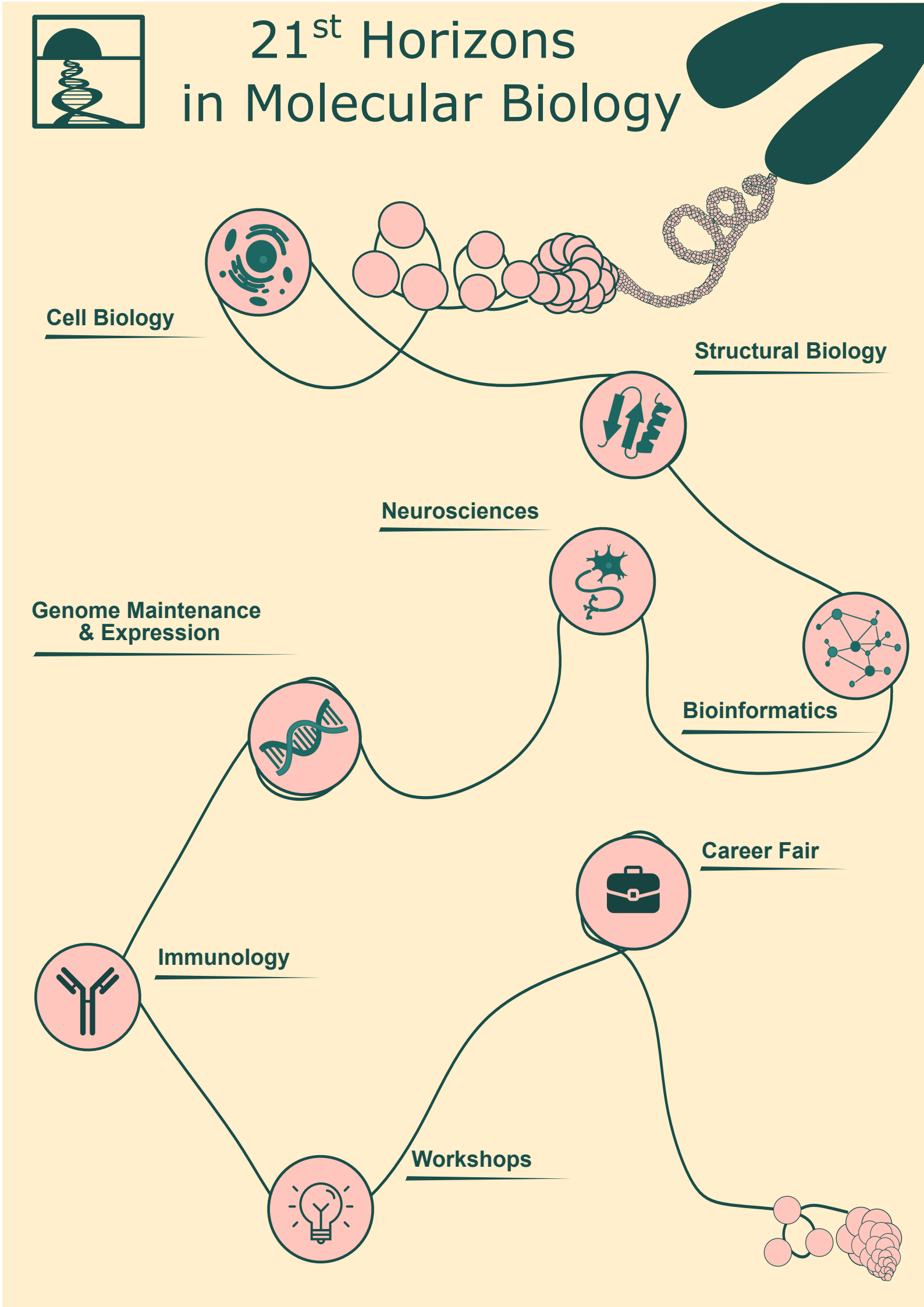
21st Horizons in Molecular Biology



21st HORIZONS IN MOLECULAR BIOLOGY

International PhD Student Symposium

and

Career Fair for Life Sciences

9th-12th September 2024

Göttingen, Germany

Booklet by Horizons Organizing team 2024

Edited by: Sara Ahrari, Yi Zhu, Pooja Mehta and Maria Groshkova

Group Picture: Irene Böttcher-Gajewski, Media Service MPI-NAT

Acknowledgements

Horizons in Molecular Biology was first conceived as an idea 20 years ago by students of the IMPRS Molecular Biology. Twenty-one years later, it has grown to one of the biggest scientific events in Göttingen and one of the biggest student-organized symposia in Germany. The conference has ceaselessly served the same goal: bringing together scientists from around the globe in a multicultural environment that favors scientific exchange. In many cases, this came with difficulties, such as the COVID-19 pandemic, that were overcome by the team efforts of each organizing committee. As the world slowly came out of the pandemic shadows, Horizons returned to its in-person nature that allows extensive peer interaction and gives the chance to all participants to share their passion for science.

The journey of organizing an international conference always comes with hurdles, which, in the case of Horizons, are dealt with by the enthusiastic team spirit of the organizers and our extensive support network. Therefore, we would like to first of all thank the coordinator of the IMPRS Molecular Biology program, Dr. Steffen Burkhardt, and the program assistant, Ms. Kerstin Grüniger, without whose experience and constant guidance Horizons would have never been feasible.

We would also like to thank the Federal Ministry of Education and Research, represented by the Federal Minister Bettina Stark-Watzinger, for offering their patronage and encouraging student initiative and involvement in international actions. Moreover, we would like to thank all our partners and donors, whose support and financial aid made Horizons possible and allowed us to offer our participants food, prizes and also the opportunity to take part in parties, city tours and many more social events.

We would like to thank the Georg-August University of Göttingen and the Max Planck Institute for Multidisciplinary Sciences, for their support and help, as well as for providing their facilities and resources for the Symposium. We appreciate the support of Michael Hartig, Steffen Schmäring and Peter Lösel, without whom we would have no technical setup, and a very empty foyer. We would also like to thank the MPI-NAT Media Service, especially Irene Böttcher-Gajewski and Johannes Pauly, for their help and contribution in taking wonderful (and fun) photographs of Horizons over the years, printing our posters, schedules, name tags, coupons and banners, as well as putting our events on the screens in the MPI-NAT foyer. The Happy Hour Community also has our gratitude for letting us share this tradition with our conference participants and helping us organize a joint MPI-Horizons Happy Hour on September 12th. We would also like to share our appreciation for the MPI-Fahrbereitschaft, who are kind enough to help transport our speakers so that we can enjoy their knowledge and company.

We would like to take a moment and share our appreciation for past organizers and friends who have supported us. Thank you for guiding us and giving advice when we needed it the most. Thanks also to our labs and colleagues for supporting us so that we could give our best to Horizons. Last but not the least, a big thank you to the entire organizing team for their commitment, creativity and sheer grit! We gave it our best, learnt a lot, and are now ready to march forward towards Horizons, welcoming all our guests, and hoping to have a wonderful event!

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Welcome to the 21st Horizons in Molecular Biology!

Horizons in Molecular Biology was conceived as a symposium by PhD students, for PhD students. Established by the students of the International Max Planck Research School for Molecular Biology, it was meant to provide a platform for young researchers to learn about the cutting-edge advancements taking place in the field of Molecular Biology beyond their own niche area. Further, it provides an opportunity to interact with leading scientists and network in an informal and fun environment.

The 21st Horizons promises a 4-day festival with scientific talks, career fair, poster sessions, a panel discussion and lots of opportunities to socialize and engage with scientists at all stages of their career.

Our distinguished speakers will be joining us from around the world not only to share their amazing research, but also to engage with students, possibly during the poster sessions, social activities and the plentiful number of coffee breaks planned.

For those who are more focused on the next steps in their career, our career fair offers many talks as well as workshops. Special speed dating sessions further give students a chance to network and personally interact with the guests from different fields.

This year we also want to address the topic “Is the current pressure to publish restricting curiosity-driven research?” in our panel discussion and hear opinions from different perspectives – PIs, Post-docs and students. The discussion follows a highly dynamic format, and, time permitting, allows for a great amount of audience participation.

As Horizons is a student symposium, we would like to encourage and motivate our peers. The awarded talks and poster sessions provide students an opportunity to share their work with peers and experts alike. Amongst the many awards being offered for poster presentations, we have a popular vote award, where all participants are welcome to vote for their favorite poster!

Our endeavor is to provide an opportunity for all participants to network and interact with graduate students from across the globe and enjoy themselves during the social events! We hope all our guests enjoy the symposium and take back with them fond memories and unforgettable experiences!

From the Horizons Organizing Committee 2024

Organizing committee

The 21st PhD Student Symposium Horizons in Molecular Biology is organized by a group of PhD students of the International Max Planck Research School for Molecular Biology in Göttingen.

