Career Fair, which is an integral part of Horizons aiming to provide a more personalized insight into career options for PhD students in natural sciences. It also offers an opportunity for



participants to learn more about what it takes to build a successful career and what kind of a skill set is likely to be helpful. On that note, this year we organized workshops advising on scientific communication as well as on how to shift from an academic environment to industry. Additionally, we hosted several talks by PhD graduates who have successfully transitioned into a corporate world and were kind enough to present their personal career paths.

After the Career Fair we commenced with our scientific program. Throughout the three and a half days of scientific lectures we had the pleasure to host some of the most distinguished scientists from around the globe who have significantly advanced their field of research, such as Ulrike Kutay, Polly Matzinger and Roeland Nusse. Moreover, we are proud to say that this year we had put a special emphasis on bringing many young investigators whose revolutionary ideas have already set them apart and made them prominent figures in the scientific

community. To mention a few: Daniel Gerlich, Florian Jug, Yamuna Krishnan and Elizabeth Villa.

Apart from the scientific talks, it is our tradition to give PhD students a chance to present their work in front of the international audience of the Horizons. We provided an opportunity for three students to give a talk in a segment called "Awarded Student Talk". In addition, numerous students got a chance to present a poster during our two poster sessions. This year we received more than 70 applications for the Awarded Student Talk and 120 abstracts for poster presentations. We are delighted to say that this was one of the most successful years in terms of student contributions to the Horizons scientific program. We would like to congratulate our Awarded Student Talk winners Mireia Sola, Ivan Sorokin and Harvijay Singh, as well as the poster prize winners Salma Sohrabi-Jahromi, Claudia Schmidt and Joshua Philippe Olorocisimo, who all received valuable prizes kindly provided by our sponsors.



15th Anniversary of Horizons in Molecular Biology (continued)



During the final day, we organized a panel discussion, where participants had the chance to receive valuable advice on how to shape their ideas into insightful research questions that are likely to be fruitful. Although we did not receive a definite recipe on how to achieve this, the overarching message was that discussing and sharing seem to be powerful tools that make your ideas better. Reading, says Polly Matzinger, is also not a bad habit if one aims for success.

to join us in 2018, Sjors Scheres and Leo James, are already confirmed as speakers of the next year's symposium. Together with Jen Heemstra, Gaia Pigi- no, Michael Rosbash and many others, they will join us on 9-12 September 2019 at the Max Planck Institute for Biophysical Chemistry in Göttingen. So save the date in your calendars and see you at the 16th Horizons in Molecular biology!

Katarina Harasimov and Sofiiia Reshetniak

Celebrated with a glass of champagne, the 15th anniversary edition of Horizons in Molecular Biology was definitely a success! Of course, not everything always goes as planned and injured knees and passport retentions can result in last minute schedule changes. Luckily, scientists who were unable

Horizons speakers 2019

Clive Brown, Bianxiao Cui, Mara Dierssen, Anne-Claude Gavin, Daniel Gerlich, Florian Jug, Yamuna Krishnan, Ulrike Kutay, Danielle Laurencin, Juliane Liepe, Polly Matzinger, Osamu Nureki, Roland Nusse, Katherine Pappas, Anna Marie Pyle, Floyd Romesberg, Neville Sanjana, Michael Sheehan, Peter Lenart, Elizabeth Villa

Joining the program in 2018

Alex Faesen completed his PhD studies in 2011 at the Netherlands Cancer Institute in Amsterdam. He continued as a postdoctoral fellow at the Max Planck Institute of Molecular Physiology in Dortmund before he joined the Max Planck Institute for Biophysical Chemistry in Göttingen as a Max Planck Group Leader in 2017. Shortly after having established his new lab, Alex started hosting three Molbio lab rotations in 2018, joined the Molbio faculty and contributed to the Molecular Biology methods training with a DNA course. The primary interest of his research group is in a less studied alternative process in cellular signaling, which is operational in cell division, DNA damage signaling, and autophagy. The signal transduction mechanism relies on the reversible change of a protein's three-dimensional structure to regulate its protein-protein interaction potential. The crucial paradigm emerging from his previous studies in cell division is that structural conversion of HORMA domains is catalyzed, both at the assembly and the disassembly level, by specialized protein machinery, allowing dynamic control of signaling. The research group of Alex is interested in the molecular mechanisms that regulate the topological changes in these signaling protein complexes, which are essential in the initiation of signaling.

