MAX REPORT

2020–2023

Cover Art

Science deconstructs and reconstitutes reality. It reveals complexity, simplicity and beauty, much as art does for Markos R. Kay (MRK). The London-based multidisciplinary artist explores digital generative art and its intersection with the natural sciences, dealing with themes of self-organization, emergence, and evolution. A major theme of his work is the computational paradigm of the natural sciences, as seen in the relationship between scientific observation, simulation and visualization.

Evolved from MRK's Quantum Fluctuations, the Perutz Scientific Report showcases digital abstractions that explore the virtual reconstitution of intricate shapes from basic elements. His method relies on defining specific initial parameters and harnessing artificial intelligence (AI) techniques to build elaborate patterns.

Inspired by the Max Perutz Labs' mission to analyze and reconstitute biological systems across scales, generative AI was used to transform a basic visual "seed" into intricate patterns through iterative processes, which continuously refine the seed, introducing variations and complexities at each step, similar to the growth of complex biological matter. Each image in the report captures a moment in this fascinating process.

MAX PERUTZ LABS VIENNA

A joint venture of

universität wien

MEDIZINISCHE UNIVERSITÄT WIEN

Part of

Vienna BioCenter

The Max Perutz Labs are dedicated to a mechanistic understanding of fundamental biomedical processes. By analyzing and reconstituting complex biological systems across different scales, our scientists aim to link breakthroughs in basic research to advances in human health.

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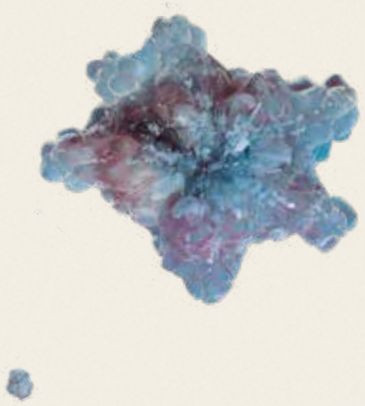

“I think of reconstitution as the art of taking bits and pieces of biological ingredients and putting them together in just the right way to recreate the magic of life. It’s like taking the letters of an ancient, forgotten language and arranging them to reveal a lost story.”

— Alwin Köhler

Fantastic Voyage

Alwin Köhler in conversation with Sarah Stoeter about the Max Perutz Labs, 60s sci-fi movies, disruptive thinking and what lies ahead

With your appointment as the scientific director in 2020, the Max Perutz Labs have seen major changes. Can you tell us about them?
Transitions naturally prompt questions about an institute's evolution, its core values, the scientific priorities and the balance between focus and diversity. How can we pay tribute to our strengths and at the same time use the opportunity to think differently? How can we increase communication and collaboration to improve the Perutz further? These are questions that the leadership team and I have asked from the onset. We have reinvigorated the search for talented scientists and increased the cooperation with our stakeholders and public outreach in general. The building's architecture and appearance have changed. I hope this has energized our community.

You were a strong advocate for renaming the institute. What was behind the change?
Quite simply, there was no compelling reason to obscure Max Perutz's name through an abbreviation, MFPL. We wanted to acknowledge the individual whose legacy underpins the institute. To break a habit takes time, but I am optimistic that, in due course, people will come to know and refer to the institute by its full name, or even as simply "the Perutz."

You assumed leadership of the institute just as Austria entered its initial lockdown in response to the COVID-19 pandemic. How was that start?
Besides the impact on public health, my main concern was the disruption to the careers of scientists. So, my priority was setting up the Vienna COVID-19 Detection Initiative, known as the VCDI, which started as a network of 21 research institutes. SARS-CoV-2 testing allowed the Perutz to operate almost without interruptions during the pandemic. VCDI scientists have also led large-scale testing in nursing homes, which has saved lives. This success rests on the shoulders of many colleagues at the Vienna BioCenter. It shows what collaboration across boundaries can accomplish.

Alwin Köhler is professor of molecular biology and scientific director of the Max Perutz Labs. He is an ERC investigator, NOMIS researcher, EMBO member, member of the Austrian Academy of Sciences and a Moore Distinguished Scholar at Caltech. Köhler studies the cell nucleus, focusing on lipids, nuclear pores and chromatin. He was interviewed by the editor of this scientific report, Sarah Stoeter.

How has the pandemic affected the Perutz community?
Everybody has demonstrated a strong sense of responsibility for each other. This was one of the most inspiring experiences. My hope is that, in retrospect, this crisis has made us stronger as a community. It has also underscored the importance of mentorship, urging principal investigators to be more sensitive to their team members' feelings about their work and future. The pandemic has also reminded us of the privilege we hold as scientists. We've been fortunate to continue our research, which ultimately is our most potent weapon against future pandemics.

How would you describe the Perutz, in a few words?
It is a really great place! At the heart, we conduct ambitious research at the forefront of mechanistic biomedicine. Our groups are relatively small, agile and productive. We foster a collaborative spirit. We put particular emphasis on recruiting early-career scientists at the most creative stages in their careers. We favor disruptive thinking over following what's scientifically in fashion. We have a clear scientific vision, but also remain open to new opportunities and surprises. Finally, we are a unique partnership between two of Austria's leading academic institutions. This creates many opportunities.

According to its mission, the Perutz is committed to a mechanistic approach in biomedicine. Why is this important?
The behavior of a biological system emerges from the interactions of its molecular components, the mechanisms by which they interact. As an example, Max Perutz, one of the fathers of modern molecular medicine, looked at breathing through the lens of mechanistic biology. Hemoglobin is a breathing molecule — if you want to understand how we breathe, you have to understand the mechanism by which hemoglobin works. Max Perutz uncovered the structure of hemoglobin and understood this fundamental issue. We focus on a mechanistic understanding, in all our research areas, because it explains how life works — and we have plenty of expertise to walk that path.

The Perutz places strong emphasis on analyzing and reconstituting biological systems across different scales. What can we learn from reconstitution?
I think of reconstitution as the art of taking bits and pieces of biological ingredients — such as proteins, DNA, lipids and other molecules — and putting them together in just the right way to recreate the magic of life. It's like taking the letters of an ancient, forgotten language and arranging them to reveal a lost story. We are molecular archaeologists solving a complex puzzle in which the pieces are molecules, and the final picture is the understanding of how life functions at its most fundamental level. We learn by building, by trial and error, and this can give us deep insights.

It is exciting to see that scientists now reconstitute not only macromolecules, but entire organelles, cells and tissues. Reconstitution actually plays an important role in many disciplines, from biology to chemistry, archaeology, and even history and art. For this report, we have collaborated with Markos R. Kay, a London-based artist and pioneer of generative AI. He initiated a digital self-assembly process in which he defined a tiny visual "seed" — this could be a molecule — and used AI-powered techniques involving many iterations and variations to construct very elaborate forms on a much larger scale. We took snapshots of this experiment as it happened. His work inspires many interesting questions.

Why is it important to understand biology across scales?
There is a science-fiction movie I really like: "Fantastic Voyage," which was released in 1966, four years after Max Perutz received the Nobel Prize. It's about a submarine crew that is shrunk to miniature size. They travel through the blood vessels of a scientist to repair his injured brain. Back then, it made people think about all the amazing things we could experience if we could shrink ourselves and travel across scales. Fast-forward 60 years, and we wouldn't go to the trouble of shrinking ourselves. Now we can easily "see" into blood vessels, into cells themselves. We have tools to examine life at almost any scale — to track changes in vegetation across the globe from satellites or pinpoint a single mutation within a chromosome.

This sounds exciting, albeit challenging. Where might it lead us?
If we want to obtain a comprehensive understanding of life, we need to examine how systems function and how they interact across multiple hierarchical levels. Phenomena at one level can influence phenomena at other scales. Multi-scale thinking provides a holistic perspective on how life evolves and adapts. And you are right, as each scale becomes more transparent, what is revealed is greater complexity than we ever could have imagined. Today, the sheer amount of information has overtaken the theoretical framework to understand it.

How can scientists tackle this complexity?
A real problem is that science has been sliced up into many different fields. Too often scientists remain in their own intellectual silos. Today scientists from historically separate disciplines desperately need each other, not just to find patterns in huge datasets but also to integrate this information into better models. Much of life is emergent. It's a complex system growing out of the interaction of simple elements. If we take insights from mechanistic biology, new technologies and AI-powered computing, it's no longer a sci-fi fantasy to travel across scales and understand the logic between them. Ultimately, we have to understand how everything relates to everything else.

Technologies have evolved, but has the scientific method evolved too? How can we keep pace with these challenges?
This is a really interesting question. A recent study in Nature* suggests that the rate of scientific innovation is slowing down. Despite major investments, the proportion of publications that challenge established concepts and push science in new directions has decreased since the 1950s. Some say that there are fewer fundamental discoveries left to be made. Alternatively, and I lean toward this, the culture of science has shifted toward a more results-oriented, executive approach. The pace has also quickened. And this may leave too little time for disruptive thinking. Unfortunately, many funding agencies also emphasize predictability over surprise.

"Multi-scale thinking provides a holistic perspective on how life evolves and adapts."

How can we overcome this trend?
That's difficult, but I'd say that we should start by changing the way we teach our students. We should impart knowledge and train technical skills, of course — but how do you develop new ideas in the first place? What makes a good scientific question? How fine-grained or fundamental should it be? Joseph Goldstein described the creative process in both art and science as two phases: first, generating and exploring new and imaginative ideas — he called it "building castles in the sky"— and then narrowing in and focusing on the most feasible and practical ideas — building houses of cards that don't topple over.

Can you train creativity?
I have heard too often that creativity is an inherent trait — you either have it or you don't. I don't believe this. I think that creative abilities can be accessed and cultivated through learning and practice. So why not prioritize creativity by incorporating lessons on innovative thinking skills? Students as well as more senior scientists — including myself — should always strive to improve when it comes to asking better questions, making connections between distant concepts, exploring contradictions or reframing a question if you are stuck. Creativity always goes hand in hand with rigorous experimentation.

Could this make science more disruptive again?
I don't have a final answer. But I do think that formulating the right new question can often push science forward more significantly than answering an existing one. A focus on creative thinking would help students, who often experience feelings of failure, to embrace uncertainty in a more positive way. It may also encourage an increasing number of creative young people to pursue a career in science. In my opinion, a major misunderstanding, also in the public, is that scientists are supposed to solve problems, when in truth, scientists should be concerned with posing disruptive questions.

What is the hardest part about asking tough questions?
It's often quite uncomfortable. When you're trying to create a completely new question, it goes beyond what you can expect in your frame of knowledge. Answering a question usually follows logical steps, but inventing a new one often involves an illogical leap into the unknown.

You were trained as both a medical doctor and basic researcher. How has this influenced you?
I see a fluid transition between these domains. To me, medicine and biology are essentially two detective stories; they just happen at different scales and with different tools. I sometimes tell my students that experiments must be as carefully planned as a therapy. And I often think that scientists would benefit from thinking like doctors, and vice versa. My training as a pediatrician has also taught me a few things about synthetic thinking and how to navigate uncertainties.

What advice would you offer young people who are considering a career in science?
Do whatever you want to do, and don't be intimidated by anyone. Be fearless. Be playful.

* Park, M., Leahey, E., and Funk, R.J. (2023). Papers and patents are becoming less disruptive over time. Nature 613, 138–144, https://doi.org/10.1038/s41586-022-05543-x

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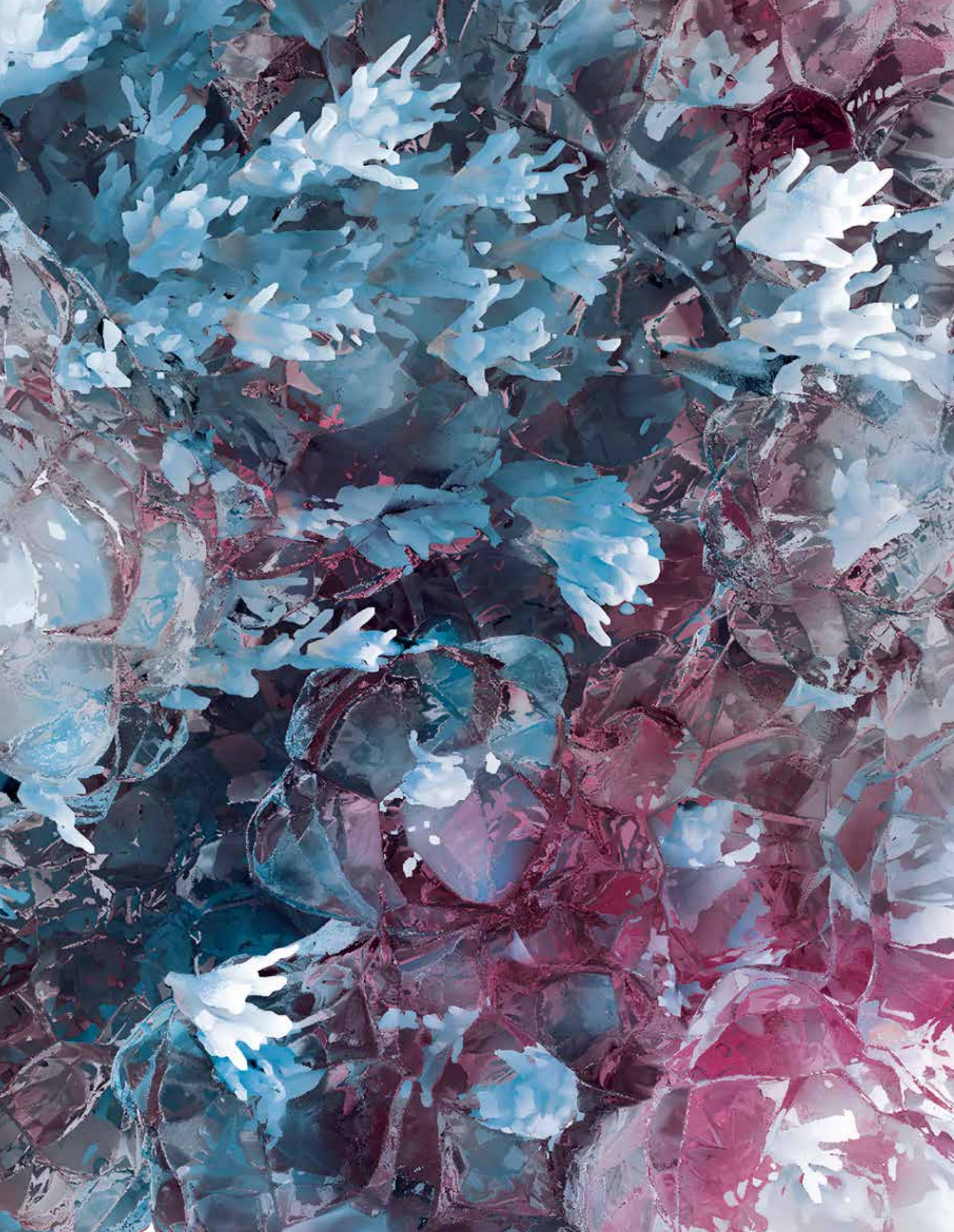


How important is public outreach for the Perutz?
We have accomplished exciting projects since 2020. Take the "Breathing at High Altitude" exhibition as an example. This exhibition about Max Perutz was a huge success. I was amazed by how many people, mostly nonscientists, came to learn about hemoglobin, the molecular basis of breathing, and the inspiring biography of Max Perutz. Last year, we had two artists paint a large mural about crystallography on the building. It's become a landmark in the 3rd district. I want the Perutz to always have an open door for curious minds.

What are the challenges ahead?
Looking at the Perutz and many other research institutions, one can easily see that the demographics of trainees and faculty unfortunately do not reflect the world around us, from gender balance to various other aspects. I am proud of the numerous people in our community who are advocating for more diversity, fairness and inclusion. With shared goals, we can promote cultural change. It will take time, but we will get there. After all, diversity is one of the ingredients that makes the Perutz such a great environment to work, teach and learn.

How will you know that the Max Perutz Labs have achieved their scientific goals?
I think we will know that when our scientists are widely recognized as leaders in their fields — creative, ambitious and impactful. And by impactful, I don't mean by publishing papers in big, fancy journals, but by generating insights that can withstand the test of time. As an institute, we should become a preferred destination for the best scientists in the world at all career stages. We should also become known for the high quality of our teaching and mentoring, for a supportive research culture that promotes collegiality and scientific integrity. These are my benchmarks. I am proud to say that a lot has been accomplished at the Perutz already. And we continue to move forward.

Any final thoughts?
After four years, I am curious to see how the next chapter in the Perutz story unfolds. I hope this scientific report and our interview will give everybody a good sense of what we've recently accomplished and what we aim to achieve.

A Word From the Rectors

Interfaces between academic institutions and scientific disciplines offer unique opportunities for exploring novel and unconventional combinations of ideas and technologies. The Max Perutz Labs exemplify this concept, as they reflect the strong commitment of the University of Vienna and the Medical University of Vienna to interdisciplinary basic research. Today's most transformative medicines owe their existence to fundamental discoveries made without immediate concern for practical applications, with their relevance to therapeutics becoming evident only many years later. In this regard, the Max Perutz Labs carry on the tradition of their namesake.

We take great pride in this joint venture, which has driven innovation across various fronts — from first-class science in mechanistic biomedicine to state-of-the-art research facilities, and from modern teaching approaches to a dedication to recruiting exceptional scientists. Ultimately, advancing science relies on creating academic environments that foster creativity and intellectual freedom, qualities that are indispensable for scientific discoveries. In the last four years, significant progress has been made, and we pledge our continued support to the mission of the Max Perutz Labs.

Markus Müller
Rector of the Medical University of Vienna

Sebastian Schütze
Rector of the University of Vienna

Max Perutz Labs Leadership Team

Leadership team (left to right): Thomas Leonard (deputy head, Medical University of Vienna), Christa Buecker (deputy head of teaching, University of Vienna), Sascha Martens (deputy head, University of Vienna), Alwin Köhler (scientific director, Max Perutz Labs), and Fabien Martins (administrative and finance director, Max Perutz Labs).

The leadership team plays a key role in guiding and overseeing the institute's operations. They are responsible for setting the institute's strategic vision, goals and priorities, as well as making decisions about the scientific infrastructure and budget management. Moreover, they are dedicated to achieving the teaching goals of the Perutz, reforming curricula and upholding ethical standards in all scientific pursuits. Collaborating closely with the faculty, the leadership team fosters an environment of innovation and cooperation while representing the institute to its two stakeholders and the public. Ultimately, the leadership team's mission is to drive scientific excellence, promote the advancement of knowledge and establish the Max Perutz Labs as a world-class institute.

A View From Outside: Scientific Advisory Board

The Max Perutz Labs Scientific Advisory Board (SAB) is comprised of internationally renowned scientists, who advise the scientific director on all aspects of the development and execution of the institute's scientific strategy. The SAB includes both permanent and ad hoc members, with the latter consulted for evaluating specific research areas.

Permanent members

Cheryl Arrowsmith

Cheryl Arrowsmith is chief scientist of the Structural Genomics Consortium (SGC) at the University of Toronto, senior scientist at the Princess Margaret Cancer Centre, and professor of medical biophysics at the University of Toronto. She is an internationally recognized expert in cancer-related structural biology, chemical biology and epigenetics.

Ivan Dikic

Ivan Dikic is a professor at the Goethe University in Frankfurt am Main and director of the Institute of Biochemistry II. He is also the founding director of the Buchmann Institute for Molecular Life Sciences (BMLS) and a fellow of the Max Planck Institute for Biophysics in Frankfurt. He is an internationally recognized leader in ubiquitin biology and autophagy research.

Benjamin G. Neel

Benjamin Neel is a professor in the Department of Medicine at New York University and director of the Laura and Isaac Perlmutter Cancer Center, where he leads a community of clinician–scientists and basic scientists, as well as a team of physicians. He is an internationally recognized authority on cell signaling in cancer and developmental disease.

Lori Passmore

Lori Passmore is a structural biologist who leads a research group at the Medical Research Council (MRC) Laboratory of Molecular Biology (LMB) in Cambridge, UK. She is a fellow of the Royal Society and a renowned expert in the study of protein complexes that regulate gene expression.

"The Max Perutz Labs are at the forefront of modern biological research. With a mission to analyze and reconstitute biological systems across scales, its scientists play a key role in addressing contemporary biological challenges — from the molecular machinery that governs the smallest cellular processes, to the complex organization of organelles, tissues and organisms. Through internationally recognized research and its commitment to interdisciplinary collaboration, I am convinced that the Perutz will make groundbreaking contributions to the field of mechanistic biomedicine for years to come."

— Ivan Dikic

Ad hoc members

M. Madan Babu (2023)
Structural and Computational Biology

M. Madan Babu is the endowed chair of Biological Data Science at St. Jude Children's Research Hospital in Memphis, Tennessee, where he is the director of the Center of Excellence for Data-Driven Discovery. He is a fellow of the Royal Society and the Academy of Medical Sciences. His group has made fundamental contributions in the field of GPCRs, disordered proteins and gene regulation.