Svenja Ahlmann
University of Göttingen, Genetics of Eukaryotic Microorganisms

Sara Ahrari
MPI for Multidisciplinary Sciences, Molecular Biology

Subhro Basu
MPI for Multidisciplinary Sciences, Structural Dynamics

Aysenur Canfes MPI for Multidisciplinary Sciences, Structure and Dynamics of Mitochondria

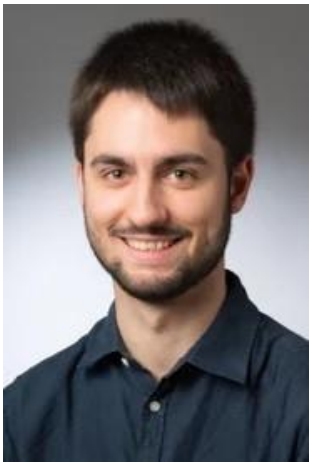
Mandira Choppella
MPI for Multidisciplinary Sciences, Structure and Dynamics of Mitochondria

Maria Groshkova
MPI for Multidisciplinary Sciences, Synaptic Nanophysiology

Hari Krishnan
MPI for Multidisciplinary Sciences, Quantitative and Computational Biology

Shantnu Kumar
MPI for Multidisciplinary Sciences, Physical Biochemistry

Pooja Mehta
MPI for Multidisciplinary Sciences, Cytoskeletal Dynamics in Oocytes



Tim Prolingheuer
MPI for Multidisciplinary Sciences, Structural Dynamics

Nandika Sahani
MPI for Biochemisty, Bacteriophages

Saruby Sharma
University Medical Center Göttingen, Cellular Biochemistry

Animan Tripathi
MPI for Multidisciplinary Sciences, Tissue Dynamics and Regeneration

Yi Zhu
MPI for Multidisciplinary Sciences, Genome Organization and Regulation

Bundesministerium
für Bildung
und Forschung

Partners

The 21st International PhD Student symposium “Horizons in Molecular Biology” is is held under the auspices of the German Bundesministerium für Bildung und Forschung, and financially supported by the following institutions through the International Max Planck Research School for Molecular Biology:

GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN IN PUBLICA COMMODA SEIT 1737

MAX-PLANCK-INSTITUT
FÜR MULTIDISZIPLINÄRE
NATURWISSENSCHAFTEN

Donors

The Organizing Committee would like to thank the following companies and organizations for their support:

Program Overview*

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18:00 - 19:30	**City tours**
20:00 onwards	**Join us for Beer (Cafe & Bar Celona)**

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* For potential last-minute changes, please refer to the schedule on our website.

SCHEDULE: Academic talks					
Tuesday (10.09.2024)		Wednesday (11.09.2024)		Thursday (12.09.2024)	
Talks		Talks		Talks	
08:00 - 9:00	Registration (open all day)	08:00 - 9:30	Registration (open all day)	8:00 - 9:30	Registration (open all day)
9:00 - 9:30	Opening Ceremony for Academic Talks				
9:30 - 10:30	**Keynote lecture: Iain M. Cheeseman** *Rewiring Cell Division*	09:30 - 10:00	**Douglas Higgs** *Switching genes on and off during haematopoiesis*	9:30 - 10:00	**Simon Bullock** *Shedding light on cytoplasmic mRNA transport mechanisms*
		10:00 - 10:30	**Anjana Badrinarayanan** *Tracking living machines: bacterial DNA replication and repair*	10:00 - 10:30	**Marco Fumasoni** *Genome maintenance and evolution*
10:30 - 10:45	Break	10:30 - 10:45	Break	10:30 - 10:45	Break
10:45 - 11:15	**Nenad Ban** *Revealing the Machinery for Production of Proteins in Human Cells*	10:45 - 11:15	**Olivia Majer** *Being in the Right Place - how sorting defects of immune receptors can cause disease*	10:45 - 11:15	**Janine Kirstein** *Chaperoning Amyloid proteins*
11:15 - 11:45	**Maria Fedorova** *Lipidome plasticity and lipid quality control*	11:15 - 12:00	**Awarded Student Talks: Carmela Cruz Arkadyuti Ghorai**	11:15 - 11:45	**Anna Wredenberg** The role of mitochondrial S-adenosylmethionine in health and disease
11:45 - 12:15	**Daniel Gerlich** *How 3D genome organization guides DNA repair*	12:00 - 13:15	Lunch	11:45 - 12:45	Lunch
12:15 - 13:15	Lunch				
13:15 - 14:15	Poster session 1	13:15 - 13:45	**Oleksiy Kovtun** *Exploring the architecture of the retromer, a cargo sorting machine of endosomes*	13:00 - 13:30	**Edward Boyden** *Tools for Analyzing, Repairing, and Simulating Biological Systems*
		13:45 - 14:15	**Robert J. Keenan** *Mechanisms of membrane protein biogenesis at the ER*	13:30 - 14:30	Poster Session 3
14:15 - 14:30	Break	14:15 - 14:45	GROUP PICTURE AND SMALL BREAK		
14:30 - 15:00	**Silvia Santos** *Our first choices: decoding signals during embryonic development*	14:45 - 15:30	**Awarded Student Talks: Somenath Dutta Mojtaba Tavakoli Magdalena Karpinska**	14:45 - 15:15	**Gregor Bucher** *Studying brain diversification by generating comparative*

					tools by genome editing in flies and beetles
15:00 - 15:30	**Ricarda Richter-Dennerlein** *A roadmap for ribosome assembly in human mitochondria*			**15:15 - 15:30**	**Break**
15:30 - 15:45	**Break**	**15:30 - 16:00**	**Sheeba Vasu** *Molecular correlates of how circadian clocks drive waveform plasticity – lessons from fly chronotypes*	**15:30 - 16:00**	**Neva Caliskan** *Old virus new biology: Translational Landscape of HIV-1*
15:45 - 17:00	**Panel Discussion** *Is the current pressure to publish restricting curiosity-driven research?*	**16:00 - 16:15**	**Break**	**16:00 - 16:30**	**Dragomir Milovanovic** *Condensate biology at the synapse*
		2:45 PM - 3:30 PM	**Awarded Student Talk 3**		
			Awarded Student Talk 4		
		16:15 - 17:15	**Poster session 2**	**16:30 - 17:15**	**Closing Ceremony**
				17:30 onwards	**Happy Hour (MPI-NAT foyer)**
20:00 onwards	**Speakers' dinner with organizers (Kartoffelhaus)**	**20:00 onwards**	**Conference Dinner and Party (Deutsches theater)**		

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* For potential last-minute changes, please refer to the schedule on our website.

General Information

Admission to Academic Talks

Admission to academic talks is free and not restricted to registered participants.

Poster Sessions

If you are presenting a poster, you will be given your poster number during registration. The number will serve as an identification mark for our poster committee.

September 10th: Poster session 1

13:15 - 14:15

September 11th: Poster session 2

16:15 – 17:15

September 12th: Poster session 3

13:30 – 14:30

Poster Prizes

A poster prize will be awarded to three participants presenting innovative research at the symposium. All registered participants presenting a poster are eligible for the prize. The participants must, however, be available and present their poster during one of our poster sessions to the jury.

Awarded Student Talks

Awarded talk 1: **Carmela Cruz, University of Göttingen**

"Understanding epigenome resetting of the human germline"

Awarded talk 2: **Somenath Dutta, Pusan National University**

"Harnessing human miRNAs to combat Zika virus: a cutting-edge computational biology approach"

Awarded talk 3: **Mojtaba Tavakoli, Institute of science and technology Austria (ISTA)**

"Dense, synapse-level reconstruction of mammalian brain tissue with light microscopy"

Awarded talk 4: **Magdalena Karpinska, Max Planck Institute for Multidisciplinary Sciences**

"CTCF depletion decouples enhancer-mediated gene activation from chromatin hub formation during cellular differentiation"

Social hours:

- **September 9th, 2024 - 8:00 PM: Join us for a beer at Cafe and Bar Celona**
  The organizers invite everyone, both participants and speakers, to join us for a beer - or any other beverage of your choice. Food and drinks are self-paid.
- **September 10th, 2024 - 8:00 PM: Speakers Dinner with Organizers at Kartoffelhaus.**
- **September 11th, 2024 - 8:00 PM: Horizons Conference Party at Deutsches Theater** (only for package holders)
  For one of the traditional highlights of Horizons, the organizers invite all conference package holders and speakers for a dinner and party in the cellar of the Deutsches Theater. Food and water are provided, other drinks are self-paid.
- **September 12th, 2024 - 5:30 PM:** Happy Hour at Max Planck Institute, Faßberg Campus
  Celebrate the end of another Horizons in Molecular Biology Symposium by joining us for a traditional MPI-NAT Happy Hour including snacks, beer, and great company! Snacks are provided, beer is self-paid.

History of Horizons

December 4th, 2003. The seminar room in Göttingen Center for Molecular Biosciences was bustling with activity. Organizers darted in and out of the room, making sure everything was in order and as it should be. Speakers attempted to look through their talking points, whilst entertaining the many curiosities of the next generation gathered around them. The graduate students themselves whispered to each other and waited apprehensively, with thinly veiled excitement, for the program to begin. There were just under a hundred eager minds crowded into that one room. Students and researchers, all brought together by a shared passion: a passion for science. This was the inaugural Horizons in Molecular Biology Conference: An International PhD Student symposium!

The conference has come a long way since then. Over the years, the number of participants grew steadily and increased in variety. Horizons now regularly attracts around three hundred participants from over thirty countries. The symposium has featured numerous renowned researchers, representing a wide range of fields in the life sciences. This exhaustive list also included several Nobel Laureates: Professors Martin Chalfie, Sir John Walker, Ada Yonath, Thomas Südhof, Kurt Wüthrich, Carol Greider, Venki Ramakrishnan, Sir John Gurdon, Tim Hunt, Michael Rosbash, Richard Henderson, Christiane Nüsslein-Volhard, and James Rothman.

Horizons has also evolved continuously as each new batch of student organizers brings a fresh perspective and new ideas, proving consistently that you can make a good thing better! In 2006, the organizers introduced a Poster Session accompanied by Student Talks. PhD students presented over a hundred posters, and a select few were given the chance to present their work to an audience of peers and professors. Building on this, in 2007, Horizons launched its first Career Fair in conjunction with the conference. The fair offered budding scientists an opportunity to connect with industry and network with life science professionals with different backgrounds and perspectives. Representatives from over twenty companies were present at the inaugural Career Fair, conducting live interviews and CV checks. Today, the Career Fair has adopted a major role in the conference, offering workshops held by professionals, and interactive discussions with key figures in the modern life science industry, all catered to the needs of a young scientist.