<http://www.uni-goettingen.de/en/577914.html>



Ufuk Günesdogan was a predoctoral fellow at the Max Planck Institute for Biophysical Chemistry in Göttingen from 2006 to 2010, when he moved to the Gurdon Institute at the University of Cambridge as a postdoctoral research associate. From 2015 to 2017, Ufuk worked at the Gurdon Institute as a Leverhulme Early Career Fellow until he returned to Göttingen to join the Faculty of Biology and Psychology as a group leader, funded by the Sofja Kovalevskaja Award of the Humboldt Foundation. All three Molbio students hosted in his lab in 2018 for lab rotations stayed in his group also for their Master's thesis. Since 2018, Ufuk contributes to the Molecular Biology methods training with a course on expression analysis. The research of his group focuses on understanding the development of mammalian primordial germ cells (PGCs), addressing the fundamental questions of how the transcriptional program is controlled and what the functional implications of epigenetic modifications in PGCs are. To address these questions, Ufuk's group makes use of *in vivo* and *in vitro* model systems of PGC differentiation, genome-wide techniques and the CRIPSR/Cas9 genome editing tool.

<http://www.uni-goettingen.de/en/577973.html>



Argyris Papantonis received his PhD from the National & Kapodistrian University of Athens, Greece in 2008. Until 2013, he worked as a postdoctoral fellow at the Sir William Dunn School of Pathology, University of Oxford and as a lecturer at University College, Oxford. After five years as a Junior Research Group Leader at the Center for Molecular Medicine, University of Cologne, Argyris was appointed as W2 Professor at the University Medical Center Göttingen in 2018. In the Molecular Biology program he is giving lectures on chromatin structure and epigenetics, and contributes to the Molecular Biology methods training with a course on the analysis of protein-protein and nucleic acid-protein interaction. His research group is interested in uncovering the rules governing gene expression in response to developmental and extra-cellular cues. Particularly, they strive to understand how chromatin (re)folders to accommodate responses to such cues in 3D nuclear space and dynamically over time. In the end, they anticipate these rules to be general ones which, once deciphered, will allow them to predict how a cell might respond upon signaling, in the context of disease, or during cellular ageing.

<http://www.uni-goettingen.de/en/595200.html>



Leaving the program in 2018

Wolfgang Fischle joined the Molecular Biology Program in 2006, when he moved from Rockefeller University to the Max Planck Institute for Biophysical Chemistry as Head of the Chromatin Biochemistry Group. Wolfgang taught lectures on chromatin structure and epigenetics. His group also hosted a methods course on the spectroscopic characterization of nucleic acids. Three Molbio PhD students graduated under his supervision. When Wolfgang joined the King Abdullah University of Science and Technology (KAUST) as a Professor of Cellular and Molecular Biology in 2015 he continued as a guest scientist at the MPI and with his lectures till 2018. We thank Wolfgang for his continuous commitment and invaluable contributions to the success of our program.



Steven Johnsen contributed to the Molecular Biology Program already during his time as an Assistant Professor at the University Medical Center Göttingen (2007-2012). In 2014, he re-joined the Molbio faculty, when he returned from Hamburg to assume the position of a Full Professor (W3). In addition to numerous Molbio lab rotations, Steve's group hosted MSc methods courses on cell culture and on the analysis of protein-protein and nucleic acid-protein interaction. Steve supervised several Molbio Master's thesis projects. Three Molbio PhD students graduated under his supervision, one PhD project is ongoing. Many thanks to Steve for his great job in our program. We wish him all the best for his new position as Professor at the Mayo Clinic, Rochester, Minnesota, USA.



Tomas Pieler belongs to the founder members of the Molecular Biology program who traveled to several East European countries for personal interviews with the first cohort of pre-selected applicants. For many years, he served as head of the examination board and coordinated the methods courses. He taught the lecture on *Xenopus* and his group hosted numerous methods courses and lab rotations over the years. Several Molbio students graduated under his supervision, most of them still holding academic positions. As a Professor of Biochemistry Tomas headed the Department of Developmental Biochemistry at the University Medical Center Göttingen before he retired in 2018. We thank Tomas for his dedicated support of our program for almost two decades.