Petr Broz (2022)
Infection and Immunity

Petr Broz holds the position of professor in the Department of Immunobiology at the University of Lausanne. He has gained recognition for his pioneering investigations into host defense mechanisms, inflammasomes and the triggering of pyroptosis — a lytic, inflammatory form of cell death.

Eric A. Miska (2022)
Chromatin, RNA and Chromosome Biology

Eric Miska is the Herchel Smith Professor of Molecular Genetics, head of department and senior group leader in the Department of Biochemistry at the University of Cambridge. He is an associate faculty member at the Gurdon Institute, University of Cambridge, and an acclaimed scientist in the field of RNA biology.

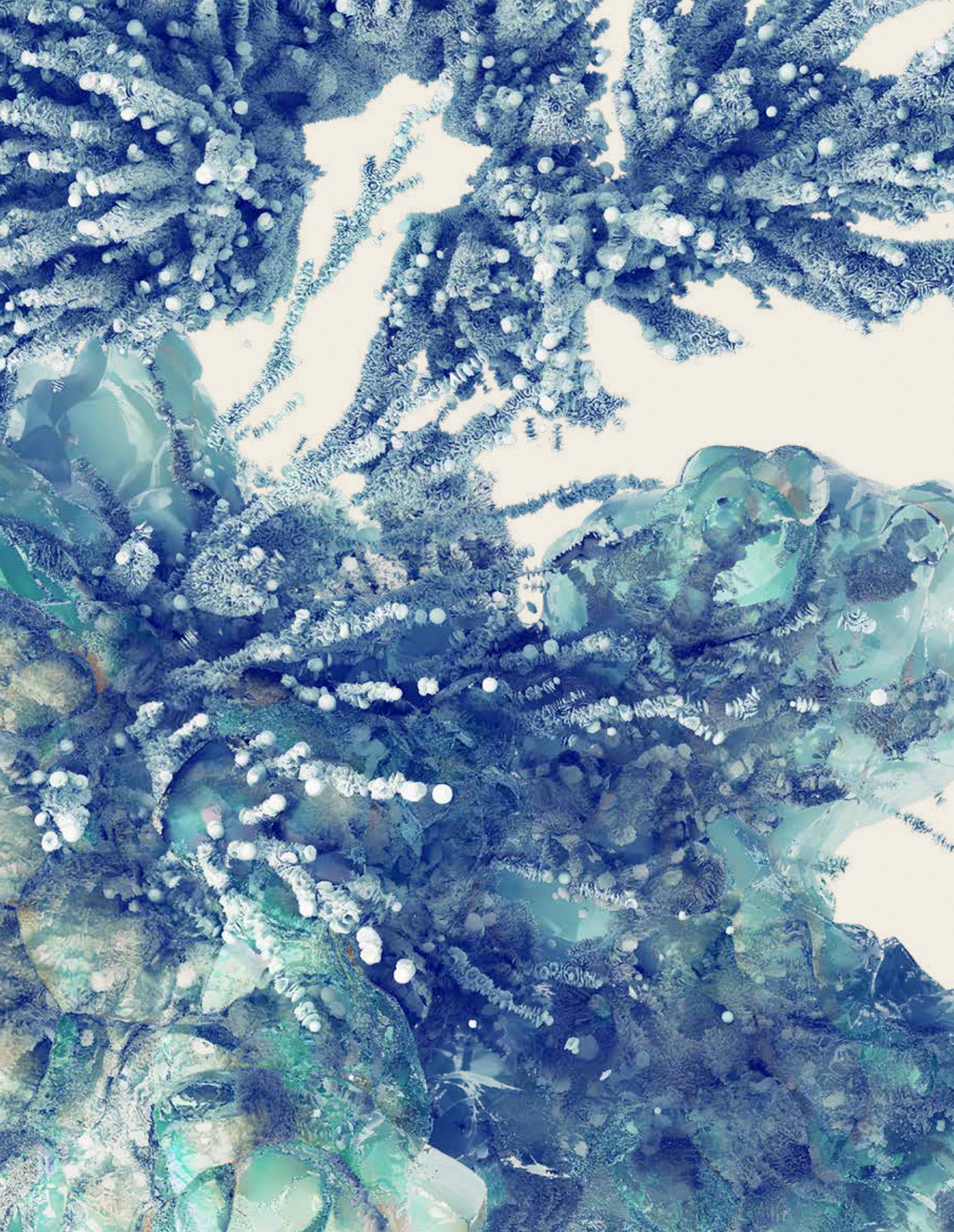
Ulrike Kutay (2021)
Mechanistic Cell and Developmental Biology

Ulrike Kutay is a professor at the Institute of Biochemistry and head of the Strategy Commission at ETH Zurich. She is recognized as a world-leading expert in the study of the cell nucleus, with a special focus on nuclear organization and proteostasis, ribosome biogenesis, and nuclear envelope function and remodeling.

Former permanent member

Peter Parker (2013–2021)

Peter Parker is a research group leader at The Francis Crick Institute, director of the King's Health Partners Integrated Cancer Centre, and professor of cancer cell biology at King's College London. His research is centered on cellular signal transduction and how faulty signaling can lead to disease.



Research Groups

With a strategic focus on fostering collaboration among researchers in the field of mechanistic biomedicine, our science program is both diverse and evolvable.

Mechanistic Cell and Developmental Biology

Infection and Immunity

Chromatin, RNA and Chromosome Biology

Structural and Computational Biology

Our research groups are associated with one of the four overarching research areas shown above. Group leaders choose a primary research area, though they could have interests in several. This broad framework encourages the pursuit of new research avenues.

Our strategy promotes the exchange of ideas across research areas. Instead of physically clustering scientists in each research area, we mix experts from different fields with the goal of increasing interdisciplinarity and synergies between individual research groups.

Focusing on the continuous recruitment of early-career researchers, the Perutz remains flexible, adjusting its research portfolio when new opportunities arise.

Collaborations between our two universities are important. These can range from informal interactions to jointly organized courses and network grants.

The following section details the four research areas and the biological questions that Max Perutz Labs scientists are interested in.

Mechanistic Cell and Developmental Biology

The instructions that make us who we are translate into a diverse array of complex and highly regulated processes that occur precisely and on time in every single cell. Mistakes in these processes can lead to disease. Scientists at the Max Perutz Labs study fundamental cellular and developmental processes at a mechanistic level.

Manuela Baccarini

Deciphering the MAPK pathway in vivo

The Question

The RAF/MEK/ERK pathway is constitutively activated in human malignancies and developmental disorders, and its components are attractive therapeutic targets. We focus on the role of the paralogs in each tier — three RAF, two MEK and two ERK in vertebrates — and have shown that RAF and MEK paralogs are required for pathway cross talk, with functional consequences for homeostasis at the molecular, cellular and organismal levels.

The Approach

We use a blend of genetics, molecular biology, biochemistry and cell biology. Since the essential functions of RAF and MEK paralogs rely primarily on protein–protein interactions with other signaling molecules, we use proximity labeling techniques coupled with mass spectrometry to understand the context in which these complexes operate. We study the functional consequences of pathway perturbation in primary cells using single-cell technologies.

Key Publications

An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion (2018). Baumgartner et al., Cell Stem Cell

A cell-autonomous tumour suppressor role of RAF1 in hepatocarcinogenesis (2016). Jeric et al., Nature Communications

MEK1 Is Required for PTEN Membrane Recruitment, AKT Regulation, and the Maintenance of Peripheral Tolerance (2013). Zmajkovicova et al., Molecular Cell

Andreas Bachmair

Protein modification in plants

The Question

Human health is linked to nutrition and profits from a healthy environment. Improving the growth of cultured plants impacts both food quality and environmental sustainability. Our group is interested in finding out how plants can grow well, even when environmental conditions are not optimal. This knowledge can help to generate improved seed material for high-quality and high-quantity harvests via sustainable agricultural practices.

The Approach

Adaptation of plants to changing environmental conditions requires signal transduction. Virtually all signal transduction pathways encompass steps to modify proteins already present in the cell. We study the impact of so-called modifier proteins, in particular via the N-degron pathway for ubiquitin conjugation, and in a pathway that links several SUMO proteins as a chain to its substrates, as part of signal transduction cascades.

Key Publications

A Yeast-Based Functional Assay to Study Plant N-Degron–N-Recognin Interactions (2022). Kozlic et al., Frontiers in Plant Science

Transcriptome, metabolome and suppressor analysis reveal an essential role for the ubiquitin-proteasome system in seedling chloroplast development (2022). Talloji et al., BMC Plant Biology

Christa Buecker

Transcriptional regulation during early embryonic development

The Question

During development, cells undergo tightly regulated differentiation steps characterized by distinct changes in gene expression. Enhancers are short DNA sequences that regulate the expression of a gene from a distance. Changes in the enhancer landscape have been mapped in numerous cell states, but how enhancers function to activate their target gene remains enigmatic. My lab wants to understand how enhancers orchestrate transcriptional changes.

The Approach

We study enhancer activity and regulation in a highly controlled in vitro developmental system: the exit from naive pluripotency. Through a combination of NGS-based approaches, imaging to follow transcriptional changes using reporters, and CRISPR-Cas9-based genome-wide screening methods, we dissect enhancer function in detail. We recently established a novel synthetic locus that allows for bottom-up reconstitution and dissection of enhancer clusters.

Key Publications

Transient upregulation of IRF1 during exit from naive pluripotency confers viral protection (2022). Romeike et al., EMBO Reports

Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements (2021). Thomas et al., Molecular Cell

Alexander Dammermann

Centriole assembly and function

The Question

Centrioles perform two important functions in eukaryotic cells: 1) They form centrosomes that organize the microtubule cytoskeleton and contribute to cell division, and 2) They form cilia, cellular projections that perform critical sensory and motile functions. Work in my lab seeks to understand the fundamental and conserved molecular mechanisms underlying centriole assembly and their function in centrosome and cilium biogenesis.

The Approach

We are using a combination of biochemical, cell biological and genetic approaches in *C. elegans* and *D. melanogaster* to address three main questions: 1) How do centrioles assemble and what are the mechanisms that underlie their remarkable stability? 2) How do centrioles recruit pericentriolar material to form centrosomes, and what is the nature of this material? 3) Focusing on early events in ciliogenesis, how do centrioles form cilia?

Key Publications

A phylogenetic profiling approach identifies novel ciliogenesis genes in *Drosophila* and *C. elegans* (2023). Dobbelaere, Su, Erdi et al., EMBO Journal

An acentriolar centrosome at the *C. elegans* ciliary base (2021). Garbrecht, Laos et al., Current Biology

Cep97 is required for centriole structural integrity and cilia formation in *Drosophila* (2020). Dobbelaere et al., Current Biology

Stephanie Ellis

Cell competition and tissue fitness in development and disease

The Question

What are the fundamental cellular and molecular principles that govern complex tissue organization? Our lab tackles this question through the lens of cell competition, a tissue-level quality control phenomenon that enables cells to sense the fitness of their neighbors and eliminate unfit, potentially disease-causing cells. By studying cell competition mechanisms, we illuminate how tissues maintain robust form and function over long lives.

The Approach

Our lab unites concepts and tools from cell and developmental biology, disease modeling and biophysics to illuminate mechanisms of cell competition in a variety of contexts including tissue assembly, repair, aging and disease. Leaning on sophisticated microscopy approaches together with functional genetics, our multidisciplinary tool kit enables study of tissue organization and growth control across scales, from molecules to whole organs.

Key Publications

Distinct modes of cell competition shape mammalian tissue morphogenesis (2019). Ellis et al., Nature

Basal Cell-Extracellular Matrix Adhesion Regulates Force Transmission during Tissue Morphogenesis (2016). Goodwin, Ellis et al,. Developmental Cell

Roland Foisner

Lamins in nuclear organization and human disease

The Question

Lamins form the nuclear lamina scaffold at the nuclear envelope. They determine mechanical properties of the nucleus and regulate spatial chromatin organization. Mutations in the LMNA gene cause various diseases, including premature aging. We study molecular functions of lamins in mechanosignaling and chromatin regulation at the mechanistic level to understand lamin functions in adult stem cell regulation and to identify molecular disease mechanisms.

The Approach

We study lamin functions in health and disease using a curiosity-driven research strategy. We apply a wide range of molecular biological, biochemical and microscopic approaches. We generate and use cellular and animal models to understand lamin dysfunction in aging and disease and to identify the contributions of impaired lamin functions to pathologies in lamin-linked diseases at the cellular, tissue and organismal levels.

Key Publications

LAP2alpha maintains a mobile and low assembly state of A-type lamins in the nuclear interior (2021). Naetar et al., eLife

Endothelial progerin expression causes cardiovascular pathology through an impaired mechanoresponse (2019). Osmanagic-Myers et al., Journal of Clinical Investigation

Peter Fuchs

Intermediate filaments in epithelial stress response

The Question

A major role of the keratin intermediate filaments in epithelia is to protect cells from stress. We recently showed that the keratin-associated protein epiplakin binds to keratin filaments only in stress situations, leading to elevated intracellular levels of Ca^{2+}, and that this interaction changes keratin dynamics. We are now investigating the influence of epiplakin binding on the formation and breakdown of keratin filaments.

The Approach

To elucidate the biological function of epiplakin in epithelia, we use cell culture, biochemistry, video microscopy and mouse injury experiments. The main goals are to investigate epiplakin's interaction with keratins in detail and to reveal the functions of epiplakin in keratin filament dynamics and network recovery after stress. In the mouse we use stress models for epithelia in different organ systems and experiments with primary cells.

Key Publications

A Ca^{2+}-Mediated Switch of Epiplakin from a Diffuse to Keratin-Bound State Affects Keratin Dynamics (2022). Ratajczyk et al., Cells

Comparative Genomics Reveals Evolutionary Loss of Epiplakin in Cetaceans (2022). Fuchs et al., Scientific Reports

Erinc Hallacli

Deciphering molecular phenotypes in neurodegenerative diseases

The Question

Neurodegenerative diseases like Parkinson's (PD) impact our aging society. To develop therapies, understanding protein aggregate toxicity in neurons is vital. We found that processing bodies (P-bodies), RNA granules, offer a new pathway in PD-linked alpha-synuclein (αSyn) toxicity. We will study P-body function in PD, RNA granule interactions with lipid membranes via αSyn, and its effect on RNA pathways.

The Approach

Our lab uses iPSC-derived cortical neurons to study P-body physiology. For large-scale experiments discovering αSyn membrane factors, we will use CRISPR and flow cytometry in human cell lines, validating in neurons. To discover new RNA pathways, we will employ ORFeome-wide protein tagging in cellular models, verifying in neurons. Our core approach: Learn what's essential to address specific problems.

Key Publications

The Parkinson's disease protein alpha-synuclein is a modulator of processing bodies and mRNA stability (2022). Hallacli et al., Cell

A genetic tool to track protein aggregates and control prion inheritance (2017). Newby and Hallacli et al., Cell

Msl1-Mediated Dimerization of the Dosage Compensation Complex Is Essential for Male X-Chromosome Regulation in *Drosophila* (2012). Hallacli et al., Molecular Cell

Erinc Hallacli will start his lab at the Perutz in April 2024.

Elif Karagöz

Protein quality control in the endoplasmic reticulum

The Question

A healthy proteome is critical for cell function. Cells constantly monitor their proteins and respond to conditions that perturb the delicate balance between protein synthesis, folding and degradation. Protein homeostasis in the endoplasmic reticulum (ER) is maintained by the unfolded protein response (UPR). How UPR sensors/transducers detect protein-folding problems and mount an appropriate response is an open question.

The Approach

In my lab, we seek to understand the UPR at a mechanistic level. We combine cell biology, biochemistry and systems-level methods to dissect how cells maintain a protein-folding homeostasis in the ER. Our long-term goal is to use the mechanistic insights derived from these approaches to restore protein homeostasis in a variety of human diseases caused by protein misfolding.

Key Publications

Optimized infrared photoactivatable ribonucleoside enhanced crosslinking and immuno-precipitation (IR-PAR-CLIP) protocol identifies novel IGF2BP3-interacting RNAs in colon cancer cells (2023). Anisimova and Karagöz, RNA

Shuffled ATG8 interacting motifs form an ancestral bridge between UFMylation and C53-mediated autophagy (2023). Picchianti et al., EMBO Journal

An unfolded protein-induced conformational switch activates mammalian IRE1 (2017). Karagöz et al., eLife

Alwin Köhler

Nuclear envelope biology — gates, chromatin and lipids

The Question

The nuclear envelope separates nucleoplasm from cytoplasm. By combining durability with plasticity, selective traffic with mass transport, spatial enclosure with sophisticated signaling, the nuclear envelope enables eukaryotes to protect and regulate their genome. How this "intelligent boundary" integrates so many functions is a mystery. We aim to understand how the nuclear envelope is built, how it breaks and how to fix it when it is broken.

The Approach

Three perspectives guide our work: lipids, gates and chromatin. We investigate at a mechanistic level how the nuclear envelope regulates its elasticity, how it opens through its NPCs and how these gates interact with the membrane. We examine how the envelope impacts the nuclear interior and affects chromatin structure and function. Additionally, we explore how membrane-less nuclear compartments shape gene expression programs.

Key Publications

Assembly principle of a membrane-anchored nuclear pore basket scaffold (2022). Cibulka et al., Science Advances

Phase separation directs ubiquitination of gene-body nucleosomes (2020). Gallego et al., Nature

The inner nuclear membrane is a metabolically active territory that generates nuclear lipid droplets (2018). Romanauska and Köhler, Cell

Martin Leeb

Molecular control of cell identity

The Question
We address fundamental questions in developmental biology: How are we made? How are cell identities defined and maintained in order to provide the right cell type at the right time for proper development? What are the central molecular players for cell-fate choice? Our main research efforts focus on some of the first differentiation decisions taken during embryonic stem cell commitment.

The Approach
The “Leeboratory” approaches cell-fate choice from multiple angles. We study epigenetics, RNA-biology and signaling to pursue a holistic approach to understand differentiation. We use genetics and high-throughput methods, combined with systems-biology approaches to delineate the molecular rules of cell-fate decision. Mouse and human embryonic stem cells and various differentiation strategies are our main experimental model systems.

Key Publications
NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation (2022). Huth et al., Genes & Development

Cooperative genetic networks drive embryonic stem cell transition from naïve to formative pluripotency (2021). Lackner et al., EMBO Journal

Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3 (2021). Santini et al., Nature Communications

Sascha Martens

Molecular mechanisms of autophagy

The Question
Autophagy is a process that cells employ to remove harmful material so that it can be replaced with new parts. During autophagy this material becomes engulfed by vesicles, the autophagosomes. How autophagosomes form around their cargoes is still enigmatic and an important question, because defects in autophagy have been associated with numerous diseases such as neurodegeneration.

The Approach
Past research has identified a plethora of factors required for autophagy. However, how these factors act together in order to couple the capturing of the cellular material destined for degradation with the formation of autophagosomes is not well understood. We focus on bottom-up approaches to understand how cells form autophagosomes. Our long-term goal is to reconstitute autophagy in vitro and compare the outcome to its working in cells.

Key Publications
Reconstitution defines the roles of p62, NBR1 and TAX1BP1 in ubiquitin condensate formation and autophagy initiation (2021). Turco et al., Nature Communications

Reconstitution of autophagosome nucleation defines Atg9 vesicles as seeds for membrane formation (2020). Sawa-Makarska et al., Science

FIP200 Claw Domain Binding to p62 Promotes Autophagosome Formation at Ubiquitin Condensates (2019). Turco et al., Molecular Cell

Johannes Nimpf

Functions of ApoER2 and VLDL receptor

The Question
During embryonic brain development, the Reelin signaling pathway orchestrates correct positioning of neurons in laminated structures of the brain. This pathway starts with the binding of Reelin to two receptors, ApoER2 and VLDL, and leads to phosphorylation of the intracellular adapter protein Dab1. The main aim of our research is to describe the actual signalosome(s) formed and to characterize their specific functions.

The Approach
To investigate the formation of specific signalosomes by Reelin, we use time-resolved anisotropy (homo-FRET) and fluorescence lifetime imaging microscopy (FLIM-FRET).

Key Publications
Disabled 1 is Part of a Signaling Pathway Activated by Epidermal Growth Factor Receptor (2021). Dlugosz et al., International Journal of Molecular Sciences

The Reelin Receptors Apolipoprotein E receptor 2 (ApoER2) and VLDL Receptor (2018). Dlugosz et al., International Journal of Molecular Sciences

Egon Ogris

Protein phosphatase 2A biogenesis and monoclonal antibodies

The Question

The phosphorylation state of a protein determines its biological functions and is regulated by the opposing activities of kinases and phosphatases. A major phosphoserine/threonine phosphatase in the cell is protein phosphatase 2A (PP2A), a large family of multisubunit holoenzymes. How PP2A holoenzymes assemble and how their biogenesis is regulated are the questions addressed by our research.

The Approach

We study PP2A biogenesis using biochemical, genetic and immunological approaches. Our analysis in yeast unraveled some of the basic principles of PP2A biogenesis. Despite the high conservation, less is known about this process in mammals. Detailed knowledge of mammalian PP2A biogenesis is required for the development of novel therapies that aim to restore the tumor-suppressive functions of PP2A.