At the heart of Horizons is an idea: An International Scientific Conference from PhD students for PhD students. Organized by students from Göttingen's International Max Planck Research School for Molecular Biology, Horizons in Molecular Biology provides an interactive experience in a relaxed environment. It aims to bridge the gap between young scientists and experienced researchers and bring together experts and novices from various fields of the life sciences to engage in a productive dialogue and exchange information. Modern discovery is persistently progressing from exploring rainforests in faraway lands to observing the nature of life under a microscope. We are the modern explorers, and are committed to keep progressing forward, in the pursuit of science, towards the Horizon.

IMPRS for Molecular Biology

For the 21st time, the Horizons symposium is organized by students of the International Max Planck Research School (IMPRS) for Molecular Biology at the University of Göttingen. The Molecular Biology Program is jointly conducted by various departments of the University of Göttingen, the University Medical Center Göttingen, the Max Planck Institute for Multidisciplinary Sciences and the German Primate Center. The common aim is to offer an intensive, research-oriented education in order to prepare the students for a professional career in the life sciences. This broad spectrum of topics is mirrored in the fields covered by Horizons. In addition to the small classes and specialized hands-on laboratory courses, the intercultural experience is extraordinary. Excursions, culture nights and workshops with students from all over the world naturally become a "seminar" on intercultural communication.

Students can join the program after completing their Bachelor studies. During the first year, students receive a broad education in molecular biology through lectures, lab rotations and methods courses delivered by the participating institutions. From the second year, the students conduct their own research during their MSc or PhD thesis projects and receive further training in specialized methods and skills courses within the Göttingen Graduate Center for Neurosciences, Biophysics and Molecular Biosciences (GGNB).

In September 2000, the first brave students from as far away as Ghana, China, Mexico and Malaysia came to Göttingen to join the new International MSc/PhD Molecular Biology Program. Today, the program has become very successful as demonstrated by excellent evaluations, awarded prizes and applications from all over the world. By now, more than 230 students have successfully defended their PhD theses within the program and kissed the Gänseliesel. Kissing this statue that stands on a fountain on the marketplace in the middle of the city and giving her flowers is an old tradition for Göttingen PhD students.

For more detailed information about the International MSc/PhD Molecular Biology Program in Göttingen, please take a look at our website:

https://www.gpmolbio.uni-goettingen.de/

About Göttingen

The renowned university town of Göttingen lies in the center of Germany in southern Niedersachsen (Lower Saxony) between the Harz mountains and the Weser river. Its establishment dates back to 953, it was chartered in 1210 and flourished as a member of the Hanseatic League.

A glimpse of this Hanseatic opulence is still present today in the medieval Town Hall, the splendid churches and quaint half-timbered houses in Gothic, Renaissance and Baroque styles. Göttingen's landmark is the "Gänseliesel", an art nouveau statue of a girl herding geese on top of the fountain on the market square, outside the Old Town Hall. Traditionally, all new doctoral graduates of the University kiss the cheeks of the statue after passing their examinations, making her "the most kissed girl in the world".

The Georg-August University was founded in 1734 and today has 14 faculties with 24,000 students. The university sends forth many famous scientists – amongst its alumni are 42 Nobel laureates. Especially many famous mathematicians come from Göttingen: Carl Friedrich Gauss, Bernhard Riemann and David Hilbert, to name only a few.

Apart from the university, the city is also home to many research institutes, such as Max Planck Institutes, and international companies.

Nearly untouched by bombings in World War II, the city center is now an attractive place to live in with many shops, small cafes, and chic bars. Consequently, many students live here, giving Göttingen a young face: in 2003, almost half of the population of the inner city was between 18 and 30 years of age. Today, Göttingen has approximately 120,000 inhabitants with the charm of a small and lively university city.

Practical Information

Certificates of attendance

Certificates of attendance will be issued via email after the conference. If you haven't registered, but need a certificate, please talk to us at the registration desk.

Insurance

The Organizing Committee accepts no responsibility for accidents or damage to participants' private property. Please make your own arrangements for all the necessary insurance.

Internet

Free Wi-Fi internet (eduroam) is available throughout the symposium in the lecture facilities. If you do not have access to eduroam, please contact us at the registration desk.

Parking

Participants can use the parking lots available near the MPI for Multidisciplinary Sciences, Faßberg campus.

Buses

The buses numbered 21, 22 and 23 to the city center leave just outside the symposium venue at the bus stop "Faßberg". Bus schedules are available at the registration desks. Tickets can be purchased with cash on the bus.

Taxi

Taxis to the city center can be arranged by calling one of the many Göttingen taxi companies:

- Göttinger-Funk-Taxi-Zentrale: 0049-0551 69300
- Puk minicar: 0049-0551 484848

Please note that taxis are considerably more expensive than public transport, and only accept cash.

Organizers

In case you have any difficulties, you are always welcome to ask for help from one of the organizers. Just look out for students wearing a Horizons T-shirt and get in touch with us regarding your issue.

Services

Registered participants are entitled to the following: Admission to plenary lectures, conference material (certificate of participation, name badge) and refreshments during coffee breaks.

Participants who opted for the conference package, in addition to the above, get vouchers for lunch, city tour (as long as spots are available) and access to conference dinner and party.

Career Fair

Welcome to the 18th Career Fair for Life Sciences

Your PhD is the starting point of your career. But have you ever wondered: what is a career in science? A Post-Doc and tenure track to become a group leader? A position in a big biotech company? What are my options?

The answer is that with a PhD in the natural sciences, you have an ocean of options. Certainly, more than two! During your PhD, you will acquire skills and a mind-set sought after everywhere.

In this year's Horizons Career Fair, you'll have the chance of meeting inspiring people, all with a background in the natural sciences, now having diverse careers in industry, bioinformatics and scientific journal editing. They will share their experience about making important career choices, alternative career paths, leadership, promoting gender equality, sustainable innovations and many more.

In addition, we offer you to take part in two different workshops, that will allow you to hone your scientific writing skills and guide you to use academia as a springboard for a future in other sectors.

Join the Horizons Career Fair 2024 and broaden your Horizons!

- Career Fair Organizers

Workshops

Making effective career choices & Effective self-presentation

Sarah Blackford

PhD Career Specialist

Abstract

Making effective career choices

This career workshop aims to help PhD participants to feel more confident about their next career move, using tools and techniques to assist them in assessing their skills and interests. With a career planning overview, they will understand how to apply this knowledge, in particular their skills and interests, to make informed career decisions and investigate options, whether they are planning for a career within or outside of academia.

Effective self-presentation

Whether it's in-person or online, at interview or during networking, effective self-presentation is vitally important to create the 'right' impression. In this workshop, you will have the opportunity to consider what's important to you in terms of your interests and career goals and how you can communicate your unique 'identity' confidently to other people, whether it's on social media or at a conference.

Monday, 09.09.2024

10:15 - 12:15 (Making effective career choices)

13:30 - 15:30 (Effective self-presentation)

Biography

Sarah Blackford is a qualified academic careers adviser (MA, Warwick University), MBTI practitioner and an honorary teaching fellow (Lancaster University). A Senior Fellow of the Higher Education Academy (SFHEA), Sarah specializes in providing career development support to PhD students and postdoctoral researchers and has been delivering career workshops and one-to-one coaching for over 20 years in research institutions, universities, EU consortia and doctoral training programmes.

Sarah's career workshops are well-renowned for being both informative and enjoyable, with plenty of opportunity for discussion as well as individual reflection. Broadly based on her book, 'Career planning for research bioscientists', much of her advice and resources are also published on her blog, www.biosciencecareers.org. As a registered practitioner with the Career Development Institute and active member of the Association of Graduate Careers Advisory Services (AGCAS), Sarah adheres to a recognized ethical code of practice.

Career Fair Talks

Nurturing roots of bioinformatics and genomics in Armenia: the story of ABI

Lilit Nersisyan

Founding Director,
Armenian Bioinformatics Institute

Abstract

The Armenian Bioinformatics Institute (ABI), established in 2021 by a dedicated group of scientists, addresses the critical shortage of bioinformatics and genomics specialists in Armenia. Our mission is to nurture the next generation of genomics researchers, equipping them with leadership skills to modernize Armenia's medical, biotech, research, and educational sectors. Our journey began with intensive two-month summer schools to bridge knowledge gaps for students interested in bioinformatics. Through our international network, we involved students in diverse research projects, providing hands-on experience with real-world problems. Today, ABI is home to three research units and around 20 young researchers. Our alumni have gone on to train at top universities worldwide or work in local biotech companies. At ABI, we focus on research areas such as human genomics for complex disorders, plant genomics, and microbiome research. Additionally, we collaborate with biotech companies on cancer genomics and microbiome research, offering bioinformatics data analysis services. Our three-year journey has provided globally relevant insights. We've learned that bioinformatics expertise is in high demand and short supply worldwide. Similar challenges exist in other countries, and we believe prioritizing bioinformatics research and training can significantly benefit the field of biomedical science globally.

Biography

Lilit Nersisyan holds a PhD from the Institute of Molecular Biology in Armenia and Leipzig University in Germany (2017). Her thesis focused on computational approaches to investigate telomere length and sequence regulation in aging and cancers. She was later a Marie Curie postdoctoral fellow at the Science for Life Laboratory and Karolinska Institutet in Sweden, where she developed a new approach to identifying fast bacterial responses to antibiotics in complex microbiome communities based on mRNA degradation patterns. In 2021, Lilit returned to Armenia and became the founding director of the Armenian Bioinformatics Institute (ABI), established to address the lack of bioinformatics experts in the country. Presently, she leads research teams at ABI and the Institute of Molecular Biology in Armenia.