Michael Hörner, a very respected member of our faculty, sadly passed away after a prolonged battle with illness in October 2018. Since 2005 he had been the coordinator of our Neuroscience program and in 2009 he became the speaker of the GGNB PhD Program Molecular Physiology of the Brain. Additionally, he established the electrophysiology training lab at the ENI and was highly engaged in teaching and lecturing neuroscience, covering a wide spectrum of neuroscientific topics.

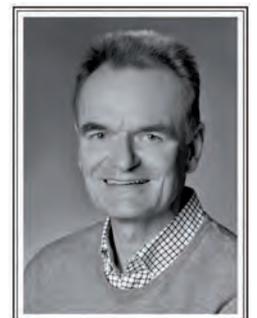
Under the supervision of Prof. Schürmann Michael completed his PhD at the Department of Cellular Biology, University of Göttingen in 1989. In the following years he had worked as an assistant

professor at the Institute of Zoology in Göttingen but also as a guest researcher in Tuscon, Woods Hole and Boston, where he stayed as a Feodor-Lynen-Humboldt Fellow from 1994 to 1995. After finishing his habilitation in Zoology in 1997 he was promoted as an Associate Professor at the University of Göttingen. In 2002 Michael moved to Hong Kong where he stayed as a guest professor and representative of the DAAD German Center at the Hong Kong University of Science & Technology. In 2004 he returned to Göttingen as an Applied Professor at the Institute for Zoology, Anthropology and Developmental Biology.

Through his diverse activities, Michael was well-known in the neuroscience

community and beyond and we are very lucky to have had him here in Göttingen, running the Neuroscience program and turning it into a great success.

He was remarkably talented in student mentoring and, together with his team, he organized memorable student retreats. His passing leaves a huge gap in our midst and we miss him very dearly. Our thoughts are with his family and especially with his son.



Our new Alumni Mentoring Program

Our alumni activities of the year 2019 will focus on our new Alumni Mentoring Program. This specific one-to-one mentoring offers a targeted and intensified relationship over a period of 6 months. The mission is to facilitate meaningful connections between experienced alumni and current PhD students and junior postdocs across a wide variety of careers and research fields in- and outside of academia. Focusing on career advancement, professional development and networking, this program aims to be a rewarding and inspiring experience for all participants. In addition to the regular individual contact of the mentor-mentee pairs, the mentees can apply for travel support to meet their mentors at their workplace. Our IMPRS Offices and Career Service will offer guidance throughout the mentoring process and organize joint events and career-related workshops.

The pilot phase starting in 2019 with the first intake of 6-10 mentees will be run within the IMPRS Molbio/Neuro community. Subject to successful evaluation it will be expanded to the GGNB and GAUSS community in subsequent years. Both mentees as well as mentors need to apply for the program. The matching of each pair will be based on the mentee's successful application and interview as well as relevant expertise of the mentor. Following our basic rules set out in the mentorship agreement, they are flexible to decide together on the timing, format and content of the meetings.

We hope that this exciting opportunity will be well-received by our alumni and PhD students. We are very much looking forward to the applications for the first call in spring.

Stefanie Klug

Current profession and location of our PhD alumni

Profession

Academia / Research (55%)

Professor, PI,
academic staff 13%
Group leader,
senior scientist 4%
Postdoc 34%
Science management 4%

Private Sector (34%)

Scientist, team leader,
manager R&D 26%
Staff, team leader,
manager non-R&D 20%
Consulting 5%

Other Profession (4%)

Media, publishing 2%
Patent attorney 2%
Scientific software development 1%

Other (7%)

Other professions, internships,
job applications, family
management etc. 7%

Country Distribution

Europe (75%)

Germany 51%
United Kingdom 8%
Switzerland 5%
Austria 1%
Belgium 1%
Denmark 1%
France 1%
Luxemburg 1%
Malta 1%
Netherlands 1%
Norway 1%
Poland 1%
Spain 1%
Sweden 1%
Turkey 1%

North America (18%)

United States 15%
Canada 4%

Asia / Australia (7%)

Australia 1%
China 1%
India 1%
Iran 1%
Qatar 1%
Saudi Arabia 1%
Singapore 1%

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