Key Publications

Loss of LCMT1 and biased protein phosphatase 2A heterotrimerization drive prostate cancer progression and therapy resistance (2023) Rasool et al., Nature Communications

PP2AC phospho-Tyr307 antibodies are not specific for this modification but are sensitive to other PP2AC modifications including Leu309 methylation (2020). Frohner et al., Cell Reports

The Myc tag monoclonal antibody 9E10 displays highly variable epitope recognition dependent on neighboring sequence context (2020). Schüchner et al., Science Signaling

Shotaro Otsuka

Intra-cellular communication between the ER and the nucleus

The Question

Inter-organelle communication needs to be tightly controlled. One of the key organelles is the endoplasmic reticulum (ER). Our lab investigates the mechanism of how the ER regulates inter-organelle communication and cell fate. We aim to reveal: 1) the structure, function and regulation of the ER–nucleus connection; 2) how the identity of the nucleus is maintained; and 3) how ER inheritance is ensured during cell division.

The Approach

The correlative live imaging with electron microscopy that we have established, allows us to visualize intra-cellular structures at high spatiotemporal resolution. We combine this imaging technology with quantitative live imaging and molecular perturbation. Our approach delivers a quantitative and dynamic high-resolution view of inter-organelle communication and provides a mechanistic understanding of the underlying molecular mechanism.

Key Publications

A quantitative map of nuclear pore assembly reveals two distinct mechanisms (2023). Otsuka et al., Nature

Visualizing Nuclear Pore Complex Assembly In Situ in Human Cells at Nanometer Resolution by Correlating Live Imaging with Electron Microscopy (2022). Bragulat-Teixidor et al., Methods in Molecular Biology

Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings (2018). Otsuka et al., Nature Structural & Molecular Biology

Florian Raible

Stem cells, regeneration and developmental plasticity

The Question

Neural regeneration is likely an ancestral feature secondarily lost in mammals and other taxa. Annelid worms modulate regenerative capacity through brain-derived factors. These also orchestrate other developmental features — ranging from bristle shapes to reproductive maturation — and even the time of death. Research into such factors therefore provides unique experimental and mechanistic access to fascinating and fundamental aspects of biology.

The Approach

Our research combines functional work (knockouts, transgenics), cell biology, multimodal imaging, cellular profiling (scRNAseq), and physiological and behavioral strategies. Most of our work focuses on the marine bristleworm *Platynereis dumerilii* , which we have helped to push as an experimental system. Our efforts are embedded in a larger Vienna-wide effort to address the molecular mechanisms of stem cell differentiation and regeneration.

Key Publications

Two light sensors decode moonlight versus sunlight to adjust a plastic circadian/circalunidian clock to moon phase (2022). Zurl et al., Proceedings of the National Academy of Sciences

Characterization of cephalic and non-cephalic sensory cell types provides insight into joint photo- and mechanoreceptor evolution (2021). Revilla-I-Domingo et al., eLife

A versatile depigmentation, clearing, and labeling method for exploring nervous system diversity (2020). Pende et al., Science Advances

Kristin Tessmar-Raible

Biological timers set by sun and moon

The Question

How is time information from the sun and moon decoded by organisms to adjust their physiology and behavior from the protein complex to the population level?

The Approach

We study the aspect of biological time from actimetry and cognitive questionnaires in healthy versus endocrinologically impaired humans, to the molecular regulation and biochemical complexes that control the inner daily, monthly and seasonal timers. One focus is on the marine worm *P. dumerilii* that times with moon- and sunlight, which we can use to test causality by techniques including transgenesis, inducible cell ablations and genome engineering.

Key Publications

Rhythms and Clocks in Marine Organisms (2023). Häfker et al., Annual Review of Marine Science

A Cryptochrome adopts distinct moon- and sunlight states and functions as sun- versus moonlight interpreter in monthly oscillator entrainment (2022). Poehn et al., Nature Communications

Seasonal variation in UVA light drives hormonal and behavioural changes in a marine annelid via a ciliary opsin (2021). Veedin Rajan et al., Nature Ecology & Evolution

Georg Weitzer

Molecular aspects of cardiomyogenesis

The Question

We investigate the signaling and genetic regulation of self-renewal, commitment and differentiation of cardiac stem cells. We also try to identify feasible strategies for paracrine stimulation of endogenous cardiac stem cells in the diseased heart to facilitate regenerative therapy and to improve the quality of life.

The Approach

We investigate the interaction of SPARC and desmin and their influence on the transcription factor network regulating homeostasis in cardiac stem cells.

Key Publications

Desmin enters the nucleus of cardiac stem cells and modulates Nkx2.5 expression by participating in transcription factor complexes that interact with the nkx2.5 gene (2016). Fuchs et al., Biology Open

Embryonic stem cells facilitate the isolation of persistent clonal cardiovascular progenitor cell lines and leukemia inhibitor factor maintains their self-renewal and myocardial differentiation potential in vitro (2013). Hoebaus et al., Cells Tissues Organs

Chromatin, RNA and Chromosome Biology

Genetic information is encoded in genes, embedded in chromatin and organized in chromosomes. Its implementation is dynamically regulated at different levels, from DNA to RNA. At the Max Perutz Labs, scientists focus on fundamental processes of inheritance, nuclear architecture, genome organization and RNA biology, from bacteria to humans.

Stefan Ameres

Mechanism and biology of RNA silencing

The Question

Gene regulation is the fundamental process that controls genome function, and it pervades most biology. The control over RNA fate and function has emerged as a central hallmark of gene regulation with enormous biological, technological and biomedical implications. Our goal is to understand how the quality and quantity of the transcriptome is controlled at the molecular level in flies and mammals.

The Approach

Our studies aim to: 1) provide insights into the emerging role of RNA modifications in the regulation of RNA fate and function; 2) determine possible causes for aberrant gene expression profiles that have been associated with human diseases; and 3) establish technologies that unravel the molecular signatures of RNA decay, as well as its functional components and their organization in pathways.

Key Publications

SLAMseq resolves the kinetics of maternal and zygotic gene expression in early zebrafish embryogenesis (2023). Bhat et al., Cell Reports

Time-Resolved Small RNA Sequencing Unravels the Molecular Principles of MicroRNA Homeostasis (2019). Reichholf et al., Molecular Cell

SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis (2018). Muhar et al., Science

Christopher Campbell

Causes and consequences of chromosomal instability

The Question

The accurate distribution of chromosomes to daughter cells is one of the most fundamental requirements of cell division. However, errors are frequently made during the attachment process, resulting in cells with an abnormal number of chromosomes, which is called aneuploidy. Our lab aims to determine the mechanisms that cells use to prevent the formation of aneuploidy as well as the repercussions of aneuploidy.

The Approach

We use a combination of cell biology, genome engineering, and molecular biology techniques to perform mechanistic studies of fundamental processes related to chromosome segregation, primarily in budding yeast and human cell culture. In addition, we conduct long-term adaptation experiments to determine how the structure of the genome changes to cope with elevated instability.

Key Publications

Adaptation to spindle assembly checkpoint inhibition through the selection of specific aneuploidies (2023). Adell et al., Genes & Development

Adaptation to high rates of chromosomal instability and aneuploidy through multiple pathways in budding yeast (2022). Clarke et al., EMBO Journal

Aurora B activity is promoted by cooperation between discrete localization sites in budding yeast (2022). Marsoner et al., Molecular Biology of the Cell

Boris Görke

Signal transduction and post-transcriptional regulation in bacteria

The Question

Our research aims to unravel novel principles and pathways underlying signal perception, transduction and cellular regulation in the model organism *Escherichia coli*. We aim to understand a regulatory network consisting of trans-envelope and ribonucleoprotein complexes as well as a phosphotransferase system, which integrates extra-cytoplasmic signals and information about the metabolic state of the cell to achieve cell envelope homeostasis.

The Approach

We are devoted to the power and art of genetic screens and mutational analyses that often reveal novel regulatory connections and pathways. We use genetics, biochemistry and molecular biology combined with global techniques such as NGS, mass spectrometry and metabolomics in collaboration with facilities on the campus. Structural and biophysical techniques and bioinformatics were applied in the past in the framework of excellent collaborations.

Key Publications

Structure of a bacterial RNP complex central to the control of cell envelope biogenesis (2023). Islam et al., EMBO Journal

Small RNA-binding protein RapZ mediates cell envelope precursor sensing and signaling in *E. coli* (2020). Khan et al., EMBO Journal

Feedback regulation of small RNA processing by the cleavage product (2019). Durica-Mitic et al., RNA Biology

Pim Huis in 't Veld

Preventing DNA damage during mitosis

The Question

The propagation of life relies on the accurate distribution of copied genomes when cells divide. As sister chromatids segregate in anaphase, pieces of DNA that link the sisters are stretched. These bridges threaten the transmission of an intact genome — a hallmark and driver of disease. We aim to understand how an ensemble of DNA helicases, translocases and topoisomerases recognizes and processes DNA bridges in dividing human cells.

The Approach

Biochemical reconstitution is a powerful tool to study the protein machinery that orchestrates a process as intricate as a mitotic cell division. We get quantitative and molecular insight into isolated parts of the machinery by systematically mixing and modifying purified components. We complement this approach with structural biology and single-molecule biophysics and investigate the implications of our discoveries in dividing cells.

Key Publications

Stable kinetochore-microtubule attachment requires loop-dependent Ndc80-Ndc80 binding (2023). Polley et al., EMBO Journal

Reconstitution of highly active human CDK1:Cyclin-B:CKS1 complexes (2022). Huis in 't Veld et al., Protein Science

Molecular determinants of the Ska-Ndc80 interaction and their influence on microtubule tracking and force-coupling (2019). Huis in 't Veld et al., eLife

Verena Jantsch

Meiosis in *Caenorhabditis elegans*

The Question

In each generation, the two parental genomes must pair, recombine and segregate as a newly mixed set of haploid chromosomes in a specialized cell division called meiosis. Failures lead to miscarriages and congenital diseases. We identify genes and processes essential for accurate chromosome segregation during meiosis. The identification of new risk factors leading to unfaithful partitioning of chromosomes into gametes is of high relevance to human health.

The Approach

Excellent forward and reverse genetics, easy cytological observation of all meiotic stages and the transparency of the animal make the nematode *C. elegans* a model system of choice. CRISPR/Cas technologies are established and allow the rapid generation of novel alleles and tagging of individual factors followed by high-resolution imaging. This way, we have generated numerous novel meiotic mutants that provide(d) us insight into events of prophase I of meiosis.

Key Publications

Release of CHK-2 from PPM-1.D anchorage schedules meiotic entry (2022). Baudrimont et al., Science Advances

Transient and Partial Nuclear Lamina Disruption Promotes Chromosome Movement in Early Meiotic Prophase (2018). Link et al., Developmental Cell

Meiotic chromosome homology search involves modifications of the nuclear envelope protein Matefin/SUN-1 (2009). Penkner et al., Cell

Franz Klein

Yeast chromosomes in meiosis

The Question

Chromosomes are the form of organization of the genome in all living organisms. Eukaryotes undergo sexual reproduction, shuttling between haploid and diploid states via fertilization and meiosis. In meiosis, homologous chromosomes are identified and physically linked during repair of programmed, Spo11-mediated DNA double-strand breaks (DSBs). We study the interplay of meiotic DSB repair and the associated dynamic changes in chromosome structure.

The Approach

We use the best-suited technology in budding yeast to answer biological questions. Our technical strengths are genomics, bioinformatics, genetic engineering, genetic screens and chromosome visualization. We perform experiments in vivo with high precision methods, such as acute protein depletion or dimerization, followed by molecular analysis, such as ChIPseq or super-resolution microscopy, but also use in vitro approaches, when necessary.

Key Publications

Spo11 generates gaps through concerted cuts at sites of topological stress (2021). Prieler et al., Nature

Smc5/6-Mms21 prevents and eliminates inappropriate recombination intermediates in meiosis (2013). Xaver et al., PLOS Genetics

Spo11-accessory proteins link double-strand break sites to the chromosome axis in early meiotic recombination (2011). Panizza et al., Cell

Javier Martinez

Connecting RNA processing to metabolism, cellular homeostasis and disease

The Question

We combine curiosity, expertise and a collaborative spirit to study the enzymatic machinery for non-canonical RNA splicing at the biochemical, structural and physiological level. We uncovered the oxidoreductase PYROXD1, a key regulator of the tRNA ligase complex, with a central role in cellular iron metabolism. RNA biology and iron metabolism "merge" in dissecting the ribosomopathy Diamond–Blackfan anemia (DBA) with a new, biochemistry-based approach.

The Approach

We use biochemistry, molecular biology, and genetics to identify and characterize key mammalian RNA processing factors. Structural biology is mainly based on collaborations. We also employ proteomics, metabolomics and next generation sequencing provided by the VBC Core Facilities. When appropriate, we venture into patient cells and animal models to dissect diseases caused by defects in RNA processing factors or ribosomal proteins.

Key Publications

Assembly defects of human tRNA splicing endonuclease contribute to impaired pre-tRNA processing in pontocerebellar hypoplasia (2021). Sekulovski et al., Nature Communications

The oxidoreductase PYROXD1 uses NAD(P) + as an antioxidant to sustain tRNA ligase activity in pre-tRNA splicing and unfolded protein response (2021). Asanovic et al., Molecular Cell

ANGEL2 is a member of the CCR4 family of deadenylases with 2',3'-cyclic phosphatase activity (2020). Pinto et al., Science

Joao Matos

Mechanisms of genome stability and haploidization

The Question

How do cells rewire DNA repair according to the specialized requirements of mitotic proliferation and meiosis — i.e., genome stability and genetic diversity? In a newer research line in the group, we are also trying to understand how meiotic cells "pack" in gametes all of the components that are necessary to restart life, while also performing the quality control that is required for gamete rejuvenation.

The Approach

Our group uses a combination of methodologies (cell biology, biochemistry and structural biology) and model systems (budding yeast, mouse and human tissue culture) to obtain mechanistic insight into how cells modulate the function of DNA repair enzymes according to cellular context.

Key Publications

Meiotic nuclear pore complex remodeling provides key insights into nuclear basket organization (2023). King et al., Journal of Cell Biology

The CDK1-TOPBP1-PLK1 axis regulates the Bloom's syndrome helicase BLM to suppress crossover recombination in somatic cells (2022). Pogliano et al., Science Advances

Regulation of the MLH1-MLH3 endonuclease in meiosis (2020). Cannavo et al., Nature

Isabella Moll

Ribosome heterogeneity in bacteria

The Question

Traditionally, the ribosome is viewed as a highly conserved machinery with an invariable RNA and protein complement. We aim to challenge this assumption and to decipher mechanisms in bacteria that modulate the translational program by ribosome heterogeneity. In particular, we focus on modifications of ribosomal RNAs and proteins that alter ribosome specificity in response to environmental stress.

The Approach

We study ribosome heterogeneity and reprogramming of protein synthesis in vivo and in vitro employing a multifaceted approach combining state-of-the-art methods of molecular biology and bacterial physiology using the model organism *E. coli*. We complement our studies with structural analyses to gain detailed insights into the molecular basis of ribosome heterogeneity and specificity.

Key Publications

Autoregulation of mazEF expression underlies growth heterogeneity in bacterial populations (2018). Nikolic, et al., Nucleic Acids Research

The RNA ligase RtcB reverses MazF-induced ribosome heterogeneity in *Escherichia coli* (2017). Temmel et al., Nucleic Acids Research

The MazF-regulon: a toolbox for the post-transcriptional stress response in *E. coli* (2016). Sauert et al., Nucleic Acids Research

Peter Schlögelhofer

Molecular mechanisms of meiotic recombination

The Question

Sexual reproduction, and at its core meiosis, is one of the drivers of evolution: Genetic information is mutually exchanged between maternal and paternal chromosomes, leading to novel combinations of genetic traits in the following generation. How is this actually achieved? Which proteins mediate DNA double-strand break (DSB) formation, DSB processing and DNA repair to ensure meiotic recombination? What are the underlying molecular mechanisms?

The Approach

We study meiosis in the plant *Arabidopsis thaliana* by employing biochemical assays with purified proteins (including single-molecule approaches) and hypo- and hyper-morphic mutants to investigate the spatial and temporal distribution of key meiotic proteins by regular und super-resolution microscopy. We also adapted various approaches, including next-generation sequencing, to determine genome-wide genetic recombination rates.

Key Publications

ATM controls meiotic DNA double-strand break formation and recombination and affects synaptonemal complex organization in plants (2021). Kurzbauer et al., The Plant Cell

Conservation and divergence of meiotic DNA double strand break forming mechanisms in *Arabidopsis thaliana* (2021). Vrielynck et al., Nucleic Acids Research

Meiotic DNA Repair in the Nucleolus Employs a Nonhomologous End-Joining Mechanism (2019). Sims et al., The Plant Cell

Dea Slade

DNA damage response and transcription regulation

The Question

Posttranslational protein modifications (PTMs) such as phosphorylation, acetylation and poly(ADP-ribosyl)ation regulate protein interactions. Our aim is to understand how protein interactions and PTMs fine-tune the dynamics of DNA damage response and transcription. Revealing the function and regulation of DNA repair and transcription factors will help to understand how their deficiency or misregulation leads to a broad range of diseases.

The Approach

We apply an integrative approach including biochemistry, molecular cell biology, structural biology or stem cell biology.

Key Publications

The SPOC domain is a phosphoserine binding module that bridges transcription machinery with co- and post-transcriptional regulators (2023). Appel et al., Nature Communications

PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC (2021). Appel et al., Nature Communications

Infection and Immunity

Malfunctions in our defense systems account for more than 85% of all human deaths. Max Perutz Labs scientists dissect the molecular mechanisms underlying the regulation of immune tolerance, signaling pathways in sterile and pathogenic inflammation, including cancer, as well as the principal mechanisms of immune surveillance in healthy, autoimmune and infectious disease settings.

Thomas Decker

Interferons: signals and immunobiology

The Question

The innate immune system uses a group of polypeptide mediators (or cytokines), the interferons (IFNs), to produce cell-autonomous immunity. Our interest is to understand how signals from IFN receptors control expression of IFN-stimulated genes. We further seek to understand how transcriptional cooperativity manages and coordinates the complexity of intracellular signals produced by immunological challenges.

The Approach

We use biochemical and proteomic tools to study JAK-STAT pathway signaling downstream of IFN receptors in mouse macrophages. Protein interactors of the JAK-STAT pathway are identified by in vivo affinity labeling. Changes of promoter occupancy, chromatin structure and gene expression are examined by NGS-based technologies. Mouse knockouts and gene editing technologies are used for genetic hypothesis testing.

Key Publications

A molecular switch from STAT2-IRF9 to ISGF3 underlies interferon-induced gene transcription (2019). Platanitis et al., Nature Communications

Marco Hein

Systems biology and viruses

The Question

What happens to a cell when it gets infected with a virus? Viruses remodel host cells into virus factories, repurposing cellular pathways while evading the host's immune system. Studying virus–host systems offers us a unique perspective to understanding the fundamental principles of life at the molecular level. It helps in the development of drugs to combat viral replication, as well as the prevention of an overactive immune response.

The Approach

We design systems-level experiments that yield systems-level insights in two important areas of virus–host biology: 1) We use CRISPR-based genetic perturbations combined with a single-cell transcriptomics readout to functionally connect host pathways with the stages of the viral life cycle where they play a role. 2) We develop proteomics methods to map the host cell's subcellular architecture and its dynamics upon infection.

Key Publications

Systematic functional interrogation of SARS-CoV-2 host factors using Perturb-seq (2023). Sunshine et al., Nature Communications

Functional single-cell genomics of human cytomegalovirus infection (2021). Hein & Weissman, Nature Biotechnology

A human interactome in three quantitative dimensions organized by stoichiometries and abundances (2015). Hein et al., Cell

Pavel Kovarik

Signaling and gene expression in inflammation

The Question

Defense against infectious agents requires an efficient inflammatory response and timely re-establishment of immune homeostasis once the hostile challenge has been eliminated. Our research aims to understand basic mechanisms defining the duration and amplitude of immune responses, focusing on transcription, mRNA decay and signaling.

The Approach

We employ genome-wide approaches, biochemistry, cell biology, animal models, and bioinformatics to reveal molecular mechanisms of how: 1) mRNA decay controls the fidelity of the inflammatory responses; 2) the Mediator kinase determines the quantity of inflammatory transcription; and 3) cytokines orchestrate host resistance against infection and host tolerance.

Key Publications

Nonredundancy of IL-1α and IL-1β is defined by distinct regulation of tissues orchestrating resistance versus tolerance to infection (2022). Eislmayer et al., Science Advances

Transcriptional Responses to IFN-gamma Require Mediator Kinase-Dependent Pause Release and Mechanistically Distinct CDK8 and CDK19 Functions (2019). Steinparzer et al., Molecular Cell

The RNA-binding protein tristetraprolin schedules apoptosis of pathogen-engaged neutrophils during bacterial infection (2017). Ebner et al., Journal of Clinical Investigation

Karl Kuchler

Host–pathogen interactions and mechanisms of drug resistance and fungal pathogenesis

The Question

We aim to decipher the dynamics of fungal pathogen – host interactions, and the molecular basis of virulence. We identify mechanisms of innate/adaptive antifungal immune surveillance, including mechanisms selected HDACs/HATs employ to control fungal virulence and antifungal inflammation. Finally, a main goal is reaching a detailed mechanistic understanding of human ABCG family efflux transporters and their roles in anticancer multidrug resistance.