Monday, 09.09.2024

10:15 - 10:45

A new direction: transitioning from academia to industry

Katherine Wood

Development Scientist,
Oxford Nanopore Technologies

Abstract

The decision whether to pursue a career in academia or industry is a difficult choice that many PhD students face at the end of their doctoral studies. Following two years as a postdoctoral researcher, Katherine made the transition to industry in 2023. Her talk will focus on her own experiences of both academia and industry as an early career researcher and why she changed paths when she did. She will look more broadly at the upsides and downsides of both career options and why other colleagues made the academia-to-industry move at different points in their lives. Katherine will also discuss the diverse roles with a biotechnology company, how the skillset obtained during a PhD can prepare researchers for these varied career options, and offer practical advice for applying for jobs post-PhD.

Monday, 09.09.2024

10:45 - 11:15

Biography

Katherine Wood studied Biochemistry at the University of Oxford, UK, for her undergraduate degree. She then moved to the University of Manchester, UK, to pursue a PhD in Genetic Medicine under the supervision of Professors William Newman and Ray O'Keefe. After successfully completing her doctoral studies, she returned to Oxford to work as a Postdoctoral Research Associate in Molecular Medicine. Following the birth of her first child, Katherine decided to leave academia and joined Oxford Nanopore Technologies as a Development Scientist in the Sequencing Chemistry Development team. She is passionate about translating our understanding of basic biochemical processes to real-world applications, advocating for scientific outreach and public engagement, and supporting women in STEM fields.

Being a structural biologist at GSK

Tim Nierhaus

Structural Biologist at GSK

Abstract

My talk will focus on my experiences of being a structural biologist at GSK, and in the pharmaceutical industry more broadly. I will share my motivation and thoughts behind my transition from academia to industry and reflect on key steps in the process. I am going to explain differences in mindset and priorities in an academic and industrial setting and illustrate how these translate into different ways of working. Based on my experience at GSK over the last two years, I will give insights into how to make your career start in industry a success. I will conclude on a comparison of living and working in the UK and Germany.

Monday, 09.09.2024

11:30 - 12:00

Biography

Tim Nierhaus obtained his Bachelor of Science and Master of Science degrees in Medical Biology from the University of Duisburg-Essen, Germany. During the second year of his master's program, he joined Dr. Jan Löwe's lab at the MRC Laboratory of Molecular Biology in Cambridge, UK, supported by the German National Academic Foundation (Studienstiftung). With funding from a Boehringer Ingelheim Fonds PhD fellowship, he continued in Dr. Löwe's lab to complete his PhD in Biological Science, focusing on the in vitro reconstitution of bacterial cell division processes using X-ray crystallography and cryo-EM. Following his PhD, he undertook a two-year postdoctoral position, working on cryo-EM studies of archaeal cell division in collaboration with Dr. Buzz Baum's group. At the end of 2022, Tim Nierhaus joined the Structural and Biophysical Sciences Department at GSK Stevenage, where he focuses on the structural characterization of biopharmaceuticals.

Big pharma to biotech

Markus Lechner

Principal Scientist,
Eisbach Bio GmBH

Abstract

Having worked both for a big pharmaceutical company and a small biotech startup, I will discuss some key differences between big pharma and startups, focusing on innovation, risk management, and career prospects for scientists. Big pharma is characterized by incremental innovation, extensive resources, and risk-averse strategies. The strong company structure offers stability, professional guidance and personal development in a stepwise career ladder. In contrast, biotech startups thrive on disruptive innovation, agility, and high-risk, high-reward projects, providing dynamic opportunities at the costs of greater job uncertainty. Drawing from personal experiences and industry insights, this talk will highlight the pros and cons of working in each environment, helping scientists make informed career choices based on their professional goals and personal preferences.

Monday, 09.09.2024

13:45 - 14:15

Biography

Markus Lechner got his MSc in Disease Biology at the University of Constance, Germany and joined the DKFZ in Heidelberg for an external Master thesis. He then obtained his PhD in Immunology from the Helmholtz Center Munich, studying the developmental processes of B cell maturation and differentiation. He decided to turn down interesting offers for academic postdoc positions and decided to join big pharma as a scientist in Pharma and Early Development at Roche Diagnostics, working on an interesting internal innovation project in a small x-functional team. After almost two years, he switched gears to join an uprising Biotech Startup Eisbach Bio as a Principal Scientist and Head of Laboratory. Here, he can contribute basically to the whole process of drug development from early idea, pre-clinical development all the way to clinical studies.

A career as a scientific editor

Sara Osman

Senior Editor at Nature Structural & Molecular Biology

Abstract

A scientific editor is a professional (as opposed to academic) editor of a scientific journal holding a PhD in the relevant subject area, and who applies their scientific expertise to the evaluation, selection, curation and management of the peer review of research articles to ensure the publication of impactful and high-quality science. Moreover, a scientific editor participates in coordinating the scientific discourse and growth directions of their respective fields by providing a platform for discussion and writing about the latest advances in editorials and features. This requires a knowledge of the scientific subject area that is up-to-date and both deep and broad, as well as a set of communication and interpersonal skills. In my talk, I will outline what these skills are, how to acquire them, and provide details about how the day of a scientific editor looks like, and reflections on things to consider if you are interested in pursuing an editorial career.

Biography

Sara Osman joined the International Max Planck Research School for Molecular Biology, which brought her to Göttingen where she gained her first lab experience during lab rotations in X-ray crystallography, protein biochemistry and NMR spectroscopy. She did her PhD work on the structural biochemistry and cryo-EM of the Mediator complex in Pol II transcription regulation, with Patrick Cramer at the Max Planck Institute for Biophysical Chemistry. Her interest in gene regulation then led her to study epigenetic silencing of chromatin in yeast with Ann Ehrenhofer-Murray in Berlin. Sara joined Nature Structural & Molecular Biology in 2021.

Monday, 09.09.2024

14:15 - 14:45

Academic Talks

Cell Biology

Rewiring cell division

Iain M. Cheeseman

Whitehead Institute, Massachusetts Institute of Technology

Abstract

The Cheeseman lab is fascinated by the molecular machinery that drives core cellular processes, particularly how these processes are modulated and rewired across different physiological contexts. The lab focuses on the proteins involved in chromosome segregation and cell division, processes that, while essential, are remarkably flexible in their composition and properties. This machinery can vary significantly between species and is modulated within the same organism across the cell cycle, during development, and in diverse physiological situations. To understand how core cellular structures adapt to varying functional requirements, the lab investigates transcriptional, translational, and post-translational mechanisms that create proteomic variability within cells and across tissues, cell states, development, and disease. Current research explores alternate translational isoforms and changes in translational control throughout the cell cycle to ensure proper cell division.

Tuesday, 10.09.2024

9:30 – 10:30

Biography

Iain Cheeseman is a Member of the Whitehead Institute and a Professor of Biology and Associate Department Head at MIT. He earned his Ph.D. in Molecular Cell Biology from UC Berkeley in 2002, working with David Drubin and Georjana Barnes, and completed his post-doc with Arshad Desai at the Ludwig Institute and UCSD. His research focuses on the molecular mechanisms of cell division, specifically the kinetochore, a structure on centromere DNA that serves as the attachment site for microtubules during chromosome movement. His work spans various experimental organisms, including yeast, *C. elegans*, human cells, starfish, and mouse models. The Cheeseman lab currently investigates chromosome segregation and cell division in human cells, employing cell biology, functional genetics, biochemistry, and proteomics. They are particularly interested in how the cell division machinery is modulated across different physiological conditions, such as cell state, tissues, development, aging, evolution, and disease.

Mechanisms of membrane protein biogenesis at the ER

Robert J. Keenan

The University of Chicago

Abstract

My group seeks to understand, in molecular detail, the steps taken by each of the major classes of membrane proteins to achieve their final assembled state. Our recent focus has been on the thousands of human proteins containing more than one transmembrane domain. These multipass membrane proteins function as receptors, channels, enzymes, anchors and transporters, and many human diseases are linked to defects in their biogenesis. In the first part of my talk I will describe our discovery of an endoplasmic reticulum (ER) translocon dedicated to the biogenesis of multipass membrane proteins, and our ongoing efforts to define the molecular basis of its function. A surprising result from this work is that the "multipass translocon" is assembled dynamically in response to features of the nascent chain. In the second part of my talk I will discuss our recent studies to understand more generally how the ER translocon adjusts its subunit composition co-translationally to accommodate the changing biosynthetic needs of its diverse set of clients.

Biography

Robert Keenan received his undergraduate degree in biology from Bates College, a small liberal arts school in Lewiston, Maine. He carried out his graduate and postdoctoral research at the University of California, San Francisco (UCSF), studying protein targeting under Robert Stroud and Peter Walter. After spending the next five years doing directed enzyme evolution at a biotechnology startup in Redwood City, California, he joined the faculty at the University of Chicago, where he is currently a Professor in the Department of Biochemistry and Molecular Biology. Research in the Keenan lab focuses on the discovery and mechanistic dissection of secretory and membrane protein biogenesis pathways, and employs a variety of strategies including in vitro reconstitution, cryo-electron microscopy and cell-based assays.