The Approach

We employ systems biology approaches by integrating various omics technologies (NGS, proteomics, metabolomics) to identify inherent and emerging properties of biological systems in the context of host–pathogen interactions and immune surveillance. Further, we use structural biology approaches such as docking, homology modeling and mutagenesis to study the dynamics of drug efflux transporters during transport cycles.

Key Publications

Type I Interferon Response Dysregulates Host Iron Homeostasis and Enhances *Candida glabrata* Infection (2020). Riedelberger et al., Cell Host & Microbe

The ABCG2 multidrug transporter is a pump gated by a valve and an extracellular lid (2019). Khunweeraphong et al., Nature Communications

Inhibition of CBLB protects from lethal *Candida albicans* sepsis (2016). Wirnsberger et al., Nature Medicine

Gijs Versteeg

Cellular control mechanisms of protein degradation

The Question

Many principles of how ubiquitination is achieved in the crowded intracellular space remain unknown. The main questions we address are: 1) How are immune- and cancer-associated proteins targeted to the proteasome? 2) Which other cellular factors control their degradation? 3) Are these processes deregulated in cancer and immune disease? 4) How do they mechanistically determine cellular protein fate decisions?

The Approach

Genome-wide genetic screening approaches are used to identify novel regulators of proteasomal degradation, with a strong focus on the degradation of immune- and disease-associated proteins. Following identification of key players in protein stability, we aim to determine the molecular mechanisms by which these regulators control degradation of their targets using cell-biology approaches and biochemical in vitro reconstitution.

Key Publications

SPOP targets the immune transcription factor IRF1 for proteasomal degradation (2023). Schwartz et al., eLife

HUWE1 controls tristetraprolin proteasomal degradation by regulating its phosphorylation (2023). Scinicariello et al., eLife

Human tripartite motif protein 52 is required for cell context-dependent proliferation (2018). Benke et al., Oncotarget

Structural and Computational Biology

Biological processes are driven by the coordinated interaction of molecules within cells and tissues. The Max Perutz Labs study how structure is related to function, the dynamics and energetics of the macromolecules that are at the heart of these processes, and the networks in which they operate. We aim to elucidate the mechanisms that shape our normal physiology and rationalize the role of aberrant macromolecules in disease.

Kristina Djinovic-Carugo

Structural biology of the cytoskeleton

The Question

Sarcomeres are the smallest contractile units of striated skeletal and heart muscles. The Z-disc is the attachment region for adjacent sarcomeres and plays a pivotal role not only in sustaining muscle architecture, but also in signaling, mechanosensing and mechanotransduction, protein turnover and autophagy. We are interested in the molecular mechanisms underlying the architecture and assembly of the Z-disc.

The Approach

In order to dissect the Z-disc structure and assembly at molecular level we are using a combination of biochemical, molecular biophysics and complementary structural biology methods on reconstituted complexes and their individual components. These structural and functional data are validated in vitro and in cellula. Finally, we combine diverse experimental data in integrative modeling to generate structural models of mini Z-disc assemblies.

Key Publications

Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with α-actinin (2021). Sponga et al., Science Advances

Molecular basis of F-actin regulation and sarcomere assembly via myotilin (2021). Kostan et al., PLOS Biology

Gang Dong

Structural biology of ciliogenesis and membrane trafficking

The Question

Our research focuses on three main topics: ciliogenesis, parasitology and membrane trafficking. Cilia are conserved organelles present in almost every organ of the human body, and their dysfunction causes a plethora of disorders (ciliopathies). We also work on proteins and protein complexes from the human parasites *T. brucei, T. gondii* and *Plasmodium*. Moreover, we study vesicle targeting and membrane fusion in membrane trafficking.

The Approach

The approaches we use include molecular biology, biochemistry, biophysics, structural biology, etc. We employ X-ray, NMR and cryo-EM to determine 3D structures of our target biological macromolecules. We also routinely use homology modeling, SAXS, SLS/DLS, CD, ITC, etc. in our studies. Our structural studies are often coupled with site-directed mutagenesis and in vivo assays to validate our mechanistic hypotheses.

Key Publications

Double NPY motifs at the N-terminus of Sso2 synergistically bind Sec3 to promote membrane fusion (2022). Peer et al., eLife

Structural and functional studies of the first tripartite protein complex at the *Trypanosoma brucei* flagellar pocket collar (2021). Isch et al., PLOS Pathogens

Sec3 promotes the initial binary t-SNARE complex assembly and fusion (2017). Yue et al., Nature Communications

Sebastian Falk

Biogenesis and action of small RNAs

The Question

Small RNAs function together with Argonaute proteins in RNA interference (RNAi) pathways to regulate gene expression. sRNA biogenesis pathways determine the identity and quantity of sRNAs loaded into Argonautes. Thus, sRNA biogenesis pathways dictate which genes are silenced by RNAi. Therefore, we want to understand how sRNAs are produced (biogenesis), and how sRNAs induce gene silencing in the nucleus through the nuclear RNAi pathway (action).

The Approach

We are using bottom-up and top-down approaches to build the protein complexes, allowing us to reconstitute the biological process with defined components in the test tube. Moreover, we employ an integrated structural biology approach, with structural biological techniques forming the core (X-ray crystallography and single-particle electron microscopy), complemented by biochemical and biophysical methods.

Key Publications

piRNA processing by a trimeric Schlafen-domain nuclease (2023). Podvalnaya et al., Nature

Structural basis of PETISCO complex assembly during piRNA biogenesis in *C. elegans* (2021). Perez-Borrajero. et al., Genes & Development

A ribonuclease III involved in virulence of Mucorales fungi has evolved to cut exclusively single-stranded RNA (2021). Cánovas-Márquez et al., Nucleic Acid Research

Joachim Hermisson

Mathematics and biosciences

The Question

The research theme at the mathematics and biosciences group is the mathematical biology of evolution. Our aim is to design mathematical methods and models that account for the biological complexity on all levels of biological organization: molecular, organismal and ecological. Recent projects range from the evolution of speciation to the study of polygenic adaptation and so-called footprints of selection in DNA sequence variation.

The Approach

Our work is concerned with the construction of mathematical models for eco-evolutionary processes. Analytical methods combine deterministic modeling approaches based on differential equations and probabilistic approaches. We use large-scale computer simulations to extend our results beyond analytically tractable cases. Finally, we develop statistical tools to test our model predictions with biological data.

Key Publications

Polygenic adaptation: a unifying framework to understand positive selection (2020). Barghi et al., Nature Reviews Genetics

VolcanoFinder: genomic scans for adaptive introgression (2020). Setter et al., PLOS Genetics

Polygenic adaptation: From sweeps to subtle frequency shifts (2019). Höllinger et al., PLOS Genetics

Thomas Juffmann

Quantum microscopy and biophysics

The Question
In any micrograph, the number of detected probe particles is fundamentally limited, either due to finite acquisition times or probe-induced sample damage. How can we optimize the sensitivity of a microscope and maximize the information that can be extracted from each detected probe particle?

The Approach
We approach imaging from an information–theoretical perspective and quantify the achievable estimation precision regarding certain parameters of interest. We then design and build microscopes that overcome state-of-the-art sensitivities, and approach the limits we found theoretically. We look for solutions in optical microscopy as well as in electron microscopy.

Key Publications
Transverse Electron-Beam Shaping with Light (2022). Mihaila et. al., Physical Review X

Electro-optic imaging enables efficient wide-field fluorescence lifetime microscopy (2019). Bowman et al., Nature Communications

Multi-pass Microscopy (2016). Juffmann et al., Nature Communications

Robert Konrat

Computational biology and biomolecular NMR spectroscopy

The Question
It is now recognized that an increasing number of proteins lack stably folded tertiary structures and that this intrinsic flexibility contributes to their biological functionality. The emerging picture is that proteins have evolved to increase the diversity of their conformational ensembles and that, even in disordered proteins, there is a hidden structure that needs to be addressed by appropriate experimental techniques and theoretical concepts.

The Approach
A hallmark of our research is the integrative application of a novel computational biology concept (meta-structure concept) and information-rich NMR spectroscopy directed toward a better understanding of the underlying mechanisms of important biological problems. We develop approaches that combine biochemistry, bioorganic chemistry and NMR spectroscopy to unravel the microscopic details of functionally important protein plasticity.

Key Publications
High-resolution structural information of membrane-bound α-synuclein provides insight into the MoA of the anti-Parkinson drug UCB0599 (2023). Schwarz et al., Proceedings of the National Academy of Sciences

Long-range structural preformation in yes-associated protein precedes encounter complex formation with TEAD (2022). Feichtinger et al., iScience

A Step toward NRF2-DNA Interaction Inhibitors by Fragment-Based NMR Methods (2021). Brüschweiler et al., ChemMedChem

Thomas Leonard

Molecular mechanisms of signal transduction

The Question
Important cellular processes are often compartmentalized by membranes, which necessitates the flow of information between subcellular compartments. How is this information integrated to drive the appropriate response? We try to understand the basic principles that govern the flow of information in cells. By elucidating the mechanisms by which these signals are transduced and propagated, we can better answer why and how things go wrong in disease.

The Approach
We use biochemical and cell biological assays supported by biophysical and structural techniques to deduce how, where and when signals are transduced. Our work is underpinned by quantitative biochemistry of precisely defined macromolecules. The insights we derive have the potential to rationalize disease pathogenesis at the molecular and atomic levels with implications for the development of precise and efficacious therapeutics.

Key Publications
PKD autoinhibition in *trans* regulates activation loop autophosphorylation in *cis* (2023). Reinhardt et al., Proceedings of the National Academy of Sciences

Activation of the essential kinase PDK1 by phosphoinositide-driven trans-autophosphorylation (2022). Levina et al., Nature Communications

Structure of autoinhibited Akt1 reveals mechanism of PIP_3-mediated activation (2021). Truebestein et al., Proceedings of the National Academy of Sciences

Jörg Menche

Quantitative modeling of biological networks

The Question

Biological processes rely on the careful orchestration of a multitude of components, from molecules to cells, organs and entire organisms. Networks provide a powerful framework for describing and understanding these complex systems. Our interdisciplinary group uses tools and concepts from network theory to better understand how biological networks are organized and how they are perturbed in diseases.

The Approach

Our backgrounds include biology, computer science, physics and mathematics, but also architecture and arts. This diversity is also reflected in the wide range of methodologies that we develop and apply. With network expertise as common denominator, we also routinely use bioinformatics methods, machine learning techniques, advanced mathematical concepts and Virtual Reality technology for exploring big biological datasets.

Key Publications

Network analysis reveals rare disease signatures across multiple levels of biological organization (2021). Buphamalai et al., Nature Communications

The VRNetzer platform enables interactive network analysis in Virtual Reality (2021). Pirch et al., Nature Communications

Mapping the perturbome network of cellular perturbations (2019). Caldera et al., Nature Communications

Irma Querques

Genome plasticity and engineering

The Question

Genomes are subjected to changes in their structure and content. Much of this plasticity is attributed to transposons. By driving variation and transfer of genes, transposons shape the biology and the evolution of organisms. How do they move? How can we leverage them to artificially modify genomes? We study the molecular mechanisms of transposon mobilization and use these insights to develop genome engineering tools for research and medicine.

The Approach

To study the mechanisms, functions and applications of transposons, we combine structural biology methods with biotechnological approaches. We analyze the mechanisms of DNA mobilization using cryo-electron microscopy and biochemistry. Our lab explores the use of transposons as genetic tools using cell-based functional assays and genome engineering. We extend these studies to therapeutically relevant cells to develop transposon-based applications.

Key Publications

Structural basis for the assembly of the type V CRISPR-associated transposon complex (2022). Schmitz et al., Cell

Target site selection and remodelling by type V CRISPR-transposon systems (2021). Querques et al., Nature

A highly soluble Sleeping Beauty transposase improves control of gene insertion (2019). Querques et al., Nature Biotechnology

Jonas Ries

Super-resolution microscopy for structural cell biology

The Question

Life is based on the action and interaction of biomolecules. A prime example for a complex and dynamic protein machinery is clathrin-mediated endocytosis, an essential cellular process for the uptake of molecules from the environment. But how can we measure the structural organization and dynamic functional changes of such cellular protein assemblies?

The Approach

Our research vision is to develop optical super-resolution microscopy technologies that will allow us to visualize the structure and the dynamics of molecular machines in living cells on the nanoscale. We are developing new approaches for single-molecule localization microscopy to measure the precise 3D locations of proteins at high throughput and for MINFLUX to probe conformational changes of protein machines in the living cells.

Key Publications

Direct observation of motor protein stepping in living cells using MINFLUX (2023). Deguchi et al., Science

Maximum-likelihood model fitting for quantitative analysis of SMLM data (2023). Wu et al., Nature Methods

Systematic nanoscale analysis of endocytosis links efficient vesicle formation to patterned actin nucleation (2018). Mund et al., Cell

Kelly Swarts

Tree-ring genomics

The Question

Conifers have been successfully adapting to changing climates over the past 250 million years, resulting in high genetic diversity and broad environmental ranges. However, long generation times combined with climate change globally challenges trees' ability to adapt. We seek to understand the biological basis of climate adaptation in conifers and predict individuals that can make populations more resilient to the changing climate.

The Approach

We use quantitative, computational and population genetic approaches to understand climate adaptation in Norway Spruce, an economically and ecologically critical tree species with cultivated and natural stands across Europe. Our conifer research is informed by crop genomic approaches, and we employ deep learning approaches for fast and replicable phenotyping.

Key Publications

Dysregulation of expression correlates with rare-allele burden and fitness loss in maize (2018). Kremling et al., Nature

Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America (2017). Swarts et al., Science

Arndt von Haeseler

Integrative bioinformatics

The Question

What are the evolutionary forces that have shaped the genomes of contemporary organisms, and how can we infer the relevant parameters from multiple sequence alignments? Can we develop mathematical, statistical and computational tools that help to analyze big data as generated by high-throughput technologies in molecular biology?

The Approach

Mathematical models and bioinformatics tools are the cornerstones to work on both questions. We develop such models and turn them into software for a wide user community. To understand the evolutionary forces, we are developing complex models of sequence evolution that, in conjunction with tree reconstruction algorithms, provide a comprehensive picture of the relationship of organisms and the changes that occur in a gene over time. Our approaches address the special needs of high-throughput technologies. We also develop "stand-alone tools" that can infer all relevant parameters from the input data.

Key Publications

SVhound: Detection of regions that harbor yet undetected structural variation (2023). Paulin et al., BMC Bioinformatics

Gruffi: an algorithm for computational removal of stressed cells from brain organoid transcriptomic datasets (2022). Vertesy et al., The EMBO Journal

Distinguishing Felsenstein Zone From Farris Zone Using Neural Networks (2020). Leuchtenberger et al., Molecular Biology and Evolution

Bojan Zagrovic

Molecular biophysics

The Question

We aim to decipher the fundamental rules behind nucleic-acid/protein interactions, understand the impact of these interactions on shaping life's evolutionary history and study their role in present-day systems. Our central hypothesis is that direct nucleic-acid/protein interactions have contributed to the establishment of the genetic code and that, in turn, the code may be a Rosetta stone for understanding present-day RNA-protein interactions.

The Approach

By combining atomistic descriptions of individual biomolecules obtained using advanced techniques of computational biophysics and structural bioinformatics with the richness of modern-day proteomic and genomic datasets, we strive to discover new fundamental principles behind the organization of biological matter and explain essential biological phenomena from a quantitative, physicochemical perspective.

Key Publications

Coding from Binding? Molecular Interactions at the Heart of Translation (2023). Zagrovic et al., Annual Review of Biophysics

Widespread autogenous mRNA–protein interactions detected by CLIP-seq (2022). Kapral et al., Nucleic Acids Research

Frameshifting preserves key physicochemical properties of proteins (2020). Bartonek et al., Proceedings of the National Academy of Sciences

March 2020 – September 2023

Grants, Awards and Promotions

ERC Grants

Irma Querques	Starting Grant	2023
Thomas Juffmann	Proof of Concept Grant	2022
Kelly Swarts	Starting Grant	2022
Joao Matos	Consolidator Grant	2021

START Programme of the Austrian Science Fund (FWF)

Stephanie Ellis	START grant	2023

Network Grants

Kristina Djinovic	The Human Frontier Science Program	2023
Jörg Menche	Horizon Europe Grant (Repo4EU)	2022
Javier Martinez	doc.funds “RNA@core”	2022
Karl Kuchler, Markus Hartl	SFB “HIT”: “HDACs as regulators of T cell-mediated immunity in health and disease” — extended	2022
Verena Jantsch	SFB “Meiosis”	2022
Bojan Zagrovic	doc.funds “Liquid-liquid phase separation in biology”	2021
Manuela Baccarini	SMICH Doctoral Program — extended	2020
Sascha Martens	Aligning Science Across Parkinson’s (ASAP) Initiative Grant	2020
Bojan Zagrovic	Volkswagen Foundation	2020
Florian Raible	University of Vienna — Research platform	2020

Individual Grants

Shotaro Otsuka	FWF	2023
Thomas Leonard	FWF	2023
Gijs Versteeg	FWF	2023
Martin Leeb	FWF	2022
Manuela Baccarini	FWF	2022
Pavel Kovarik	FWF	2022
Sebastian Falk	FWF	2022
Roland Foisner	FWF	2022
Thomas Leonard	FWF	2022
Gijs Versteeg	FWF	2022
Sebastian Falk	FWF (International programs)	2022
Elif Karagöz	WWTF	2022
Alexander Dammermann	FWF	2021
Kristina Djinovic	FWF (International programs)	2021
Sascha Martens	WWTF	2021
Javier Martinez	FWF	2021
Sascha Martens	FWF	2021
Martin Leeb	FWF	2021
Boris Görke	FWF	2021
Gang Dong	FWF	2021
Robert Konrat	FWF	2021
Karl Kuchler	FWF	2021
Manuela Baccarini	FWF	2021

Karl Kuchler	FWF	2020
Roland Foisner	FWF (International programs)	2020
Gang Dong	FWF (International programs)	2020
Udo Bläsi	FWF	2020
Christa Buecker	FWF	2020
Alwin Köhler	WWTF COVID-19 Rapid Response Call	2020
Alexander Dammermann	FFG	2020
Bojan Zagrovic	Ministry of Education, Science and Research	2020
Joao Matos	Swiss National Science Foundation (SNSF)	2020
Sascha Martens	Regents of the Universtity of California	2020

Contract Research Projects

Kristina Djinovic	Biomin	2022
Jörg Menche	F. Hoffmann-La Roche Ltd.	2022
Robert Konrat	Cebina GmbH	2021
Thomas Decker	Boehringer Ingelheim Contract Research	2020

Institutional Grants

Max Perutz Labs (together with UBB)	DataLife (Ministry of Education, Science and Research)	2023

Promotions

Dea Slade	Associate Professor, Medical University	2023
Manuela Baccarini	Vice Rector for Research and International Affairs, University of Vienna	2022
Christa Buecker	Associate Professor, University of Vienna	2022
Peter Schlögelhofer	Full Professor, University of Vienna	2022
Thomas Juffmann	Associate Professor, University of Vienna	2021
Karl Kuchler	Professor, Medical University	2021
Thomas Leonard	Professor, Medical University	2021

Honors

Alwin Köhler	Moore Distinguished Scholar, Caltech	2023

Awards

Climate@MaxPerutzLabs Initiative	Austrian Sustainability Award	2022
Stephanie Ellis	Vallee Scholar Award	2022
Irma Querques	Branco Weiss Fellowship	2022
Sebastian Falk	EMBO Young Investigator	2022
Kristin Tessmar-Raible	Ignaz Lieben Award	2021

Memberships

Alwin Köhler	Corresponding member Austrian Academy of Sciences (ÖAW)	2022
Alwin Köhler	EMBO member	2021
Kristin Tessmar-Raible	EMBO member	2021
Sascha Martens	EMBO member	2020

New Group Leaders

Hiring new talent brings fresh perspectives to the Max Perutz Labs. We recruit tenure-track junior group leaders and full professors. Since 2020, we have welcomed nine scientists from diverse backgrounds to the Perutz community, all dedicated to strengthening our scientific mission.

Stefan L. Ameres was born in Germany. He obtained his PhD in biochemistry from the University of Vienna in 2006. After postdoctoral training with Phillip Zamore at the University of Massachusetts Medical School (US) from 2007 to 2011, he joined the Institute of Molecular Biotechnology (Vienna, Austria) as group leader in 2012. In 2020 he was appointed professor of RNA biology at the Max Perutz Labs. Having received an ERC Starting Grant and FWF START Grant in 2013, Ameres was awarded an ERC Consolidator Grant in 2019.

Stefan L. Ameres

Mechanism and biology of RNA silencing

Gene regulation is a crucial process that governs genome function, and it pervades most aspects of biology, from organismal development to cellular differentiation and physiological responses to external stimuli and pathogens. At the post-transcriptional level, controlling the fate and function of RNA is a hallmark of gene regulation with significant biological, technological and biomedical implications. Ameres and his research group are investigating the molecular-level regulation of transcriptome quality and quantity in both flies and mammals.