Wednesday, 11.09.2024

13:45 – 14:15

Shedding light on cytoplasmic mRNA transport mechanisms

Simon Bullock
MRC Laboratory of Molecular Biology

Abstract

Subcellular mRNA localization controls where proteins function in various cell types. While cytoskeletal motors are known to play a key role in mRNP trafficking, how mRNAs are recruited to motors and how motor activity is regulated in these assemblies remains unclear. To address these questions, two experimental models are used: early *Drosophila* development and human cancer cells. High-resolution cryo-EM structures of the *Drosophila* RNA adaptor Egalitarian (Egl) complexed with the dynein motor activator Bicaudal-D (BicD) and three double-stranded RNA targets reveal how mRNA is recognized. Single-molecule resolution in vitro motility assays show that two RNA stem-loops are required to activate dynein motility, a finding supported by Alphafold-assisted modeling of RNA-protein complexes. This work uncovers common organizational principles of mRNA transport complexes across divergent eukaryotic cell types, with RNA cargo determined by the specificity of interchangeable RNA-binding proteins.

Thursday, 12.09.2024

9:30 – 10:00

Biography

Simon trained with Rosa Beddington FRS at the National Institute for Medical Research and David Ish-Horowicz FRS at the CRUK London Research Institute before establishing his own group in the Cell Biology Division of the MRC Laboratory of Molecular Biology in 2004. He received the Lister Institute Research Prize in 2008 and was elected a member of EMBO in 2015. He also co-founded the Microscopes4Schools outreach project.

Simon is intrigued by how the internal space of cells is organized, focusing on microtubule-based transport of organelles and macromolecules. His group uses biochemistry, in vitro reconstitution, advanced microscopy, and genetics to study the molecular mechanisms and principles of cargo transport by microtubule motors. Key research highlights include identifying factors that link the dynein motor to diverse cargoes in *Drosophila* and mammalian cells, uncovering regulatory mechanisms for dynein and kinesin motors through single-molecule resolution in vitro motility assays, and discovering novel regulators of motor and microtubule biology through biochemical and genetic screens. Additionally, Simon's team has developed CRISPR tools widely used by the Drosophila research community.

Chaperoning amyloid proteins

Janine Kirstein
Fritz Lipmann Institute

Abstract

The Kirstein lab studies protein folding challenges in aging and pathologies, focusing on amyloid proteins associated with late-onset neurodegenerative diseases. The research examines the folding landscape of mutant amyloid proteins such as Huntingtin, Abeta, and tau, using C. elegans models in vitro and in vivo. The lab has identified chaperones that suppress and reverse Huntingtin aggregation. Their work shows that amyloid protein aggregation correlates with early neuronal decline and that certain neurons are more vulnerable to specific amyloid proteins. The lab aims to understand how proteostasis network components—molecular chaperones, the proteasome, and autophagic flux—can be modulated to counteract amyloid-induced proteotoxicity. They have developed sensors to explore these interactions and demonstrated that autophagy activates when chaperone-mediated folding fails.

Biography

Janine Kirstein is a Professor for Biochemistry of Aging at the Friedrich Schiller-University and the Leibniz Institute on Aging in Jena, Germany. Her research focus is on protein folding and pathologies associated with protein folding defects such as Huntington's and Alzheimer's disease. She uses biochemical techniques to study how molecular chaperones maintain the fold and function of the proteome and proteins at risk. These mechanistic studies are complemented by analyses using the aging model system Caenorhabditis elegans. Her lab uses the nematode to study the aggregation and pathology of the human disease proteins Ab42, tauand mutant Huntingtin with aging.

Thursday, 12.09.2024

10:45 – 11:15

Our first choices: decoding signals during embryonic development

Silvia Santos
The Francis Crick Institute

Biography

Silvia is a quantitative stem cell biologist specialized in cell decision-making. Originally from Portugal, she did her undergraduate studies in Molecular and Cellular Biology in the UK. Silvia moved to Heidelberg for a PhD at the EMBL where she showed how signalling dynamics affects cell fate choices. Silvia then moved to Stanford University for her post-doctoral training (EMBO and HFSP fellow) to explore spatial-temporal control principles in cell division. Silvia joined the Francis Crick Institute in 2018 as a group leader to establish the Quantitative Stem Cell Biology lab. Silvia's lab combines single cell experimental and theoretical approaches to understand decision-making during developmental transitions. In this context, her lab studies cell cycle remodelling, cellular differentiation and the interplay between cell division and fate choice in early development, using human embryonic stem (hES) cells and 3D models of mammalian development as model systems. Her work has an impact in the understanding of health and disease states.

Tuesday, 10.09.2024

14:30 – 15:00

A roadmap for ribosome assembly in human mitochondria

Ricarda Richter-Dennerlein
University Medical Centre Göttingen

Abstract

Mitochondrial ribosomes have a central importance as they synthesize the core subunits of the oxidative phosphorylation system, which produces the majority of cellular energy. Defects during mitochondrial ribosome biogenesis leads to OXPHOS deficiency and subsequently to severe early-onset diseases, yet how this complex machinery assembles is poorly understood.

Here, we reconstructed the first comprehensive assembly map for the human mitochondrial ribosome – from very early to late assembly steps. In contrast to bacterial ribosomes, mitochondrial ribosomes assemble via protein-only modules, which are produced in excess and which present primed states for subunit biogenesis. The formation of these protein-only complexes is independent of the ribosomal RNA and our data suggest that rRNA synthesis is the rate-limiting step in the progression of ribosome assembly in human mitochondria. This also rationalizes how mitochondria coordinate the formation of these large protein-rich complexes from dual genetic origin.

Biography

Ricarda studied Molecular Biotechnology at the Technical University Dresden (Germany). For her PhD, she chose the laboratory of Robert Lightowlers and Zofia Chrzanowska-Lightowlers at the Newcastle University (UK). After a successful PostDoc period in the research group of Thomas Langer at the University of Cologne, funded by the EMBO-long-term Felllowship, she selected Göttingen and its University Medical Center (UMG) for her further scientific career. After a postdoctoral fellowship in the research group of Peter Rehling, she established her own independent research group at the UMG in 2016 funded by the DFG Emmy-Noether grant. In 2023 she was appointed to a W2 Professor for Biochemistry at the UMG, Institute for Molecular Biology, and awarded with the first “Lower Saxony Impulse Professorship” by the Lower Saxony Ministry of Science and Culture and the Volkswagen Foundation.

Tuesday, 10.09.2024

15:00 – 15:30

Neuroscience

Tools for analyzing, repairing, and simulating biological systems

Edward Boyden

Massachusetts Institute of Technology

Abstract

Analyzing and repairing biological systems, such as the brain, requires tools for systematically mapping, dynamically observing, and dynamically controlling these systems. We are discovering new molecular principles to enable such technologies. For example, we discovered that one can physically magnify biological specimens by synthesizing dense networks of swellable polymer throughout them, and then chemically processing the specimens to isotropically swell them. This method, called expansion microscopy, enables ordinary microscopes to do nanoimaging. As a second example, we serendipitously discovered that microbial rhodopsins, genetically expressed in neurons, could enable their electrical activity to be precisely controlled in response to light. These molecules, now called optogenetic tools, enable causal assessment of how neurons contribute to behaviors and pathological states, and are yielding new candidate treatment strategies for brain diseases. Finally, in order to reveal relationships between different molecular signals within a cell, we are developing spatial and temporal multiplexing strategies that enable many signals to be imaged at once in the same living cell. Scientifically, we are focusing on the application of these tools to collect ground truth-oriented data for the worm C. elegans and the larval zebrafish, with the goal of creating biologically accurate computer simulations of entire brains.

Biography

Ed Boyden is Y. Eva Tan Professor in Neurotechnology at MIT, an investigator of the Howard Hughes Medical Institute and the MIT McGovern Institute, and professor of Brain and Cognitive Sciences, Media Arts and Sciences, and Biological Engineering at MIT. He leads the Synthetic Neurobiology Group, which develops tools for analyzing and repairing the brain, and applies them systematically to reveal ground truth principles of brain function and to repair the brain. These inventions include optogenetics, expansion microscopy, tools for spatially and multiplexed imaging of biological signals, and new noninvasive brain stimulation methods. He co-directs the MIT Center for Neurobiological Engineering and the MIT K. Lisa Yang Center for Bionics. Amongst other recognitions, he has received the Croonian Medal (2019), the Canada Gairdner International Award (2018), and the Breakthrough Prize in Life Sciences (2016), and is an elected member of the National Academy of Sciences (2019)

Thursday, 12.09.2024

13:00 - 13:30

Condensate biology at the synapse

Dragomir Milovanovic

German Center for Neurodegenerative Diseases (DZNE)

Abstract

Brain functioning critically relies on neuronal communication that mainly occurs by chemical signaling at the specialized contacts known as synapses. At synapses, messenger molecules are packed into synaptic vesicles (SVs), which are secreted upon the arrival of an action potential. Indeed, loss of SVs and synaptic deficits are associated number of neurodegenerative diseases. Hundreds of SVs accumulate at each synaptic bouton. Despite being held together, SVs are highly mobile, so that they can be recruited to the plasma membrane for their rapid release during neuronal activity. However, how such confinement of SVs corroborates with their motility remains unclear. To bridge this gap, we employ ultrafast single-molecule tracking (SMT) in the reconstituted system of native SVs and in living neurons. SVs and synapsin 1, the most highly abundant synaptic protein, form condensates with liquid-like properties. Two-color SMT and super-resolution imaging in living axons demonstrate that synapsin 1 drives the accumulation of SVs in boutons. Even the short intrinsically-disordered fragment of synapsin 1 was sufficient to restore the native SV motility pattern in synapsin triple knock-out animals. Thus, synapsin-driven condensation is sufficient to guarantee reliable confinement and motility of SVs, allowing for the formation of mesoscale domains of SVs at synapses and functional neurotransmission.