The Ameres lab aims to shed light on the role of RNA modifications in the regulation of RNA fate and function; identify possible causes for abnormal gene expression associated with human diseases; and develop technologies to decipher the molecular signatures of RNA decay and its functional components and organization in pathways. The team is employing quantitative biochemical methods, cell culture experiments and in vivo genetics, and combining time-resolved transcriptomics and functional genetics with bioinformatics to unravel the timescales and functional organization of posttranscriptional gene regulation at the molecular and genomic scale.

What do you turn to for inspiration in your research?

"When I'm trying to write grants and papers, my guitar is basically at arm's length on the wall of my office, and from time to time that's what I reach for to get out of this complex mindset one has when dealing with science, to just immerse myself in a different state of mind. It's very inspiring to me."

Why did you choose to join the Max Perutz Labs?

"The Max Perutz Labs provide a highly supportive environment with an excellent community spirit. The research landscape covers a broad array of topics, allowing for ample possibilities to engage in cross-fertilizing discussions to expand upon and connect to our own research interests in my lab, which I find very stimulating."

Born in Canada, Stephanie Ellis obtained her PhD from the University of British Columbia (Canada) where she studied cell adhesion in the fly embryo with Guy Tanentzapf. She then completed her postdoctoral training with Elaine Fuchs at Rockefeller University (US). Ellis established her research group at the Max Perutz Labs in 2022. She has received the 2022 Vallee Scholar Award from the Vallee Foundation and a START Grant from the Austrian Science Fund in 2023.

Stephanie Ellis

Cell competition and tissue fitness in development and disease

Mechanisms of quality control that act to maximize tissue health, or "fitness," on the cellular and tissue level have not been well defined. Ellis and her research group are studying quality control during tissue morphogenesis and maintenance through the lens of cell competition. Cell competition is a conserved, yet poorly understood, phenomenon of growth control that is likely to have serious implications for heterogeneous cell–cell interactions within tissues and in stem cells during development and homeostasis and in disease. Ellis explores the molecular and cellular mechanisms that underlie competitive behaviors, testing the hypothesis that cell competition plays a central, protective role in shaping the tissue-level response to stress.

The team is employing a multidisciplinary toolkit — drawing from genetics, cell biology and quantitative biology — to ask mechanistic questions about epithelial tissue organization and growth control across scales. They use mouse skin as a model system because it has a well-defined developmental program, is genetically tractable, and is compatible with immunofluorescence and live imaging — favored approaches to studying cell behavior and cell–cell interactions. The Ellis lab previously established the skin as a physiologically relevant system in which to study mammalian cell competition. The research group aims to use their tools to uncover basic principles of growth control in complex epithelial tissues as they grow, differentiate, reach their final size and contend with threats to their homeostasis.

Why did you choose to join the Max Perutz Labs?

"Vienna has a dense community of internationally renowned researchers and this energy about it that I think is pretty unique in the whole world. This spirit of interaction and cross talk really drew me to the Perutz."

What do you hope to achieve at the Perutz?

"The research question that my lab is focusing on borrows ideas from Darwinian biology, thinking of our tissues as communities of cells that have to coordinate in a survival-of-the-fittest way to build a healthy tissue development and then to keep that tissue healthy as we age. We are trying to develop tools and experiments to dissect how these cellular interactions might be mediated. It would be a major contribution to broaden our fundamental understanding of how cells sense the health of their neighbors and collectively decide who survives and who is pushed out. I also want to build a strong team and to inspire a new generation of researchers to be excited about science and discovery."

Erinc Hallacli, born in Turkey, received an MS in molecular and cellular biology from Heidelberg University (Germany) and a PhD at the European Molecular Biology Labs (EMBL) in Heidelberg under the mentorship of Asifa Akhtar. He was a postdoc at the Whitehead Institute and Massachusetts Institute of Technology (MIT) in the lab of Susan Lindquist, and later a postdoc and instructor at Brigham and Women's Hospital and Harvard Medical School in the lab of Vikram Khurana (Boston, US). He is assistant professor of neurology at Brigham and Women's Hospital and Harvard Medical School and will join the Max Perutz Labs in April 2024. Erinc was recently awarded an NIH R01 Grant as a co-investigator.

Erinc Hallacli

Deciphering molecular phenotypes in neurodegenerative diseases

The global population is aging, escalating the impact of neurodegenerative diseases like Parkinson's disease (PD), the second-most prevalent after Alzheimer's. Although 25 years have passed since the discovery of α-synuclein (αSyn) as a key component of PD Lewy bodies — abnormal aggregations of proteins inside nerve cells — its full role remains elusive. While αSyn is known to disrupt lipid homeostasis, its predominant presence in the cytosol, including in non-neuronal cells, suggests other functions.

Research by Hallacli and colleagues indicates αSyn's role in RNA condensates, specifically processing bodies (P-bodies). Using iPSC-derived neuronal models, Hallacli and his team will explore P-bodies' role in healthy and diseased neurons. αSyn's transient membrane interactions, without lipid anchors, hint at a broader interplay between membranes and RNA granules. Yet, current technology can't measure these transient protein–membrane interactions. The team aims to innovate tools to study these interactions and, using CRISPR and drug screens, discern the factors influencing αSyn's membrane localization. This could pave the way for PD treatments balancing RNA and lipid pathways. Finally, to truly grasp αSyn toxicity mechanisms, the researchers will investigate the sequence of molecular events during synuclein accumulation. They hope to develop a "phenotype machine" to observe protein perturbations over time, starting with αSyn models, with potential applications for other proteinopathies.

Why did you choose to join the Max Perutz Labs?

"I chose the Max Perutz Labs due to its supportive scientific community and swift problem-solving. The science, facilities and integration within the Vienna BioCenter infrastructure are top-notch. The Perutz's communal equipment use allows experimentation from day one. The generous startup package and rare tenure-track position stand out. And with a steady influx of global graduate-level talent and Vienna's cultural richness, affordability and excellent transport, the decision was straightforward."

What do you hope to achieve at the Perutz?

"At the Max Perutz Labs, I aim for scientific excellence, focusing on RNA and lipid metabolism in Parkinson's disease. But it takes a village, and collaborating with other Perutz researchers will be key. Furthermore, effective communication of our research will be vital, and I aim to simplify complex ideas and mentor future researchers. I hope to stay informed, curious and embrace new technologies. I believe this is essential for progress and fostering a thriving lab environment."

Erinc Hallacli will start his lab at the Perutz in April 2024.

Marco Hein grew up in Germany, obtaining his PhD with Matthias Mann at the Max Planck Institute of Biochemistry (Germany) in 2014, where he used proteomics to map the human protein interactome. As an EMBO postdoc fellow, he studied virus–host interactions using single-cell functional genomics with Jonathan Weissman at the University of California, San Francisco (US). Following a stint as a Chan Zuckerberg Biohub fellow, he established his lab at the Perutz in 2022.

Marco Hein

Systems biology and viruses

Viruses are intracellular parasites that remodel host cells into virus factories, exploiting cellular metabolism and repurposing signaling pathways. At the same time, viruses must constantly evade the host's immune system. Through the power of evolutionary pressure, viruses have turned into the ideal cell biologists. Studying virus–host systems can shed light on the fundamental principles of the organization of life at the molecular level. Understanding the principles of virus–host interactions will also help in the development of drugs to combat viral replication, as well as the prevention of an overactive immune response.

Using cutting-edge technology, Hein and his research group are studying two complementary aspects of virus–host biology to better understand the processes within an infected cell: The repurposing and/or counteracting of host pathways by the virus, and the physical reorganization of the host cell upon infection. The team is employing CRISPR-based genetic perturbations combined with a single-cell transcriptomics readout to functionally connect host pathways with the stages of the viral life cycle where they play a role. They are also developing proteomics methods to map subcellular architecture and its dynamics upon infection. The Hein lab aims to design systems-level experiments that yield systems-level insights, going beyond what one can see by studying one gene or protein at a time.

What inspires or motivates you?

"In systems biology, the hypothesis is in the approach — you design an experiment to look at, for example, all the proteins in the system, and see how they respond to perturbation. And the hypothesis is that that approach will guide you toward forming your hypothesis about what's going on in a certain process. I'm motivated by understanding those principles of how life is organized at the molecular level that you could not have if you only looked at one protein at a time."

Why did you choose to join the Max Perutz Labs?

"Vienna is a very livable city where they also do great science. There is the critical mass of the science community: The Perutz is part of the Vienna BioCenter, which hosts more than 2,000 scientists, so you have experts in every area across the different institutes. There's a lot of cross talk happening — we have shared seminars that everyone's invited to, there's a joint PhD program, and collaboration is fostered under the Vienna BioCenter umbrella."

Joao Matos was born in Portugal. In 2007 he received his PhD in biology with Wolfgang Zachariae at the Max Planck Institute of Molecular Cell Biology and Genetics (Germany). In 2009 he began postdoctoral work with Stephen West at the London Research Institute (UK). Matos was appointed assistant professor of cellular biochemistry at ETH Zurich (Switzerland) in 2014. He joined the Max Perutz Labs in 2020 as professor of cell and developmental biology. Among other awards, Matos received an ERC Consolidator Grant in 2020.

Joao Matos

Mechanisms of genome stability and haploidization

The life cycle of sexually reproducing eukaryotes depends on two specialized chromosome segregation programs: mitosis and meiosis. While mitosis drives cellular proliferation and the stable propagation of the genome, meiosis promotes genetic diversity and the formation of haploid gametes, which combine at fertilization to restore the diploid state. Remarkably, both genome stability and genetic diversity depend on the cell's ability to repair damaged chromosomes using homologous recombination.

Using a combination of approaches (cell biology, biochemistry and structural biology) and model systems (budding yeast, mouse and human tissue culture), the Matos lab is investigating how cells rewire DNA repair according to the specialized needs of mitotic proliferation and meiosis to promote genetic diversity and haploidization during meiosis; prevent genomic instability — and cancer — during mitotic proliferation; and ensure the efficient disengagement of recombination intermediates prior to chromosome segregation and cell division.

What is it about basic research that appeals to you?

"I particularly enjoy the moments in which we discover something that is very unexpected, which forces us to learn about other fields. I like this transition from initially having the sense of being lost and knowing very little about this new thing that we are exploring, into having the feeling, as time goes on, of discovering how things are connected and how things work."

Why did you choose to join the Max Perutz Labs?

"There were different aspects to my motivation to join the Perutz from abroad. Perhaps the most important were the research focus of the institute and the collaboration on campus. I think it's a really good fit for the type of scientific questions that I'm trying to address. I see a lot of synergies with the surrounding groups, and my colleagues are excellent. Of course, all of that is helped by the fact that Vienna is a fantastic city for families."

Jörg Menche was born in Germany. In 2010, he received his PhD in theoretical physics with Reinhard Lipowsky at the Max Planck Institute of Colloids and Interfaces (Germany), specializing in network theory. He did postdoctoral work at Northeastern University with Albert-László Barabási and the Dana Farber Cancer Institute (US) from 2010 to 2012. He was a postdoctoral fellow at the Central European University (Hungary) from 2013 to 2015. Menche formed a research group in 2015 at the CeMM Research Center for Molecular Medicine (Austria). In 2020 he began a joint professorship at the Max Perutz Labs and the Faculty of Mathematics of the University of Vienna.

Jörg Menche

Quantitative modeling of biological networks

The intricate interplay of molecules, cells, organs and entire organisms is crucial for almost all biological processes. Networks offer a powerful framework for describing and understanding these complex systems. Menche and his research group specialize in applying network theory to biology and medicine, particularly in molecular networks that form the mechanistic basis of all biological processes. The group is investigating how these networks are organized and how they are affected in diseases.

Menche's diverse team comprises biologists, computer scientists, physicists, mathematicians, architects and artists with network expertise, who use bioinformatics methods, machine learning techniques, advanced mathematical concepts and virtual reality technology to explore large biological datasets. They tackle both fundamental and practical problems, ranging from deciphering the cellular arithmetic of perturbations to identifying mutations that cause genetic diseases.

What motivates you as a scientist?

"My team! I work with extraordinary individuals who also are fantastic as a group. Working with this young, bright, enthusiastic, extremely diverse set of people is what gets me out of bed for sure. It's very humbling — and a bit terrifying — to think of all the great mentors I've had and to know that, at some point, I may be one of these people as I grow older, but it's also cool."

Why did you choose to join the Max Perutz Labs?

"The Max Perutz Labs is the perfect environment for pursuing our diverse research interests. Our ambition is to better understand the basic principles that govern how complex biological systems work. At the Perutz, we can work closely with passionate scientists who share this ambition and approach it from many different directions. Their deep expertise on a wide range of topics in molecular biology, together with their enthusiasm for basic research, offer exciting opportunities for collaborative projects that go beyond what each of us could achieve individually."

Pim Huis in ’t Veld was born in the Netherlands. He obtained a master’s degree from the University of Nijmegen (Netherlands) and a PhD working with Jan-Michael Peters at the Research Institute of Molecular Pathology (Austria) in 2015. He then joined Andrea Musacchio at the Max Planck Institute of Molecular Physiology (Germany) as a postdoctoral scientist. In 2023 he was appointed group leader at the Max Perutz Labs.

Pim Huis in ’t Veld

Preventing DNA damage during mitosis

The accurate distribution of copied genomes during cell division is essential for the propagation of life. As sister chromatids segregate in anaphase, pieces of DNA that connect them are stretched and challenge the completion of mitosis. Huis aims to understand how DNA helicases, translocases and topoisomerases work together to recognize and process these DNA bridges to maintain genome stability.

The Huis lab obtains quantitative and molecular insight into this protein machinery through biochemical reconstitution. Systematically mixing and modifying purified components, combined with structural biology, cell biology and single-molecule biophysics, is a powerful way to study a process as intricate as mitotic cell division.

What inspires you?

“It’s really cool to be able to do basic research. I still find it amazing that I get to make a living doing exactly that — zooming into some of the molecular machines that are at work inside our bodies all the time, that we don’t fully understand. To unravel bits and pieces of how that machinery operates is really fascinating, rewarding, humbling.”

Why did you choose to join the Max Perutz Labs?

“The Perutz is a great place to do both chromosome biology research and reconstitution biochemistry. With over 40 research groups, there are enough people to have scientific discussions, get input and ideas, and share infrastructure; this collaborative atmosphere extends through the campus and also makes the Vienna BioCenter very attractive. The Perutz is committed to mechanistic cell biology, and that’s precisely what I want to do — to understand complex biological processes by studying their building blocks and regulators in a quantitative molecular manner. That is a mission I hope to contribute to.”

Born in Italy, Irma Querques studied biotechnology at the University of Bologna (Italy) and received a PhD at the European Molecular Biology Laboratory in Heidelberg (Germany), where she worked on eukaryotic transposons with Orsolya Barabas. She joined the lab of Martin Jinek at the University of Zurich (Switzerland) as a FEBS and EMBO postdoctoral fellow to study CRISPR-guided transposons. She is the recipient of an ERC Starting Grant for her research project "BROADCAST." Querques joined the Max Perutz Labs in 2023.

Irma Querques

Genome plasticity and engineering

Genomes regularly experience alterations in their structure and content. Much of this plasticity can be attributed to transposons, pieces of DNA that autonomously "jump" between and within genomes. By driving variation and interspecies transfer of genetic data, transposons shape the biology and the evolution of organisms. In bacteria, for instance, CRISPR-Cas genome defense systems are functionally and evolutionarily linked to mobile DNA. But how transposons move and interact with their hosts and how they could be used to artificially modify genomes remains elusive.

Querques and her team aim to better understand the mechanisms, functions and applications of transposons, combining structural biology methods with biotechnological approaches. Through their integrative approach, they are analyzing the macromolecular organization and the mechanistic details underlying DNA mobilization using cryo-electron microscopy and X-ray crystallography together with biochemical and biophysical methods. In addition, they are investigating the interplay between transposons and host machineries, such as CRISPR-Cas systems, and the biotechnological potential of these interactions using cell-based functional assays, protein design and genome engineering experiments. Insights from these studies could lead to the development of genome engineering tools for research and medicine.

Why did you choose to pursue basic research?

"When I was finishing high school, I wanted to become a writer of novels, because I could be creative and use my imagination. Then, at the first scientific talk I attended, I met a biotechnologist and realized how much creative ability and imagination also go into science — imagining what is happening in a test tube without being able to see the molecules, for example. When I started reading scientific papers, I understood there's a story to tell, not only about how you get to a scientific idea and research project, but also about how processes work. For me this was a great way to combine two interests. I knew this was exactly what I wanted to do."

Why did you choose to join the Max Perutz Labs?

"The Perutz's mission is not only to understand biological systems at the basic level, but also to translate them into something useful for medicine, for biotechnology. Multidisciplinary research is implicit in this mission, and to do that, you need teams that use different techniques, investigate different aspects, look at things at different scales. This possibility to collectively look at biological systems and their future applications from different perspectives distinguishes the Perutz from other institutions. It is also a diverse and multidisciplinary place where creativity and imagination find space — that's why I was very happy to join the Perutz."

Jonas Ries is from Germany. He studied physics in Bremen and Konstanz, specializing in quantum optics. After completing a PhD in biophysics with Petra Schwille at the TU Dresden (Germany) in 2008 and a postdoctoral fellowship with Vahid Sandoghdar and Helge Ewers at ETH Zurich (Switzerland) in 2012, he joined the EMBL in Heidelberg (Germany) as a group leader. In 2023 he was appointed professor of advanced microscopy and cellular dynamics at the Max Perutz Labs. Ries received an ERC Consolidator Grant in 2017.

Jonas Ries

Super-resolution microscopy for structural cell biology

Clathrin-mediated endocytosis is an essential cellular process for the uptake of molecules from the cell surface to its interior. During endocytosis, more than 50 different proteins in many copies self-assemble into a complex machinery that invaginates the membrane and forms a vesicle. The precise locations of the proteins throughout the process of endocytosis are yet unknown, and the technologies available today are limited in their ability to measure the structural organization and dynamic functional changes of cellular protein assemblies.

To address this, the Ries research group is working to develop optical super-resolution microscopy technologies that will enable them to visualize the structure and the dynamics of molecular machines in living cells on the nanoscale. The interdisciplinary team of physicists, biologists, computer scientists and engineers are developing new approaches for single-molecule localization microscopy (SMLM) to measure the precise 3D locations of proteins at high throughput and new MINFLUX technology to probe conformational changes of protein machines in the living cell with nanometer-spatial and millisecond-temporal resolution. These methods are providing invaluable mechanistic insights into endocytosis and other cellular protein machines.

What made you focus on basic research?

"I was always curious and interested in how the world works, particularly the universe and the quantum world. I started specializing in experimental quantum optics and attempted to do a PhD but broke it off after nine months, because I was too impatient and clumsy for these extremely complex experiments. So I went into biophysics, where, with smart ideas and relatively small projects, you can have a big impact and enable other groups to do their research. I like to develop new tools and technologies. It's amazing to see or discover something that people didn't know about, that we couldn't achieve before, and to add to the general knowledge of humankind. It's really motivating to then to see these technologies used in other research."

Why did you decide to join the Max Perutz Labs?

"I very much like the Max Perutz Labs because of the vibrant scientific environment with excellent research groups from many different disciplines. I hope to find biologists there who can use our technology, to set up collaborations, and find some synergies with the technology-focused groups. I also hope to establish good connections with, for example, optics experts and microscopy developers. Open science also has been very important for directly sharing our developments via software, hardware, data, preprints and so on. These are things I want to work toward and that are possible at the Perutz."

Honorary Faculty

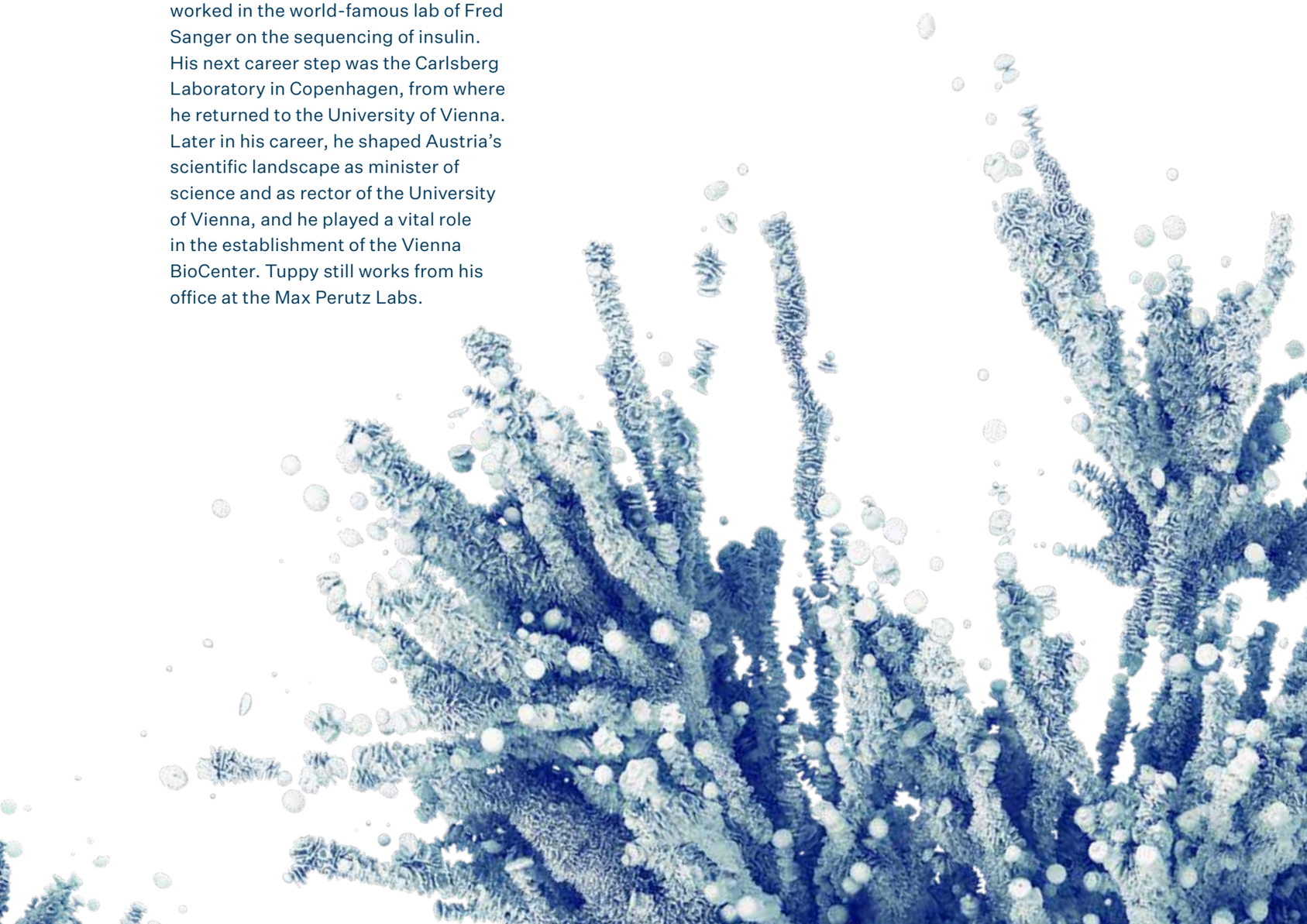
Hans Tuppy

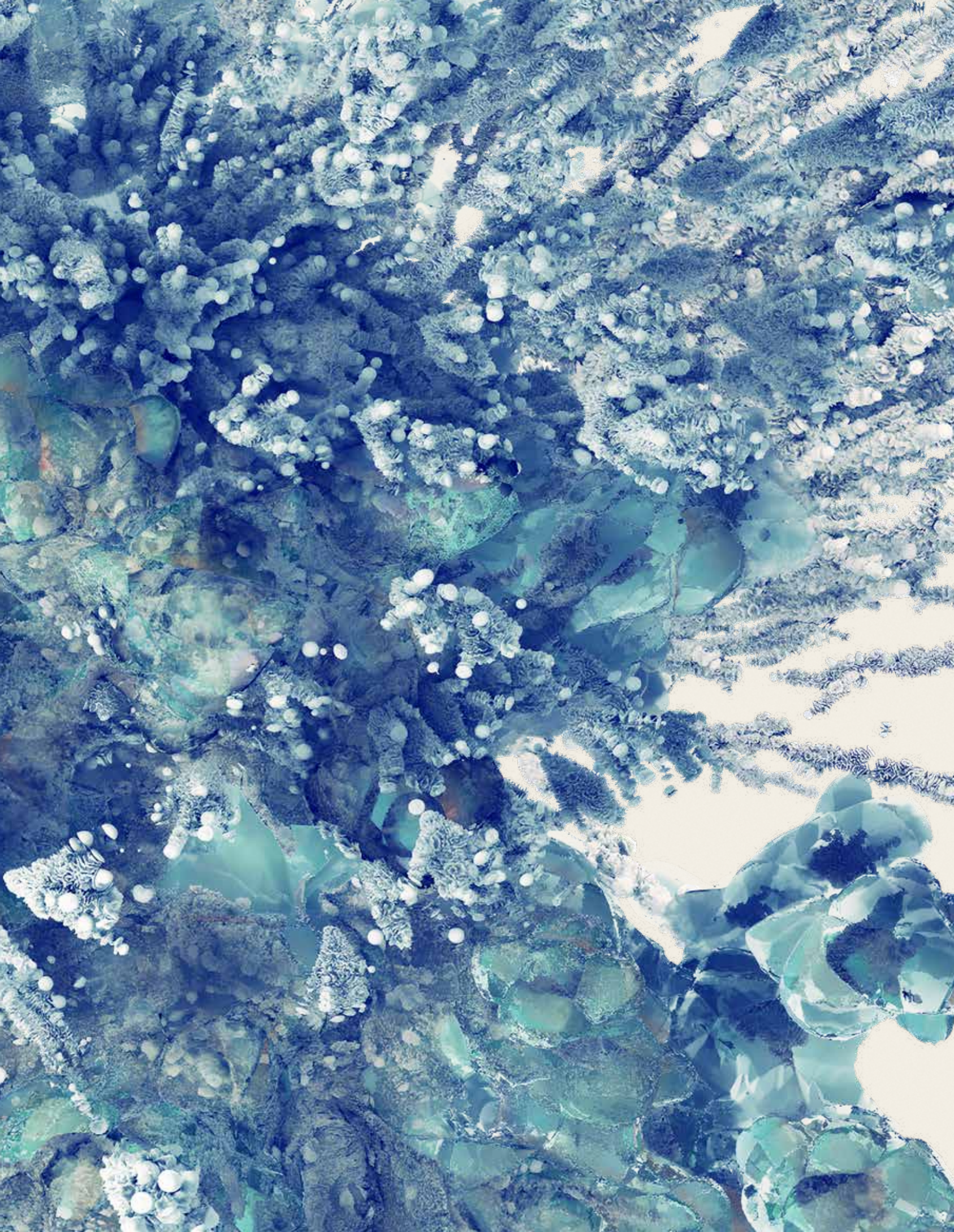
Honorary faculty member

Hans Tuppy, born in 1924, started his studies in chemistry at a time when Europe was struck by World War II. After graduation in 1945, his career brought him to Cambridge where he worked in the world-famous lab of Fred Sanger on the sequencing of insulin. His next career step was the Carlsberg Laboratory in Copenhagen, from where he returned to the University of Vienna. Later in his career, he shaped Austria's scientific landscape as minister of science and as rector of the University of Vienna, and he played a vital role in the establishment of the Vienna BioCenter. Tuppy still works from his office at the Max Perutz Labs.

"Science is my life."

— Hans Tuppy





Research Highlights

The mechanistic exploration of biological systems has yielded numerous discoveries at the Perutz. Here, we highlight a selection, including the reconstruction of an intricate RNA processing reaction, the reconstitution of autophagy initiation, the assembly of reaction chambers for ubiquitin signaling and a novel method to map DNA breaks across chromosomes. Lastly, we honor a discovery that has revolutionized biology and medicine.

RNA 3’ Ends Are Processed by an ANGEL

Javier Martinez lab

"The discovery of ANGEL2 was serendipitous. Having already selected 30 candidate enzymes, I dug deep into our data and decided to add one more protein to the list of enzymes to filter out. After a laborious approach that involved spending countless hours in the cold room using chromotography methods, it was this last protein that turned out to be ANGEL2."

— Paola Pinto

Ribonucleic acid (RNA) is a biomolecule with numerous functions. Among them, RNA can transmit the genetic information contained in deoxyribonucleic acid (DNA) for conversion into proteins, the workhorses of the cell. RNA is composed of a chain of building blocks called nucleotides, which also contain sugar groups. Chemical modifications in the last sugar of an RNA chain are critical for a variety of cellular processes.

For example, RNA molecules are frequently modified with a terminal 2',3'-cyclic phosphate group. This modification influences the stability of RNA molecules and is important for pre-tRNA splicing, the unfolded protein response (UPR) and the ribosome quality control pathway. During investigations into how this modification is generated, we discovered an enzymatic reaction leading to the removal of RNA 2',3'-cyclic phosphate groups in human cells. This reaction was previously known to occur only in bacteria and viruses. The enzyme catalyzing this reaction in human cells had, until this point, remained enigmatic.

Over the last two decades our laboratory has gained vast expertise in filtering out candidate enzymes from a complex "soup" of thousands of proteins by using protein purification techniques. Using this approach, other RNA modifying enzymes were successfully identified. Returning to the cold room once again, we started from a large volume of human cell extracts, which we passed through several columns, each one bearing a different protein-binding property. Throughout the filtering process, we followed the candidate enzyme's ability to remove the cyclic phosphate — this turned out to be ANGEL2.

ANGEL2 was identified as a 2',3' cyclic phosphatase, but in fact it belongs to a family of enzymes known as deadenylases. In a radically different reaction, deadenylases remove a string of adenosines found at the end of messenger RNAs, which encode proteins. Removal of this particular type of nucleotide usually leads to the degradation of mRNAs but might also modulate other processing reactions. By performing structural analyses we revealed the reaction mechanism of ANGEL2 and explained why it removes 2',3' cyclic phosphates rather than eliminating stretches of adenosines.

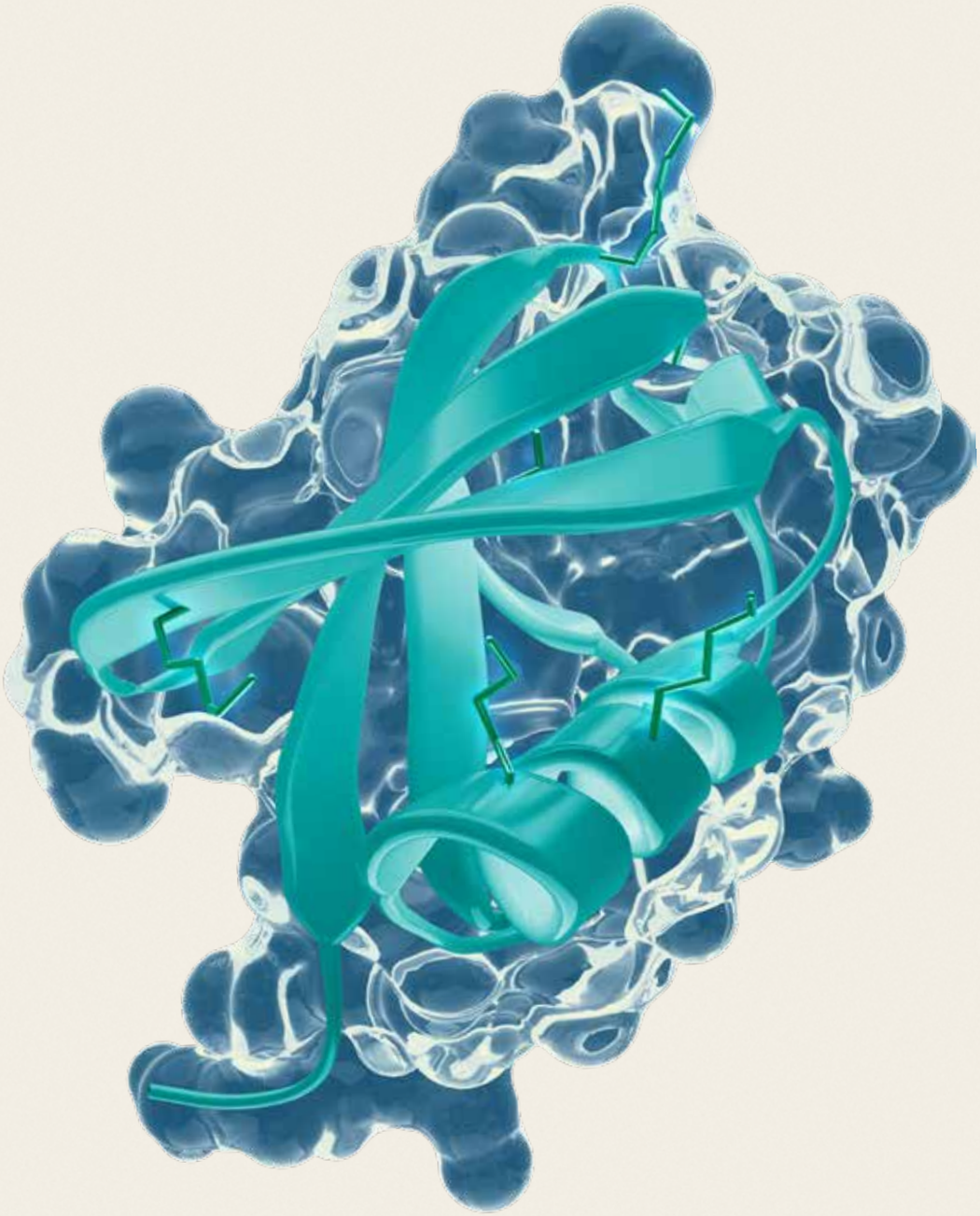
Modifying the levels of ANGEL2 in cells provided important clues about its function. For example, ANGEL2 emerged as being involved in the UPR, a type of biological stress reaction that is triggered when misfolded, nonfunctional proteins accumulate due to cellular disturbances. The UPR seeks to correct the protein-folding defect and to restore the normal function of the cell. Ultimately, we and our collaborators from the University of Zurich (Martin Jinek and Alena Kroupova) were able to show that ANGEL2 regulates the UPR and may play a key role in controlling the response to cellular stress, and it also has exciting implications for the pathology of neurodegenerative and metabolic diseases.

Paola H. Pinto, Alena Kroupova, Alexander Schleiffer, Karl Mechtler, Martin Jinek, Stefan Weitzer & Javier Martinez. ANGEL2 is a member of the CCR4 family of deadenylases with 2',3'-cyclic phosphatase activity. Science, vol. 369, issue 6503, 524-530 (2020).

https://doi.org/10.1126/science.aba9763

Building the Autophagosome

Sascha Martens lab



"As the Atg9 vesicles are incredibly tiny, cellular noise would have prevented us from doing this research in vivo. By experimenting in vitro and looking at individual proteins outside the cell, we were then able to go back to the cell to validate our observations. In the end, the in vivo and in vitro approaches actually complement each other and revealed our most interesting finding."

— Justyna Sawa-Makarska

Autophagy ensures cellular health by removing harmful material from the cytoplasm. Defects in autophagy are suspected to be involved in several human diseases. During autophagy, cargo such as misfolded proteins or damaged organelles are captured in a double-membrane compartment called the autophagosome, which forms de novo around the cargo and is targeted for degradation. The factors involved in autophagosome formation are known, but how they cooperate to initiate the formation of these membranes has so far been enigmatic. By reconstructing the first steps in the formation of autophagosomes, we demonstrated that tiny vesicles loaded with the protein Atg9 act as the seed from which the autophagosome is grown.

To understand what's really behind certain physiological phenomenon such as autophagy, we have to look at each component as a distinct piece of machinery that fulfills a certain function and then try to understand how each of the individual pieces comes together and finally understand how they interact. When our team began this research almost 10 years ago, we knew that the biogenesis of the autophagosome was catalyzed by a complex machinery of proteins. So, we set out isolating and characterizing 21 proteins, rebuilding parts of this autophagy machinery. Altering one parameter at a time, we created a controlled environment in vitro and slowly began to reconstitute the early steps of autophagosome biogenesis.

Autophagosomes first form as cup-shaped membranes in the cell, which then grow to engulf the cellular material designated for degradation. One of the factors involved in this process is Atg9, a protein whose importance in the formation of the membrane was known, but whose role was not clear. Atg9 is found in small intracellular vesicles. Over time, as the factors we explored grew in complexity, we were able to show that Atg9 vesicles form a platform on which the autophagy machinery can assemble to build the autophagosome.

Cells encapsulate cargo so that it can be correctly transported and degraded in a chemical environment that is different to the one normally found in cells. Autophagosomes therefore consist of a double membrane made of phospholipids. This fatty envelope creates a waterproof package that separates material from the aqueous surroundings of the cell and marks it for degradation. But Atg9 vesicles do not supply the bulk of the lipids to the growing autophagosome. Rather, we discovered that the vesicles actually recruit lipid transfer proteins. These proteins bridge the growing Atg9 vesicles to the endoplasmic reticulum (ER). In this way, lipids are transferred from the ER to the emerging autophagosome, enabling it to grow in size.

We are now using the toolkit we've developed to unravel the next steps in the biogenesis of the autophagosome. This research project was a collaboration of the Martens lab with Gerhard Hummer and Soeren von Bülow from the Max Planck Institute for Biophysics in Frankfurt, Germany, and Martin Graef from the Max Planck Institute for Biology of Ageing in Cologne, Germany.

Justyna Sawa-Makarska*, Verena Baumann*, Nicolas Coudevylle*, Sören von Bülow, Veronika Nogellova, Christine Abert, Martina Schuschnig, Martin Graef, Gerhard Hummer und Sascha Martens: Reconstitution of autophagosome nucleation defines Atg9 vesicles as seeds for membrane formation. Science, vol. 369, issue 6508, eaaz7714 (2020).

https://doi.org/10.1126/science.aaz7714

Layered Liquids — Reaction Chambers for Gene Regulation

Alwin Köhler lab

"Our initial findings challenged established concepts in chromatin biology. We were puzzled, too, but decided to thoroughly investigate how the droplet-like state of a chromatin-modifying enzyme accelerated its activity. The breakthrough occurred when we realized that the enzyme required a scaffold protein to form a core-shell structure with a liquid interior, similar to a reaction chamber."

— Laura Gallego

A marvel of complexity, the nucleus is the command center of the cell — harboring information, codes and controlled access. Chromosomes float amidst a seemingly chaotic sea of water, proteins, nucleic acids and other molecules, all engaged in a myriad of simultaneous reactions. These reactions have one main purpose: to turn genes on and off at the right time and place. Gene regulation is what makes a brain cell look and act different from a muscle cell.

A key question in biology and major interest of our lab, is how specific proteins become concentrated and organized on a specific gene to turn it on and off. In the nucleus, DNA is folded into chromatin, which is composed mainly of DNA wrapped around histone proteins. Enzymes can modify histones by posttranslational modifications and thereby affect chromatin structure and transcription, which regulates whether a gene is active. The mono-ubiquitination of histone H2B is an epigenetic mark, which broadly influences chromatin structure and eukaryotic transcription. How nucleosomes are recognized and ubiquitinated in a precise co-transcriptional choreography is still poorly understood.

We discovered that Bre1, a ubiquitin E3 ligase that ubiquitinates histone H2B, exists in a peculiar material state. Bre1 binds a scaffold protein, Lge1, which displays an unusual behavior when viewed under the microscope: Lge1 forms liquid-like droplets, which grow, collide and coalesce. These structures form by macromolecular phase separation, a process by which certain components separate from the surrounding environment to concentrate and assemble into biomolecular condensates.

Biomolecular condensates are thought to compartmentalize cellular matter and have been described in various forms in the cell. However, understanding how phase separation might regulate enzyme activity is still a major challenge. So, we began investigating how the liquid-like properties of Lge1 would affect the activity of Bre1 toward its substrate, chromatin. By reconstituting the process from defined components, we successfully demonstrated how Lge1, through phase separation, orchestrates chromatin ubiquitination.

Bre1 and Lge1 self-assemble into layered condensates with Bre1 forming a catalytically active shell around a liquid Lge1 core. Other components of the ubiquitination machinery and chromatin are also recruited into Lge1-Bre1 layered condensates, which we discovered to act as reaction chambers. Phase separation provides a means of concentrating the reactants of a genetic switch in the crowded chaos of the nucleus, essentially forming a crucible to accelerate the enzymatic reaction.

Moving from test tubes to cells, we found, together with our collaborators from Cornell University, that Lge1 and Bre1 are specifically concentrated on highly expressed genes and preferentially bind the nucleosomes in gene bodies, while excluding the first nucleosome of a gene. Mutations that disrupt Lge1-Bre1 phase separation affect cell fitness, underscoring the importance of these reaction chambers in gene regulation.