Biography

Drago is fascinated by how thousands of macromolecules and organelles self-organize at the synaptic boutons, the critical communication sites between neurons. Since January 2020, he has led the Laboratory of Molecular Neuroscience within the German Center for Neurodegenerative Diseases (DZNE). Drago pioneered the concept of liquid-liquid phase separation at the synapse, demonstrating that synaptic vesicles can organize into a distinct liquid phase, akin to oil droplets in water (Milovanovic et al., Science 2018, Hoffmann et al., Nat Comm 2023). The work from his lab showed that the condensates of synaptic vesicles act as a buffer recruiting disordered synaptic proteins such as alpha-synuclein, a protein implicated in the pathology of Parkinson's Disease. Recently, the lab discovered that condensates can harbor electric potential at their interfaces, suggesting a new function of condensates as mesoscale capacitors that can store charge. Condensate biology is now emerging as a key mechanism for understanding synapse organization (Sansevrino et al., Trends Neursci, 2023).

Thursday, 12.09.2024

16:00 - 16:30

Studying brain diversification by generating comparative tools by genome editing in flies and beetles

Gregor Bucher

University of Göttingen

Abstract

Evolutionary adaptations of brain structure and function are essential for animal survival and emerge during development. However, the cellular and genetic mechanisms controlling diversification remain enigmatic. In holometabolous insects, larvae differ from the adult in both behavior and brain morphology due to the divergent needs of larval and adult life.

To study brain diversification, we used homology-directed genome editing to establish transgenic lines that visualize homologous cell groups throughout development with high precision in the fly *Drosophila melanogaster* and the beetle *Tribolium castaneum*. These genetic neural lineages have allowed us comparing the development of homologous neural cells from the embryo to the adult.

Besides overall conservation, we detected conspicuous differences. Specifically, a part of the brain (the central complex) develops already in beetle embryos but only in pupae in flies. In the adult brain, we found cell clusters that diverge between those species. Finally, a clear change of retinal homeobox expression in the mushroom bodies might be linked to differences in adult neurogenesis between fly and beetle. We follow up these hypotheses by characterizing subpopulations of the genetic neural lineage by single cell sequencing and we are testing candidate regulator genes for their role in shifting developmental timing.

Biography

Gregor Bucher studied zoology and developmental genetics at the LMU Munich. During his PhD at LMU, he studied the function of patterning genes in the red flour beetle *Tribolium castaneum* and discovered parental RNAi. After two years of child care and working as scientific writer, he continued his career in Göttingen, where he established his independent group. In 2013, he was awarded a Heisenberg professorship and since 2017 he has been professor at the University of Göttingen. He is interested in the genetic basis of development and evolution of insect head and brain and in new modes of pest control using RNAi. His lab has been developing new transgenic tools for their emerging model organism. He initiated and led the first genome wide RNAi screen in an insect outsideDrosophila (DFG research unit FOR1234 “iBeetle”). He is part of the steering committee of the DFG priority program SPP2349 GEvol.

Thursday, 12.09.2024

14:45 - 15:15

Molecular correlates of how circadian clocks drive waveform plasticity – lessons from fly chronotypes

Sheeba Vasu

Jawaharlal Nehru Centre for Advanced Scientific Research

Abstract

Circadian clocks shape how organisms schedule their physiology and behaviours across the time of day. While the underlying molecular basis for clocks is now extensively investigated, we know little about how evolutionary forces shape waveforms. Using a laboratory selection approach, we have created populations of fruitflies *Drosophila melanogaster* which have now diverged dramatically in their time of emergence from pupal cases 'eclosion'. These unique populations have allowed us to discover that in the process of adapting to new temporal niches circadian clock organization is altered in multiple ways including changes in the splicing machinery for core circadian clock genes. I will present some of our recent findings in this direction.

Wednesday, 11.09.2024

15:30 -16:00

Biography

Sheeba Vasu is an Associate Professor at the Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), Bangalore, India. She received her PhD from JNCASR in 2002. Subsequently, she moved to UC Irvin, CA, USA, for her postdoctoral research. Sheeba's research tackles two distinct aspects of circadian clocks – their evolution and underlying neuronal circuitry. Having established a unique set of populations subjected to long-term selection under naturalistic environments she demonstrated evolution of both circadian clock properties and life-history traits. She showed that evolution of extremely 'early' and 'late' chronotypes is accompanied by altered circadian clock organization including heightened temperature sensitivity in the 'late' chronotypes. Employing genetic manipulations in *Drosophila melanogaster*, her studies suggest that a circadian neuropeptide signals to sleep centers via its cognate receptors. Her studies were the first to suggest a role for gap-junction proteins -Innexins, in the fly circadian circuit. She demonstrated the role of temperature-sensitive ion channel dTRPA1 in mediating rhythmic locomotion and revealed that a circadian neuropeptide pigment-dispersing factor suppresses nighttime activity under continuously warm days.

Immunology

Being in the right place - how sorting defects of immune receptors can cause disease

Olivia Majer

MPI for Infection Biology

Abstract

Our research investigates the detection of nucleic acids by the innate immune system. Microbial nucleic acids are a common feature sensed by our immune system to initiate protective responses; however, the detection of host-derived nucleic acids poses the risk of self-recognition and autoimmune disease. A specific subset of Toll-like receptors, specializing in nucleic acid detection, localizes and signals from endolysosomal compartments, a setup vital for discriminating self from foreign nucleic acids. We are mapping the specific trafficking pathways that deliver these receptors to their signaling compartments and identify sorting defects that lead to hyperactive signaling and autoreactive immune responses. Patients with mutations in these pathways develop autoimmune disease at a very young age.

Wednesday, 11.09.2024

10:45 - 11:15

Biography

Olivia Majer earned her PhD from the University of Vienna, specializing in the field of host-pathogen interactions during fungal infections. During her postdoctoral studies at the University of California, Berkeley, she focused on the cell biology of endosomal Toll-like receptors, investigating mechanisms that disrupt tolerance to self-derived nucleic acids and promote autoimmunity. Additionally, she pursued further training in super-resolution microscopy at FU Berlin, which enabled her to explore the subcellular organization of intracellular immune receptors in greater detail. Since 2020, Olivia has been leading a research team at the Max Planck Institute for Infection Biology, where they investigate the spatial subcellular organization and trafficking of innate immune receptors and their implications for autoimmune diseases.

Bioinformatics

Lipidome plasticity and lipid quality control

Maria Fedorova

Technical University Dresden

Abstract

Maintaining homeostasis is a key feature of cellular organization. The mechanism behind homeostatic control at molecular level involve machineries overseeing DNA, protein and lipid qualities. In contrast to DNA and proteins, lipid quality control (LQC) is so far poorly understood. The regulation of the cellular lipid homeostasis in response to various stimuli is important to maintain the physiological status of a cell and to allow adaptation to everchanging environment. A type of stimulus cells can experience during their life cycle is redox stress. Lipids are sensitive to variations in the levels of reactive oxygen species due to the large number of polyunsaturated acyl chains which can be oxidized leading ultimately to the membrane rupture and cell death. The mechanism behind lipidome remodeling in pro-oxidative conditions is under-examined. Here we used high resolution LC-MS/MS based lipidomics to address adaptive vs lethal responses of cellular lipidome in pro-oxidative conditions in time resolved manner. We identified specific lipid signatures up- or down-regulated upon cell death propagation and/or adaptation. Using a combination of high-resolution lipidomics screening and bioinformatics approaches we aim to reveal a detailed time-resolved image on cellular lipidome remodeling under redox stress conditions to promote a better understanding on the lipid quality control machinery.

Biography

Maria Fedorova studied Biochemistry at Saint-Petersburg State University, Russia and obtained her PhD at the Faculty of Chemistry and Mineralogy, Leipzig University, Germany. She worked as a Group Leader at the Institute of Bioanalytical Chemistry at the University of Leipzig. In 2021 Maria group moved to the Center for Membrane Biochemistry and Lipid Research, TU Dresden. Maria research is focused on understanding the mechanisms behind plasticity, adaptation and maladaptation of natural lipidomes in response to different stressors (metabolic, redox, etc). Using innovative mass spectrometry and bioinformatics solutions, her group looks at the lipid quality control machinery at subcellular, cellular and organismal levels. Maria also serves as a vice-chair of Pan-European Network in Lipidomics and Epilipidomics (EpiLipidNET; https://www.epilipid.net/), a community of researchers interested in lipid biology and lipidomics technologies, supported by European Cooperation in Science and Technology.

Tuesday, 10.09.2024

11:15 - 11:45

Genome Maintenance & Expression

Tracking living machines: bacterial DNA replication and repair

Anjana Badrinarayanan

National Center for Biological Sciences

Abstract

Genome maintenance is essential for the faithful propagation of life. Genome integrity can be challenged by endogenous stresses such as those induced by DNA replication, or by exogenous DNA damaging agents. In all cases, cells mount robust responses to detect and fix DNA damage. DNA repair itself is a double-edged sword, with some pathways also inducing mutations during repair. Cells thus have regulatory mechanisms to dictate repair pathway choice as well as regulate specific steps of the DNA repair process. Together, these genome maintenance systems facilitate cell survival as well as cellular adaptation and evolution under stress. My lab is interested in understanding how microbes organise, protect and repair their DNA. For this, we track replication and repair pathways inside cells in real-time using high-resolution and quantitative microscopy-based approaches. In my talk, I will discuss some recent insights we have gained on the mechanism of homology search during recombination.

Biography

Anjana is an Associate Professor of Microbiology at the National Centre for Biological Sciences (Bangalore, India). Using cell biological approaches, in conjunction with genetic, computational and biochemical tools, her group addresses fundamental questions about the regulation of DNA damage response and repair mechanisms in microbial systems *in vivo*. Her studies have underscored the power of single-cell microscopy to study DNA repair *in vivo,* and has provided new insights into general principles of genome integrity maintenance and its likely impact on microbial adaptation/ survival.

Wednesday, 11.09.2024

10:00 – 10:30

Genome maintenance and evolution

Marco Fumasoni

Instituto Gulbenkian de Ciência, Portugal

Abstract

Cell volume is a fundamental determinant of cellular physiology, maintained through a process known as cell size homeostasis. Studies have shown that large deviations from the typical cell size often produce harmful effects. Nonetheless, cell sizes have dramatically diverged during evolution, ranging from micrometers to millimeters. How does cell size homeostasis evolve to produce such diversity without impacting cell physiology? To address this paradox, we designed an experimental evolution strategy to select progressively smaller cells from *Saccharomyces cerevisiae* populations. Over 1500 generations, we achieved a five-fold reduction in cell volume compared to wild-type cells, marking the largest decrease observed. We show that the new size homeostasis is stably maintained. Strikingly, evolved cells maintain robust fitness, suggesting that the dramatic change in cell volume did not severely impact physiology. We investigated the genetic basis of cellular miniaturization through whole-genome sequencing of the evolving populations. The roles of known and novel players involved in cell size regulation, as well as putative suppressors of defects associated with cell miniaturization will be discussed. Our results demonstrate the evolutionary plasticity of cell size homeostasis and offer novel insights into how variability in a major cellular feature can be evolutionarily achieved.

Biography

Marco Fumasoni was trained as a molecular geneticist at IFOM (IT), studying the mechanisms that maintain genome stability during the replication of damaged DNA templates. He then moved to Harvard University (USA) for his postdoc, where he used experimental evolution combined with molecular, cellular, and quantitative approaches to study the mechanisms and dynamics of genome evolution. Since 2021, he has been a group leader at the Instituto Gulbenkian de Ciência (PT), where he studies the interplay between genome maintenance mechanisms and evolutionary forces in shaping cell biology.

Thursday, 12.09.2024

10:00 – 10:30

The role of mitochondrial S-adenosylmethionine in health and disease

Anna Wredenberg

Karolinska Institutet

Abstract

Mitochondria form a central hub in metabolism and involved in diverse pathways such as energy, lipid or amino acid metabolism, or iron-sulphur cluster formation. Dysfunction in this organelle is associated with rare inborn errors of metabolism, but numerous more common diseases show dysregulation in mitochondria. Classically, this has been attributed to changes in cellular respiration and aerobic ATP production, but recent advances show that an imbalance in different metabolites can also affect mitochondrial function. Around 30% of cellular S-adenosylmethionine reside inside mitochondria, but its role is there is only partially understood. We disrupted the mitochondrial SAM transporter, SAMC, in various murine tissues and demonstrate tissue-specific responses to a mitochondrial SAM depletion. For instance, while the skeletal muscle develops a progressive decline resembling other mitochondrial myopathies, cardiac-specific deletion causes a severe and sudden cardiac phenotype driven by a rapid loss of lipoylation of 2-oxoacid dehydrogenases. This collapse coincides with the transition from milk to solid food, causing a natural reduction in medium-chain fatty acids. Our data establish that octanoic acid becomes rate-limiting during this transition and indicate a direct route for octanoic acid into mitochondria, thus exposing a critical requirement for lipoic acid during cardiac maturation.

Biography

Anna Wredenberg is a senior consultant in clinical genetics at the Center of Inherited Metabolic Diseases at Karolinska University Hospital and a professor in mitochondrial biology at the Department of Medical Biochemistry and Biophysics at the Karolinska Institutet. Clinically, she specialises in investigating and diagnosing patients with suspected inborn errors of metabolism, including mitochondrial diseases. Professor Wredenberg has been studying mitochondrial function in various animal models since 2000 and established her own research group at the Karolinska Instituet in 2012, focusing on understanding mitochondrial gene expression and the role of methylation as post-transcriptional and post-translational modifications within mitochondria.

Thursday, 12.09.2024

11:15 - 11:45

How 3D genome organization guides DNA repair

Daniel Gerlich

Institute of Molecular Biotechnology, Vienna

Abstract

DNA double-strand breaks (DSBs) pose a severe challenge to genomic integrity. While various repair pathways exist, only homologous recombination ensures error-free repair by restoring missing information through physical interactions with a homologous region in the genome. In somatic cells, homologous recombination is much more efficient between sister chromatids of replicated chromosomes than between homologous copies of a chromosome, suggesting that homology search might be facilitated by the 3D organization of sister chromatids. To investigate the role of chromosome organization in DNA repair, we developed sister-chromatid-sensitive conformation capture methods, using high-throughput sequencing (scsHi-C) and programmable multiplexed in situ hybridization (scsFISH). Using these methods, we show that broken DNA ends scan a megabase-sized domain on the opposing sister chromatid. We find that cohesin regulates the homology scanning process both through its loop-extruding as well as its cohesive functions. Our study hence reveals how the 3D organization of replicated chromosomes contributes to DNA repair.

Biography

Daniel Gerlich graduated in Biology from University of Freiburg, Germany, in 1998. He earned his PhD from University of Heidelberg in 2002, developing computer vision tools for multi-dimensional bioimage data in the group of Roland Eils. After a postdoc on the organization of chromosomes in Jan Ellenberg's laboratory at the European Molecular Biology Laboratory (EMBL) Heidelberg, he established his own laboratory in 2005 as Assistant Professor at the Institute of Biochemistry at ETH Zurich. In 2012, he moved to the Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA) at the Vienna BioCenter to take a position as senior research group leader. His research focuses on cell division, chromosome organization, and computational methods for bioimage- and genomics data analysis. Dr. Gerlich has received several honours for his scientific contributions, including a European Young Investigator Award of the European Research Council (2005), EMBO young investigator (2009) and EMBO full memberships (2017), and ERC consolidator (2012) and Advanced (2021) grants.

Tuesday, 10.09.2024

11:45 – 12:15

Old virus, new biology: translational landscape of HIV-1

Neva Caliskan

Helmholtz Institute for RNA-based Infection Research

Abstract

Human Immunodeficiency Virus-1 (HIV-1) uses a number of strategies to modulate viral and host gene expression during its lifecycle. To characterize the transcriptional and translational landscape of HIV-1 infected cells, we employ a combination of ribosome profiling, disome sequencing and RNA sequencing. We found that the initial host response to viral infection is translationally regulated, and subsequently gives way to transcriptomic changes as the infection progresses. We show that HIV-1 mRNAs are efficiently translated at all stages of infection, despite evidence for a substantial decrease in translational efficiency of host genes that are implicated in host cell translation. We observed ribosomal collisions in Gag-Pol upstream of the ribosome frameshift site that we attributed to a novel RNA structural fold using RNA structural probing and single molecule optical tweezers. Antisense oligos designed to break this structure decreases frameshifting efficiency. Overall, our work highlights the complexity of HIV-1 gene regulation and will provide a key resource for decoding of host-pathogen interactions upon HIV-1 infection.

Biography

Neva Caliskan studied molecular biology and genetics at the Middle East Technical University in Ankara (Turkey) and worked as a visiting scholar in 2005 at EMBL in Heidelberg. She received her Master's degree at the International Max Planck Research School for Molecular Biology (Göttingen) in 2009. After completing her PhD in 2013, she first worked as a postdoctoral fellow at the Department of Physical Biochemistry at the Max Planck Institute for Biophysical Chemistry and then as a project leader at the same institute from 2015-2017. Since January 2018 she has been heading the junior research group "Recoding Mechanisms in Infections" at the Helmholtz Institute for RNA-based Infection Research (HIRI) in Würzburg. As of May 2018, she holds a junior professorship at the Faculty of Medicine of the University of Würzburg.

Thursday, 12.09.2024

15:30 - 16:00

Switching genes on and off during haematopoiesis

Douglas Higgs

MRC Weatherall Institute of Molecular Medicine

Abstract

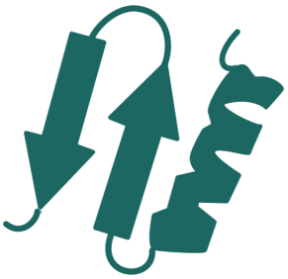
We study how transcriptional and epigenetic programmes are played out on chromatin spanning the alpha globin cluster as hematopoietic cells undergo lineage fate decisions and differentiation to form erythroid cells. This model helps to establish the general principles underlying the regulation of mammalian gene expression. The alpha globin cluster and its regulatory elements are silenced in early progenitors, poised for expression in later progenitors and fully expressed during terminal erythroid differentiation. Using a variety of approaches, we have established the order in which silencing factors are removed, activating transcription factors bind and epigenetic modifications occur. We have also studied in detail when and how the alpha globin enhancers activate transcription of their cognate genes. In addition, we have shown how chromosomal conformation and nuclear sub-localisation change during hematopoiesis. Natural *cis* and *trans* acting mutations that cause alpha thalassaemia provide additional insight into how the long-range regulatory elements may interact with the promoters of the globin genes and other flanking genes to activate their expression. Together these observations establish some of the general principles by which mammalian genes within their natural chromosomal environment are switched on and off during differentiation and development and how these processes are perturbed in human disease.