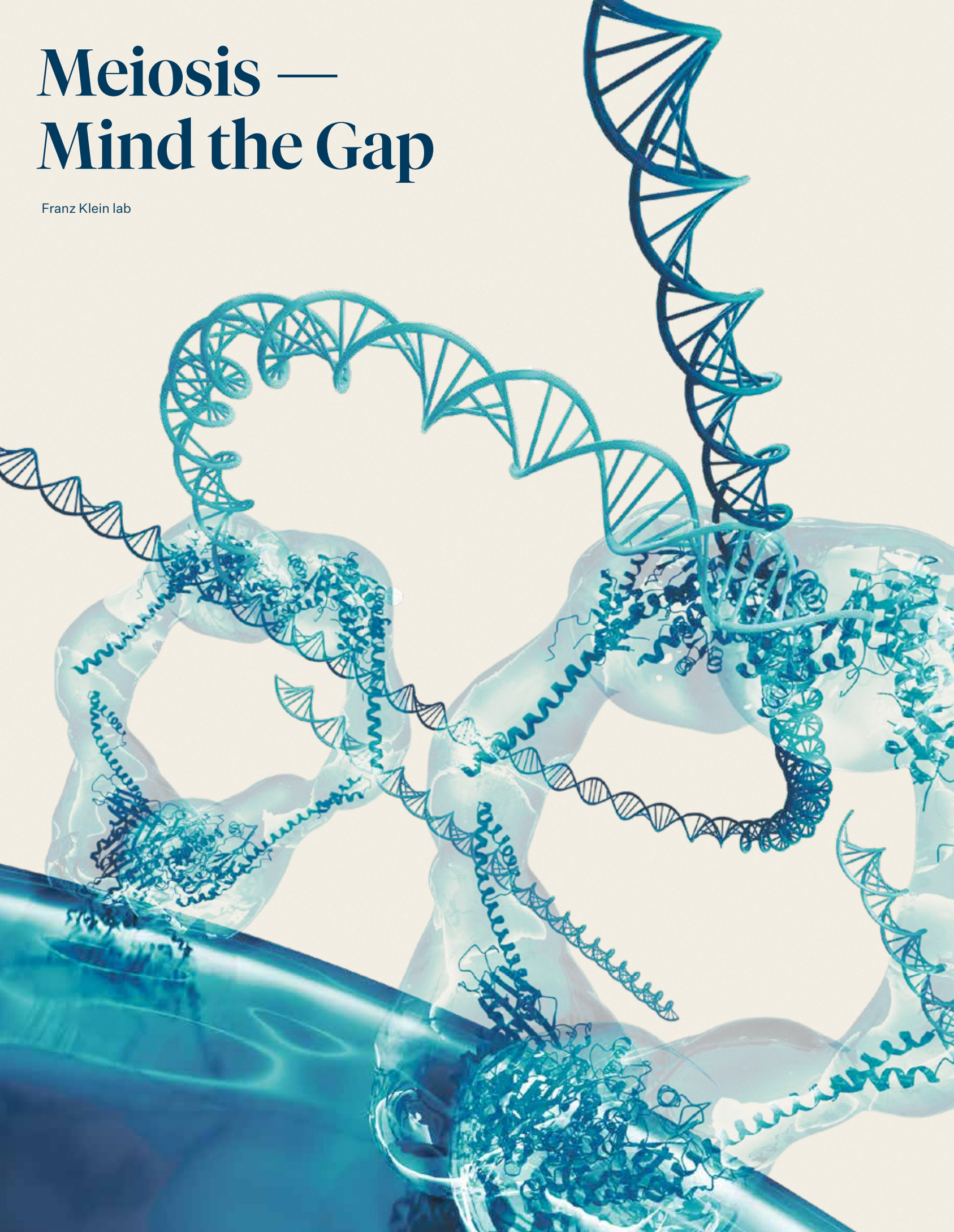
We also found a potential link to human disease. Lge1 has a functional counterpart in humans, called WAC. This protein also behaves like a liquid and when mutated causes DeSanto–Shinawi syndrome, a neurodevelopmental disorder. Thus, aberrant phase separation might have direct implications for human pathology.

Laura D. Gallego*, Maren Schneider*, Chitvan Mittal*, Anete Romanauska, Ricardo M., Gudino Carrillo, Tobias Schubert, B. Franklin Pugh & Alwin Köhler. Phase separation directs ubiquitination of gene-body nucleosomes. Nature 579, 592-597 (2020).

https://www.nature.com/articles/s41586-020-2097-z

Meiosis — Mind the Gap

Franz Klein lab



"The development of Protec-seq to generate a precise dDSB map with unprecedented resolution and the discovery of the correspondence of Spo11 cutting motifs with p53 motifs were the highlights of this project."

— Silvia Prieler, Doris Chen

Meiosis is a specialized, conserved process that generates gametes, the reproductive cells of an organism. In humans, genetic information is encoded in 23 chromosome pairs; each pair consists of two homologs, one from each parent. Gametes, however, are haploid, comprising only half the number of chromosomes. During haploidization, paternal and maternal chromosomes exchange parts of their DNA in a process called meiotic recombination, resulting in a unique combination of parental DNA. This process is initiated by the Spo11 complex, a nuclease that introduces several hundred chromosomal breaks (called double strand breaks, or DSBs; about 200 in yeast) per cell, which are repaired using the homologous copy as a template. DSBs were observed to be evenly distributed across chromosomes, with an average spacing of about 300 kilobases (kb), and enriched at gene promoter sites.

Given this spacing, we unexpectedly discovered that DSBs can occur within a distance of only 30 to several hundred base pairs (bp), thereby liberating short DNA fragments, which we termed double DSB (dDSB) fragments. We observed dDSBs in around 20% of the cases, a frequency that is too high to be explained by random events. To characterize those dDSB events, Silvia Prieler developed a special method, Protec-seq, for isolation and subsequent deep sequencing of dDSB fragments, enabling us to construct quantitative DSB maps with unprecedented high single-nucleotide precision.

To mine these dDSB maps, Doris Chen and Franz Klein developed in-depth computational analyses and novel means of visualization, revealing several striking features. We discovered a novel motif for Spo11 cleavage sites, which precisely matches that of the tumor suppressor p53. In fact, it is the signature for bendable DNA, strongly suggesting that Spo11 bends DNA during cleavage. Furthermore, dDSB fragment lengths display a periodicity of 10.4 bp, corresponding to exactly one turn of a DNA double helix. In addition, the predominant lengths imply that DNA is twisted during double-cut formation. Finally, enrichment of DSBs at highly active promoter regions and topoisomerase II binding sites led to our conclusion that Spo11 cuts DNA at sites under topological stress.

Although novel, this conclusion should not be surprising, because Spo11 is evolutionarily related to type II topoisomerases, enzymes that relax stressed and entangled DNA by initiating DSBs. Based on the observed periodicity, our model predicts that Spo11 complexes are mounted to a surface. We propose that Spo11 is usually located at the junction of two DNA strands, subsequently breaks one strand and pushes the other through the opening gate. Occasionally, two (or more) Spo11 complexes attach to a DNA strand and a second incoming strand will create two junctions, leading to two coordinated cuts.

Why cells undergo the risk to punch out chromosome pieces is still unclear. The gaps and their corresponding fragments pose an enhanced risk for mutations, caused by erroneous repair and resulting deletions or by insertion of fragments in irregular positions. Since short excised dDSB fragments are highly GC-rich, one could speculate that this phenomenon could antagonize a previously observed trend of GC enrichment at DSB hotspots. While clearly a risk to genome integrity, the creation of gaps in chromosomes may represent a mechanism for reshuffling of genetic control elements and hence enhancement of evolutionary diversity.

Silvia Prieler*, Doris Chen*, Lingzhi Huang, Elisa Mayrhofer, Soma Zsótér, Magdalena Vesely, Jean Mbogning, Franz Klein: Spo11 generates gaps through concerted cuts at sites of topological stress. Nature 594, 577–582 (2021).

https://doi.org/10.1038/s41586-021-03632-x

2020 Nobel Prize in Chemistry Awarded to Emmanuelle Charpentier

Emmanuelle Charpentier was a faculty member of the Max Perutz Labs from 2002–2009. The French microbiologist, geneticist and biochemist then moved on to Sweden and Germany. She is now the scientific and managing director of the Max Planck Unit for the Science of Pathogens in Berlin, Germany. It was at the Perutz that Charpentier laid the foundation for the groundbreaking utilization of the CRISPR-Cas9 system.

Few discoveries have revolutionized biomedicine as quickly and radically as CRISPR-Cas9, widely known as the "gene scissors." This tool promises to make many things possible that were previously unthinkable: curing genetic diseases, defeating cancer and making crops more resistant. The scientific community has been eagerly awaiting such a tool because CRISPR-Cas9 is precise, simple and affordable.

But where do the gene scissors come from? Who discovered CRISPR-Cas9? And how does it work? The story takes us from the salt pans of the Spanish Mediterranean to the basements of the French Ministry of Defense and Danish yogurt factories. We're talking about scientific pioneers who pursued seemingly exotic research outside the mainstream. It is the fascinating story of Emmanuelle Charpentier, who assembled the components of the CRISPR system and brought the molecular gene scissors to life.

In 1987, the official but completely unnoticed starting shot was fired. At that time, a peculiar pattern was reported in the genetic information of a gut bacterium from Japan: repetitive DNA sequences now known as "clustered regularly interspaced palindromic repeats" (CRISPR for short). A few years later, *Haloferax mediterranei*, an archaebacterium, came into focus. In the group of archaea, many microbes that thrive in extreme environments are known. *Haloferax* thrives in the salt lagoons of the Spanish Mediterranean and, once again, the peculiar repetitive DNA code was found. It was soon recognized that this specific DNA code is present in a wide variety of microbes. The French military, seeking forensic methods to detect bioweapons, investigated plague bacteria originating from an outbreak in Vietnam. And once again, the repetitive CRISPR code was present. Several scientists now suspected that CRISPR might be a kind of "immune memory." Every day, an invisible brutal battle for survival unfolds between bacteria and their viruses, called bacteriophages. Thus, bacteriophages infect bacteria, and bacteria must defend themselves. Did CRISPR potentially hold a license to kill this class of viruses?

Now an experimental proof was urgently needed for this extraordinary idea, and it came again from an unusual direction. The production of yogurt and other dairy products is threatened by viruses that infect and destroy lactic acid bacteria. A researcher in the dairy industry realized that lactic acid bacteria were resistant to viruses when they carried the CRISPR code. The mystery of the gene scissors slowly unraveled.

When a virus infects a bacterium, its genetic information is incorporated into the bacterium's own genetic information, specifically into the CRISPR locus. If the virus attacks the bacterium again, the CRISPR code is read. This information then serves as a "mug shot" for a protein called Cas9, enabling it to recognize and cut the foreign virus DNA. Cas9 is the gene scissors that specifically cuts the viral DNA, rendering it harmless. With the discovery of the Cas9 protein, the components of the gene scissors were almost complete, but the scissors were still dull. Something important was missing.

Charpentier, back then a researcher at the Max Perutz Labs, realized that a short ribonucleic acid (RNA) she called tracrRNA could activate the gene scissors. The puzzle was complete, and an almost unbelievable possibility emerged. What if Charpentier could simply replace the "mug shot"? In other words, what if the bacterial gene scissors could be reprogrammed to recognize and modify a different DNA, such as human DNA? Charpentier went to the University of Umeå in Sweden and, together with her colleague Jennifer Doudna from Berkeley, accomplished the masterpiece. They developed a method to apply the gene scissors to any DNA. This, in turn, allows for the removal or repair of DNA segments. For this discovery, the two researchers were awarded the Nobel Prize in Chemistry in 2020. As Louis Pasteur remarked in 1854, "Chance favors the prepared mind."

CRISPR is now everywhere. Hardly any research area in molecular biology can do without the gene scissors, and new applications are reported almost daily. In 2019, permission was granted in the United States for the world's first study using CRISPR-Cas9 on patients suffering from an inherited eye disease. Other therapeutic approaches are currently being tested for certain blood disorders. All these gene therapies are performed on somatic cells and not on germline cells. Germline therapy poses ethical issues and requires broad societal discourse and binding international regulations.

What can we learn from Emmanuelle Charpentier about the importance of basic research? The key lesson is that medical revolutions are often the product of chance, detours and an incredible amount of tenacity. A complex ecosystem of scientists was involved in the CRISPR revolution, but Charpentier was prepared and had the groundbreaking idea at the right time. Originally, she did not set out to develop a method for gene therapy — her motivation was simple curiosity. Many of the CRISPR pioneers were young, ambitious, willing to take risks, and their publications were rejected by the top journals. Perhaps therein lay the recipe for success.

Congratulations!

— Alwin Köhler, scientific director

Research Facilities

The history of science has ample evidence for technology as a catalyst for scientific breakthroughs. Iconic examples are the invention of microscopes for the observation of living cells, the construction of telescopes that led to the discovery of the moons of Jupiter, and the transformative power of DNA sequencing in biology and medicine.

"We strive to cultivate a collaborative relationship and to support users during each step of the experimental process."

— Kitti Dóra Csályi, facility head

Facility Heads, Max Perutz Labs

Josef Gotzmann (BioOptics–Light Microscopy)
Markus Hartl (Mass Spectrometry)
Kitti Dóra Csályi (BioOptics–FACS)
Andreas Bachmair (Plant Facility)
Stefan Schüchner (Monoclonal Antibody Facility)
Irmgard Fischer (Histology)

At the Perutz, state-of-the-art technologies are provided by our in-house scientific facilities. These are complemented by the Vienna BioCenter Core Facilities (VBCF). In this way, our researchers have unrestricted access to a broad spectrum of modern instruments.

Highly trained, expert scientists offer guidance on experimental design, instrument usage and troubleshooting as well as data analysis, ensuring that the facilities contribute effectively to our success.

Adoption of new tools is important in defining new scientific paths. The Perutz and the VBCF cooperate closely in identifying emerging technologies with strategic input from management, facility heads and user groups.

The Perutz Facilities

BioOptics–Light Microscopy

This facility is a backbone of our research, providing 15 state-of-the art light microscopy systems. The facility supports users with the evaluation of experimental approaches, instrument selection and all aspects of quantitative image analysis. In addition, the facility installs customized workflows for special and complex experiments and offers training for users.

Mass Spectrometry

The Mass Spectrometry Facility provides world-class proteomics services through modern liquid chromatography–mass spectrometry (LC–MS) analysis platforms and bioinformatics tools to identify and quantify peptides, proteins and their posttranslational modifications. To guarantee high-quality data, the facility regularly monitors performance using automatic quality control procedures and is continually refining protocols. New methodology is implemented to support researchers with custom projects, consulting on all steps, from planning to data analysis and publication. Data generated by the facility is routinely deposited into publicly available repositories, consistent with the latest data-sharing and transparency policies of journals.

BioOptics–FACS

Flow cytometry is a powerful technology that utilizes fluorescence labeling of marker genes or cell-specific antigens to identify cells with a specific phenotype. With a speed of thousands of events per second, it has a wide range of downstream applications in immunology, developmental and chromosomal biology, and other areas of biology including genomic tagging of proteins by CRISPR-Cas9. The facility provides high-end flow cytometers to perform cell sorting and multiparametric analysis. It also provides expertise in experimental design, sample preparation, analyzer operation and data analysis.

Plant Facility

The Perutz Plant Facility supports plant growth for educational and research purposes, providing greenhouses, growth incubators and a tissue culture room, as well as essential material for plant growth. Its services are complemented by the VBCF Plant Sciences Facility, which offers state-of-the-art phenotyping of plants grown within accurately controlled environments.

Monoclonal Antibody Facility

The facility develops mouse monoclonal antibodies and produces novel high-quality monoclonal antibodies tailored to specific requirements and applications. It generates mouse monoclonal antibodies against any custom antigen, including short peptides, recombinant proteins, posttranslational modifications or small compounds. Highly used, commercially available antibodies include CRISPR-Cas9 (Clone 7A9) and Myc-tag (clone 4A6). The facility rigorously validates its antibodies and has contributed significant efforts toward addressing the reproducibility crisis in antibody research.

Histology

The Perutz Histology Facility provides equipment for the histological and histopathological analysis of tissue samples. It provides research and validation services, establishes new histological methods, and trains and supports users. Its services are complemented by techniques offered in the VBCF Histology Facility (e.g., the detection of RNA in situ with the RNAscope Technology).

Vienna BioCenter Core Facilities (VBCF)

Electron Microscopy (EM)
The facility offers access to an extensive range of instruments, techniques, and expertise to visualize the ultrastructure of any model system — from molecules, such as RNA, DNA, or protein, to organelles, entire prokaryotic or eukaryotic cells, and tissues. The most recent addition to the EM equipment portfolio is the Thermo Fisher Scientific Glacios, a cryo-EM for high-throughput sample screening and fully automated data recording. Currently a Correlative Light and Electron Microscopy (CLEM) workflow is being set up, enabling users to switch between light and electron microscopy in one system.

Metabolomics
The facility quantifies metabolites and other small molecules to address, for example, how a high-fat diet can influence the lipid composition in the blood or other basic aspects of metabolism, such as the impact of genetic perturbations on the production of the building blocks of DNA and RNA. The team develops individualized experimental approaches, from hypothesis-free analysis of samples, to targeted analysis, assisted by isotopically labeled metabolites.

Next Generation Sequencing (NGS)
The NGS facility offers Nanopore and SMRT sequencing, single-cell and spatial transcriptomics, small- and large-scale Illumina sequencing platforms, base modifications and epigenomics, as well as many other methods, some of which were developed at the Vienna BioCenter (e.g., STARR-seq, SARSseq, SLAM-seq). NGS activities are leveraged by IT experts, who maintain and develop computational tools to manage, analyze and access information and data during all steps of the sequencing process.

"The mission of Vienna BioCenter Core Facilities is to enable groundbreaking discoveries by ensuring that all members of the VBC community have equal access to cutting-edge research infrastructure. To this end, the Perutz is an essential partner in our daily commitment to help scientists achieve their most ambitious goals."

— Daniele Soroldoni, managing director, VBCF

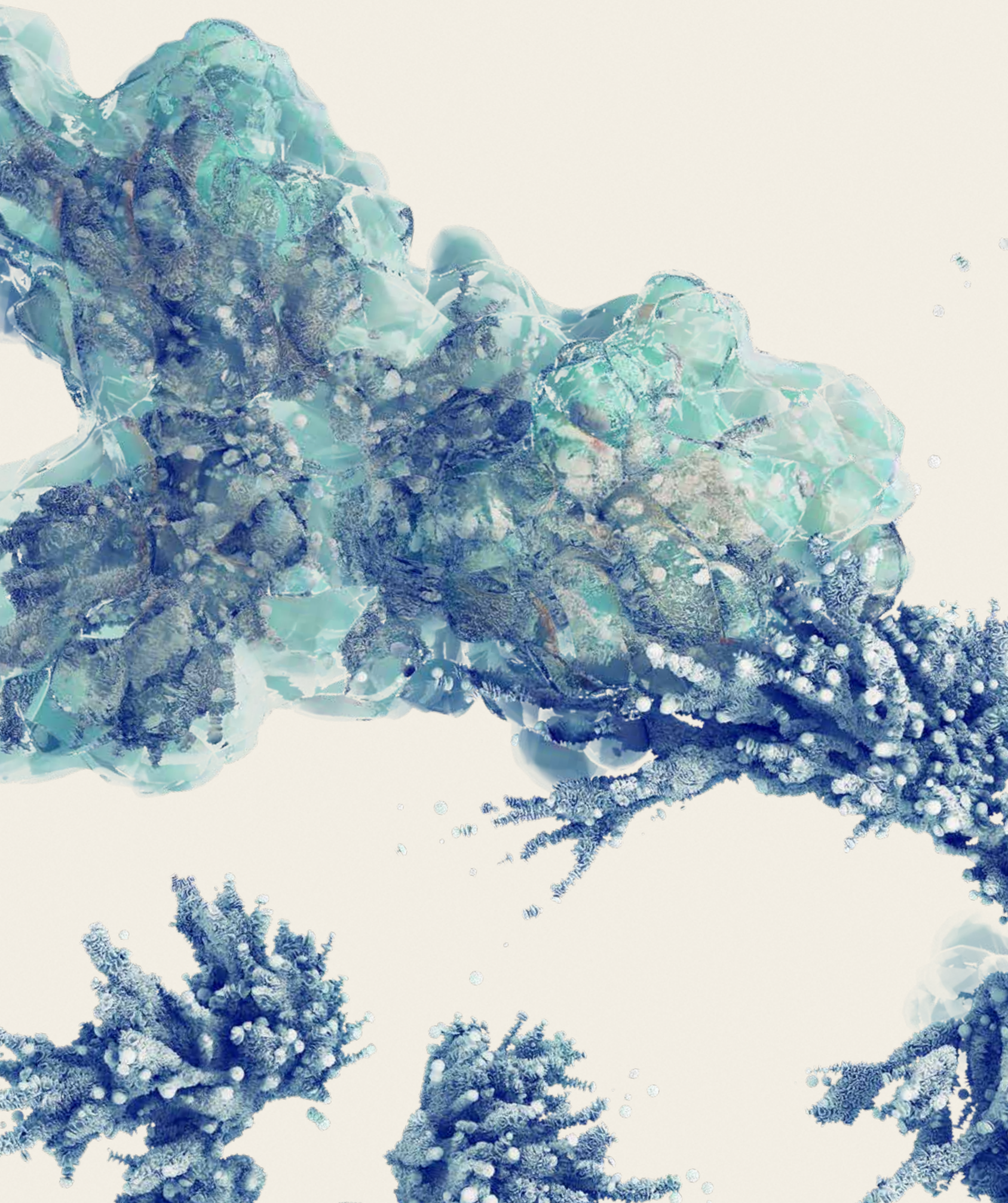
Preclinical Phenotyping
The facility provides access to state-of-the-art equipment for in vivo testing of mouse models, complementing the expertise of individual research labs. These include pharmacological treatments and various behavioral tests, specialized surgical services, optical imaging, dissection/perfusion services, cardiovascular measurements via implantable telemetry and other sensor systems, which allow the measurement of metabolic and physiological parameters in parallel.