Biography

Douglas Higgs qualified in Medicine at King's College Hospital Medical School in 1974 and trained as a haematologist. Until April 2020 he was Director of the MRC Molecular Haematology Unit and Director of the MRC Weatherall Institute of Molecular Medicine (WIMM). He is currently Professor of Haematology at the University of Oxford and a Group Leader in the WIMM. Douglas Higgs' research has made a major contribution to our understanding of how mammalian genes are switched on and off during lineage specification and differentiation using haematopoiesis as his model. He has established the alpha-globin cluster as one of the best understood models of mammalian gene expression, and thereby largely unraveled the molecular basis and improved the management of alpha-thalassaemia, a form of inherited anaemia affecting millions of individuals throughout the world. In addition to understanding how mammalian genes are normally regulated, his group has made a significant contribution to establishing the general principles by which they are perturbed in human genetic disease. His group is currently involved in using their knowledge to manipulate gene expression in patients with thalassaemia.

Wednesday, 11.09.2024

9:30 -10:00



Structural Biology

Revealing the machinery for production of proteins in human cells

Nenad Ban

ETH Zurich

Abstract

Our group is interested in understanding the process of expression of genetic information that leads to the production of functional proteins. This process requires an intricate interplay between the protein synthesis machinery and an ever-growing list of cellular components that control protein synthesis and participate in protein biogenesis. Building on our studies that provided some of the first blueprints for understanding the eukaryotic protein synthesis machinery including the cytosolic and the mitochondrial ribosomes, we are now investigating protein synthesis in human cells using a combination of structural, biochemical and biophysical experimental approaches. We are particularly interested in understanding the regulation of protein synthesis and the biogenesis of cytosolic and membrane proteins. I will present examples of recent results that contribute to our understanding of the network and the coordination of cellular factors that interact with translating ribosomes in human cells to control protein synthesis and to ensure accurate protein production.

Biography

Since 2000 Nenad Ban is a professor of structural molecular biology at ETH Zurich. He is a pioneer in studying gene expression mechanisms and the participating protein synthesis machinery in all kingdoms of life, both in terms of the chemistry of the process and with respect to molecular mechanisms of translation regulation, and of co-translational folding, processing, and targeting to membranes. His group revealed the mechanisms behind the key steps in eukaryotic cytoplasmic and mitochondrial translation with a broad impact on a wide range of fields in biology, chemistry, and biomedicine. Nenad Ban is a member of the National Academy of Sciences of the United States of America, European Molecular Biology Organization, the German Academy of Sciences, and a recipient the Heinrich Wieland Prize, the AAAS Newcomb Cleveland Prize, the Jung Prize for Medicine, and the Otto Naegeli Prize for biomedicine.

Tuesday, 10.09.2024

10:45 – 11:15

Exploring the architecture of the retromer, a cargo sorting machine of endosomes

Oleksiy Kovtun

Max Planck Institute for Multidisciplinary Sciences

Abstract

Vesicular coats select receptors and other transmembrane cargo and drive membrane curvature to generate cargo-loaded carriers for membrane trafficking pathways. Retromer assembles coats with several cargo adaptors to retrieve endosomal cargo to distinct pathways, including retrograde transport to the Golgi and recycling to the plasma membrane. This process of endosomal cargo retrieval is an essential regulator of protein localization and turnover, and its dysregulation has a pronounced fallout in highly specialized cells such as neurons. We use structural studies to understand how cargo recognition initiates the formation of membrane carriers bound to specific trafficking routes. A combination of cryo-electron tomography (cryo-EM) and sub-tomogram averaging (STA) has provided us with insights into the organization of several membrane-assembled retromer coats and revealed a modular nature of this coat.

Thursday, 12.09.2024

14:15 – 14:45

Biography

Oleksiy Kovtun is a structural biologist studying endocytosis and membrane trafficking. He received a PhD from the University of Queensland in Australia for research in in vitro protein synthesis. After graduation, Oleksiy focused on structural studies of membrane trafficking complexes, first in the Bret Collins' group at the University of Queensland, and then in the John Briggs' group at EMBL-Heidelberg, Germany, and LMB-MRC, UK. He started his group at MPI for Multidisciplinary Sciences in Göttingen in 2021 with a mission to understand the mechanistic basis of the function of vesicular coats. Currently, his team is focused on the retromer, a coat that sorts cargo in the endosome, the logistical hub of the cell. They primarily use cryo-electron tomography and subtomogram averaging to resolve retromer assembly on the membranes. This approach unravels how the retromer selects and directs cargo into diverse trafficking routes, the function critical for highly specialised cells and commonly affected in human pathologies.

Panel discussion

” Is the current pressure to publish restricting curiosity-driven research?”

In today's academic landscape, the emphasis on publications as the primary driver of research has sparked a vital conversation about its impact on the spirit of curiosity-driven research. In this panel discussion, we aim to explore the relationship between the pressure to publish and the free exploration of ideas in research. As academia increasingly emphasizes quantitative metrics and immediate impact, the question arises: Are we inadvertently stifling creativity and innovation? Join us as we navigate the complexities of fostering curiosity in a publication-focused environment.

Panelists:

Anjana Badrinarayan

Associate Professor of Microbiology at the NCBS, India

Nenad Ban

Professor of Structural Molecular Biology at ETH Zurich, Switzerland

Iain Cheeseman

Member of Whitehead Institute; Professor of Biology and Associate Department Head at MIT, USA

Lilit Nersisyan

Founding Director of the Armenian Bioinformatics Institute

Sara Osman

Senior Editor, Nature Structural & Molecular Biology

Moderators: Sara Ahrari and Svenja Groth

Poster Sessions

Tuesday, 10th September

P01	**Sanja Nikolic:** Growth and early characterization of neural organoids derived from patients with a neurodevelopmental and progeroid disease
P06	**Nilanjan Ghosh Dastidar:** Quantitative mass spectrometry analysis of aminoglycoside resistance mechanisms
P07	**Siddharth Padmanabhan**: Intersection of antibacterial autophagy with scavenger receptor function
P08	**Yi Zhu:** CTCF depletion uncouples the role of enhancer-promoter interactions and higher-order chromatin hubs in gene regulation during cellular differentiation
P09	**Tariq Tammam Ali:** Core particle modulator Blm10 increases degradation of alpha Synuclein
P10	**Bins K Chackochan:** The interplay between neurotrophic factor, CNTF, and transcription factor, Prrx1, in regulating adult neurogenesis in CNTF-treated mouse Subventricular Zone-derived neurosphere cultures
P11	**Somenath Dutta:** Exploring human miRNAs and genes for development of potential therapeutics against Zika virus using Bioinformatics approaches
P12	**Denis Šubert:** G-quadruplexes: CTCF's Hidden Ally at TAD Boudnaries
P14	**Fei Yu:** snoRNAs can shuttle into the cytoplasm during maturation in S. cerevisiae
P27	**Yaroslav Abramenko:** p53 is involved in the resistance of A549 cell line to mitotic inhibitors
P37	**Danial Hashemi:** Unveiling epigenetic signatures in non-obstructive azoospermia: insights from microarray analysis and molecular validation
P38	**Denis Šubert:** G-quadruplexes: CTCF's Hidden Ally at TAD Boundaries
P40	**Vahid Tavakolpour:** Targeting crosstalk between PD-L1 and PI3K/AKT pathway in triple-negative breast cancer via miR-34a

Wednesday, 11th September

P03	**Mojtaba Tavakoli:** Dense, synapse-level reconstruction of mammalian brain tissue with light microscopy
P04	**Ketevan Silagava**: Study of the degradation of recombinant DNA in broiler chicken feces
P05	**Sapthagiri Sukumaran:** An endogenous optical signalling pathway that activates non-visual photoreceptor opsin OPN3
P15	**Hafsa Zahid:** Odd Skipped related 1 is a master regulator of regenerative inflammation and extracellular matrix dynamics in skeletal muscle repair
P16	**Dilaray Tüfekçi:** Investigation of interaction between EML1 and Microtubules
P17	**Reshma Ramesh:** OCT4 phase separation facilitates transcriptional initiation and gene regulation
P18	**Shoval Miyara:** A macrophage-myofibroblast cell circuit reveals cold fibrosis following myocardial infarction
P19	**Jacob Elkahal:** Repurposing of Glatiramer Acetate to treat cardiac ischemia in animal models
P20	**Bidisha Bhattacharya:** Mutations in CUL4B affects cell cycle progression in the developing brain

P21	**Yuval Shapir Itai:** Bispecific dendritic-T cell engager potentiates anti-tumor immunity
P23	**Naama Darzi:** Vagotomy restores liver metabolism and prevents cancer-associated cachexia (CAC) development

Thursday, 12th September

P24	**Daniel Alfandari:** Host immune cell membrane deformability governs the uptake route of malaria-derived extracellular vesicles
P25	**Nina Sophie Bellersheim:** BTK inhibition - A potential treatment strategy for progressive MS
P26	**Justas Kvietkauskas:** Investigating membrane protein folding using SEIRAS
P28	**Cagil Urhan:** Inducible relocalization of the cytosolic transcription factors in B lymphocytes during the initiation of humoral response
P29	**Taehee Kim:** Molecular mechanisms regulating Cav1.3 Channel by CaBP2
P30	**Liudmila Ivanova**: Regions of the amyloidogenic domain of Sup35 protein essential for amyloid formation and LLPS
P31	**Sonja Schneider:** Catalytic regulation of autophagy
P32	**Viktor Martian:** Impact of the polymerization method on the biocompatibility of denture base resins in a 3D tissue engineered human oral mucosa model
P33	**Zhenglin Fu:** Structures of Importin 7 bound to RanGTP and in complex with Importinβ and histone H1°
P34	**Sabina Diusenova:** Reconstitution of autophagy initiation super-complex
P35	**Carmela Cruz:** Understanding epigenome resetting of the human germline
P36	**Anqi Jiang:** Dynamic mechanical microenvironmental control of FAPs differentiation during muscle regeneration
P39	**Tamazi Giunashvili:** Studying expression level of some genes involved in the formation of post-traumatic stress disorder associated fear memory by qPCR