Protein Technology (ProTech)
ProTech offers customized services for the production, purification and characterization of recombinant proteins. These include the design and cloning of (multigene) expression constructs, as well as the production of recombinant targets in bacteria, insect cells and mammalian cells. The facility gives advice on the feasibility of production and scaling-up and offers custom-designed chromatographic purification to yield homogeneous protein preparations for subsequent investigations.

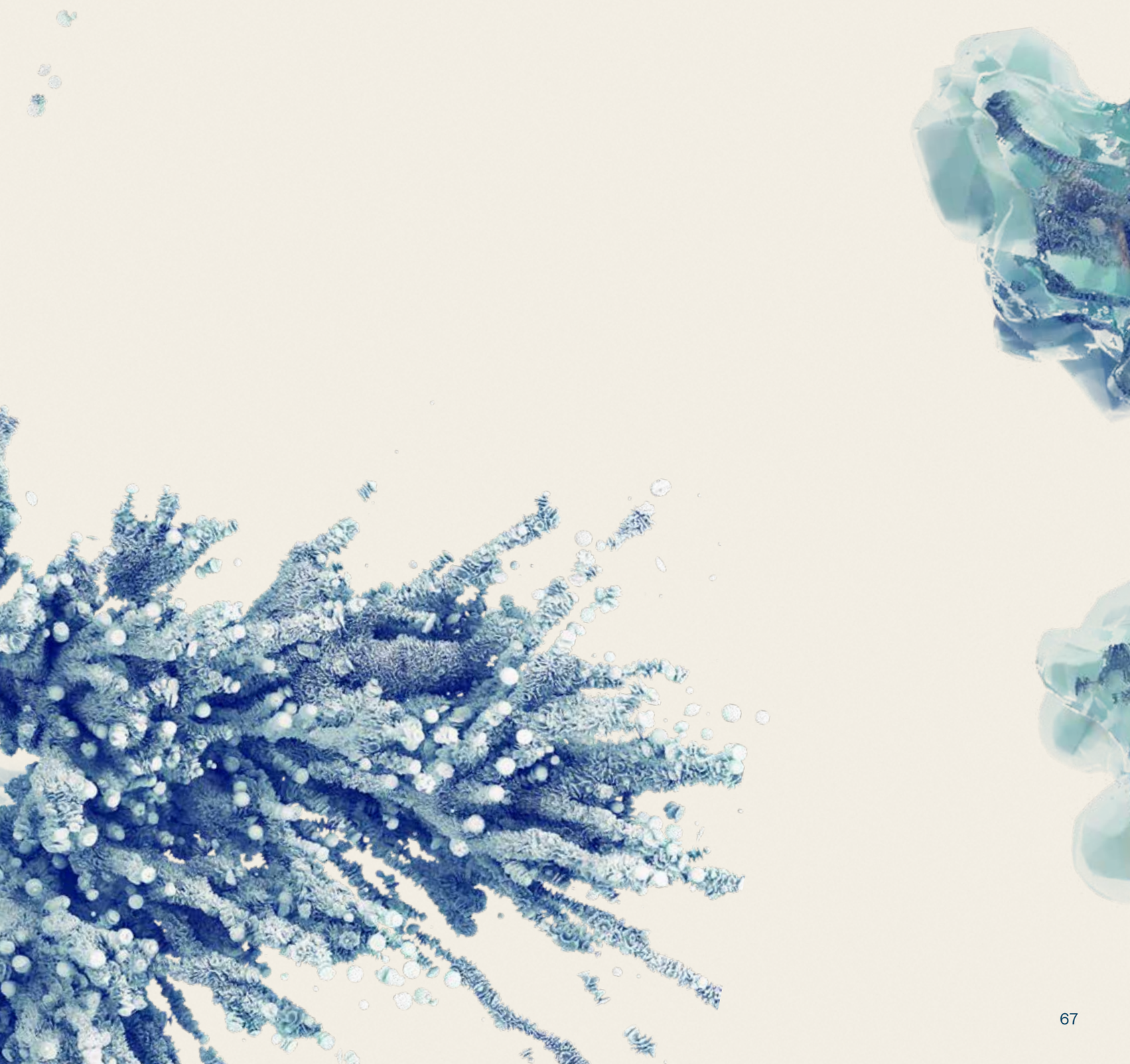
Vienna Drosophila Resource Center
The transgenic flies maintained at the facility are a unique collection of fly stocks including the world's largest collection of *Drosophila* RNAi lines. With over 1.3 million fly stocks shipped to more than 2,500 registered labs in over 50 countries, the facility is the main *Drosophila* stock center in Europe and one of the top three worldwide.

Facility Heads,
Vienna BioCenter Core Facilities

Thomas Heuser (Electron Microscopy)
Thomas Köcher (Metabolomics)
Andreas Sommer (Next Generation Sequencing)
Sylvia Badurek (Preclinical Phenotyping)
David Drechsel (Protein Technology Facility)
Lisa Meadows (Vienna Drosophila Resource Center)



Through our education programs, we aim to inspire a mindset of embracing uncertainty and to foster intellectual humility, perseverance and curiosity.



Teaching at the Perutz

"Ignorance is the natural state of mind for a research scientist."

— Neil deGrasse Tyson, astrophysicist

The Max Perutz Labs is not just a research institute. Central to our mission is the education in mechanistic biomedicine for our bachelor's, master's and PhD students, along with opportunities for postdoctoral researchers. We focus on training young researchers in the skills necessary for critical, analytical thinking across scales.

Inspiring the next generation of researchers to be experts in their field, while understanding how different subjects relate to each other, requires innovative teaching concepts and mentoring approaches. Teachers must equip students not only with technical skills, but also with the adaptability needed to take on the complexities of a fast-evolving scientific landscape. Placing too much faith in what we already know leads to inflexibility.

In a time marked by an unprecedented surge in data generation, creative problem solving also includes skills in data analysis, programming and data visualization. Machine learning and AI are increasingly used to identify patterns in cell biology, predict protein structures and make sense of complex datasets. Quantitative analyses are replacing the qualitative, descriptive language once used to characterize biological phenomena.

Team-based projects, problem-based learning, and customized curricula are essential components of an interdisciplinary education. We focus on critical thinking and effective communication through courses that train complex data analysis, literature review and problem solving. As the experimental possibilities increase, so does the importance of ethical considerations and responsible research practices.

In 2022 we introduced a new flagship master's program in molecular biology, which puts a strong emphasis on the molecular, mechanistic and quantitative exploration of biological processes across different scales. In 2021 we created an innovative master's program in molecular precision medicine (see next page).

It took Max Perutz 10 years to determine the structure of oxyhemoglobin. It took him another 10 years to determine the structure of deoxyhemoglobin with which he could work out the mechanism by which hemoglobin transports oxygen from our lungs to our tissues. This curiosity and perseverance is what we aim to inspire in students at the Perutz.

Our Teachers

Teaching requires skill and passion. While all of our faculty are involved in teaching, our lecturers place their main focus on teaching.

Full-Time Lecturers
Ivan Yudushkin (director of studies), Elisabeth Sonnleitner, Alois Schweighofer, Markus Teige, Angela Witte

Part-Time Lecturers
Andrea Barta, Dieter Blaas, Andreas Hartig, Reinhold Hofbauer, Natale-Erwin Ivessa, Heinrich Kowalski, Johann Rotheneder, Gerhard Wiche, Ursula Schöberl, Katharina Semrad

A New Era in Molecular Precision Medicine

"The mission of the program is simple: We want to furnish students with the necessary knowledge and skills to transform our understanding of the human body, what can go wrong with it and how we can fix it."

— Thomas Leonard, group leader and curriculum director

Despite centuries of studying the human body, our treatments of diseases have often been crude, ineffective and with numerous undesired side effects. An insufficient understanding of the molecular and mechanistic basis of diseases has hindered our ability to repair broken parts effectively. The discovery and development of "molecular scissors" (CRISPR-Cas9; see page 60) highlights the possibilities of treating genetic disorders at their root cause as well as the close connection between basic research and practical application.

Recognizing the opportunities of a new era in precision medicine and the unique position of the Perutz as a bridge between basic research and the clinic, we were inspired to develop a groundbreaking master's program in molecular precision medicine. This program aims to equip future researchers and clinicians with the knowledge and expertise needed to harness the full potential of mechanistic biomedicine, with the ultimate goal of revolutionizing the way we approach and treat human diseases.

Molecular Precision Medicine was introduced in 2021 as a joint program of the Medical University of Vienna and the University of Vienna. The curriculum addresses the fundamentals of pathogenesis of human disease at a molecular and mechanistic level. Students learn from both basic scientists and clinical practitioners how this information can be used to develop precision therapeutics that target the underlying cause of disease, how these therapeutics are evaluated for efficacy and toxicity, and about the future challenges facing precision medicine. Basic scientific and therapeutic concepts are rigorously illustrated with appropriate diseases and case studies, allowing students to understand disease all the way from its molecular basis to its clinical treatment. Students develop the bioinformatics skills to analyze large datasets of genomic information, including programming and applied statistics. Finally, students are exposed to current and future ethical and socioeconomic challenges in public health.

Bojan Zagrovic, group leader

Training and Careers

Careers at the Perutz can develop along several paths. Our commitment to academic excellence and modern scientific education is exemplified by strong collaborations with our partner institutes at the Vienna BioCenter Campus (VBC).

Bachelor's and Master's Programs

Anchored at the University of Vienna and Medical University of Vienna, these programs serve as a solid foundation for a scientific career. They equip students with subject knowledge, research skills, analytical thinking and a strong work ethic, preparing them to excel in a PhD program or in alternative careers. All faculty at the Perutz offer opportunities for undergraduate studies with hands-on training in our four research areas.

Vienna BioCenter Summer School

The Vienna BioCenter Summer School is an international success story. The nine-week fellowship program, tailored toward 20 undergraduate students, enables them to conduct small yet ambitious projects within a research group. Summer students receive extensive guidance, access to our cutting-edge facilities and generous stipends. The program includes an independent research project, a lecture series and final scientific symposium. Many talented students have returned to the VBC for PhD studies.

Vienna BioCenter PhD Program

Dedicated to training tomorrow's scientific leaders, the Perutz offers PhD opportunities to conduct cutting-edge research under the umbrella of the internationally renowned Vienna BioCenter PhD program. The program comprises the four academic institutes of the VBC, and students receive a joint degree from the University of Vienna and the Medical University of Vienna. The program offers a varied curriculum and strong individual support from thesis advisory committees. It includes a wide array of seminars that take place regularly, providing researchers with opportunities to deepen and broaden their areas of interest. Students can participate in a range of advanced courses such as writing, advanced microscopy, data analysis and more, along with career development workshops. Throughout their training, both students and postdoctoral researchers at the VBC showcase their research to the entire campus community through the Monday Seminars. The weekly series acts as a valuable forum for sharing knowledge and fostering inter-disciplinary communication. Students organize various activ-ities each year, including a retreat and a symposium. With English as the working language, the program draws inter-national talent. Currently around 120 PhD students from nearly 50 countries pursue their studies at the Max Perutz Labs.

Manuela Baccarini, group leader, and Kyojiro Ikeda, postdoc

Postdoctoral Opportunities

The central aim of a postdoctoral study is to cultivate self-reliance, showcasing originality, creativity and productivity as key factors that will contribute to future accomplishments in research. Much like other training endeavors, the Perutz and Vienna BioCenter environment provide exceptional research and networking opportunities as well as stepping stones toward independence. In 2020, the Vienna International Postdoctoral Program (VIP2) was initiated. This program provides three-year fellowships and a two-mentor system. It selects candidates from diverse backgrounds, whose projects have the potential to evolve into a distinct, independent research direction. Over 50 postdocs are currently employed at the Perutz.

Junior Group Leader Mentoring

The Perutz invests heavily in its future, particularly with its new junior group leaders. Selected through highly competitive, international calls, these talented scientists are fully independent. Each of them is on a track to tenure, allowing promising early-career scientists to eventually attain the rank of a tenured professor, which comes with significant job security and academic freedom. To provide assistance, tenure-track junior group leaders are mentored by one or two internationally recognized scientists. They attend leadership courses and obtain grant and manuscript writing support. Junior group leaders interact annually with our Scientific Advisory Board, meeting in a one-to-one setting. To further support their career development, the leadership team hosts an annual Junior Group Leader Recess dedicated to in-depth strategic planning. We aim to cultivate a vibrant, collaborative environment in which problems can be shared, new questions can be raised and success is celebrated.

Max Perutz PhD Fellowship

"Being chosen by the Perutz faculty strengthened my motivation to pursue my scientific goals, and the fellowship provides a platform to share my research with scientists from all over the world."

— Paulina Kettel, PhD student, Karagöz lab

Max Perutz's discovery of how hemoglobin transports oxygen from the air in our lungs to the mitochondria in all our cells established a new field of biology — molecular biology. A tour de force transcending the fields of physics and biology, Perutz's work led the way into a new dawn of molecular, mechanistic thinking. Along the way, he was supported by the UK Medical Research Council, which later established the world-famous Laboratory of Molecular Biology with Perutz as its first chairman. His work laid the foundations of molecular medicine, inspiring efforts to treat sickle cell disease based on an understanding of the pathology at a molecular level.

Perutz continued to dedicate much of his life to research, writing and the promotion of science. Following his lead, in 2021 the Max Perutz PhD Fellowship was established at the Perutz to reward visionary research in mechanistic biomedicine. Perutz PhD Fellows demonstrate innovative, outside-the-box thinking and develop curiosity-driven research projects.

Each year, students at the beginning of their studies are invited to apply for the fellowship, and awardees are endowed with a four-year scholarship to investigate a fundamental biological question. Current Perutz PhD Fellows are tackling diverse research topics that include protein quality control in the endoplasmic reticulum, membrane contact sites, microtubule organizing centers and cell fate determination.

2021 and 2022 Perutz Fellows (left to right): Helena Bragulat Teixidor, Luis Miguel Cerrón Alván, Júlia Garcia Baucells and Paulina Kettel

Student and Postdoc Fellowships and Awards

PhD Fellowships

Anzhela Pavlova	Böhringer Ingelheim Foundation Fellowship	2023
Jeanne Fesselet	Max Perutz PhD Fellowship	2023
Manuela Sophie Koller	Max Perutz PhD Fellowship	2023
Alexandra Shulkina	ÖAW DOC Fellowship	2023
Elisabeth Holzer	ÖAW DOC Fellowship	2023
Johannes Benedum	ÖAW DOC Fellowship	2023
Júlia Garcia Baucells	Max Perutz PhD Fellowship	2022
Paulina Kettel	Max Perutz PhD Fellowship	2022
Valentina Budroni	ÖAW DOC Fellowship	2022
Toni Manolova	ÖAW DOC Fellowship	2022
Alexander Stockinger	ÖAW DOC Fellowship	2022
Alexander Tsarev	ÖAW DOC Fellowship	2022
Luis Miguel Cerrón Alván	Max Perutz PhD Fellowship	2021
Helena Bragulat Teixidor	Max Perutz PhD Fellowship	2021
Dana Abdeen	ÖAW DOC Fellowship	2021
Aleksandra Anisimova	ÖAW DOC Fellowship	2021
Daria Filipczak	ÖAW DOC Fellowship	2021
Helena Bragulat Teixidor	ÖAW DOC Fellowship	2021
Konstantina Georgiou	ÖAW DOC Fellowship	2020
Sara Scinicariello	ÖAW DOC Fellowship	2020
Ameya Rakesh Khandekar	ÖAW DOC Fellowship	2020
Christina Manakanatas	ÖAW DOC Fellowship	2020
Laura Santini	ÖAW DOC Fellowship	2020

Postdoc Fellowhips

Elias Adriaenssens	Marie Sklodowska-Curie Fellowship	2022
Michel Fasnacht	ESPRIT Award	2022
Cristin Quesada Candela	VIP2	2022
Martin Xaver	VIP2	2022
Nathan Palmer	EMBO Postdoc Fellowship	2021
Elias Adriaenssens	Horizon MSCA 2021	2021
Virginia Busetto	VIP2	2021
Jose Julián Valenzuela	VIP2	2021
Audrey Mat	VIP2	2021
Egor Kiselev	VIP2	2020

PhD Student Awards

Anete Romanauska	Science & SciLifeLab Prize	2021
Anete Romanauska	Denise P. Barlow Award	2021
Anete Romanauska	Harold M. Weintraub Graduate Student Award	2020
Anete Romanauska	VBC PhD Award	2020
Borja Mateos	VBC PhD Award	2020

Prepared for the Future

Completing a PhD is a major achievement after a challenging and rewarding scientific journey. Studying at the Max Perutz Labs provides students with a strong foundation in advanced research methods and extensive experience in interdisciplinary collaboration with top scientists. Above all, they cultivate analytical skills, unconventional thinking and creativity, which have practical applications not only within the laboratory but also in academia, the biotechnology and pharmaceutical industries, and even in outer space.

We interviewed three Perutz alumni to learn how their PhD studies prepared them for their careers.

Amelie Schoenenwald

Graduated
2020, PhD in integrative structural biology, Tim Skern lab

Current position
Medical expert manager, GlaxoSmithKline, Munich, Germany; member of the European Space Agency (ESA) Astronaut Reserve

Role/responsibilities
As a reserve astronaut, participating in technical/medical courses, posing as a human test subject and doing public relations while waiting for a mission to fly to low earth orbit or beyond. In my company, working with physicians to improve diagnoses, support clinical studies, organize medical education events and execute projects.

What led you to your current position?
I had spent most of my life in academia and really wanted to see what else the world had to offer. I wanted to be challenged in novel ways and be exposed to a diverse set of new tasks while remaining true to my scientific background. In practice, I assessed where I wanted to be and what skills I would need to get there. Interestingly, what led me to the position at ESA was quite the opposite: I had never prepared or trained specifically for becoming an astronaut. Yet, it all came together: my (scientific) qualifications, my hunger for great adventures, but also things like my age and hobbies, and obviously a great deal of luck.

Daniel Serwas

Graduated
2017, PhD in cell biology,
Alexander Dammermann lab

Current position
Senior scientist, Chan Zuckerberg Institute for Advanced Biological Imaging (Chan Zuckerberg Biohub Network)

Role/responsibilities
Assemble and organize a team to research the structure and function of human organelles. We aim to create a library of organelles and their protein complexes at atomic resolution under near-native conditions.

What led you to your current position?
During my PhD at the Perutz, my PI took me to a conference in the US, which motivated me to apply for postdoc positions there. I wrote to labs I was interested in and proposed projects that would complement the lab's research and provide me with new opportunities to learn. With the support of a Human Frontier Research Program postdoctoral fellowship, I then joined David Drubin's lab at the University of California, Berkeley where I worked until moving to my current role.

What are your professional aspirations?
I aspire to make a meaningful impact on society by using my research skills and also continuously improve myself. At the same time, I also want to use my experience and mentor the next generation of scientists. The Chan Zuckerberg Imaging Institute is the perfect place for me to reach these goals.

What was the best thing about doing your PhD?
Surely, the best thing is the exuberant joy PhD students feel after finally producing publishable results and eventually seeing their research published! Nevertheless, the constant struggle to become a better researcher and a better person was also a journey worth making, especially while being surrounded by like-minded and motivating individuals. It was beautiful to explore and to venture — both in the laboratory as well as beyond!

What is the most important thing you learned during your PhD?
Fail fast and learn fast. Sometimes going back to base one and starting over leads to better results because it diminishes the risk of going down rabbit holes.

What did you learn during your PhD studies that prepared you for your current position?
We are all unique individuals with diverse strengths: But where can we unlock our full potential? And what path do we genuinely want to pursue? Asking yourself these questions regularly is key.

What advice would you give to future PhD students?
Graduate students tend to mingle among themselves and focus mainly on their own projects. Therefore, do not forget about your other passions outside of the laboratory: Everybody loves to be inspired and likes to surround themselves with enthusiastic, happy people who love what they do! Be the change.

What was the best thing about doing your PhD?
The best thing about my PhD program was the sense of community. It was very easy to get to know other people and make lifelong friends at the Perutz. It was also unique in that I had the opportunity to work together with other research institutions on campus and drive my own learning journey. One of the strengths of the Perutz is that the professors really embrace their roles as mentors, and you can always talk to people from other labs if you need help. People care about you, your future development and you as a person.

What did you learn during your PhD studies that prepared you for your current position?
I learned how to do rigorous research and present my research to people outside my field. For example, the collaborative and friendly environment of the labs made it easy to get to know other researchers and their projects. Although I was working on cilia and centrioles in a completely different organism, the friendly nature of the program made it easy for me to reach out to the lab next door and learn what they were working on. This experience of building bridges between labs and projects taught me how to communicate with people from different fields and convey the importance of my own work.

Do you have any advice for future PhD students?
My advice for future PhD students is to go for what you are passionate about even if others try to discourage you. I remember wanting to pursue electron microscopy to study cell biology, but many said it was a dated method. Now, it's one of the most desired skills to have. One of the most important choices in my career was that I went for it because I found it interesting.

Yamile Marquez

Graduated
2014, PhD in genomic sciences, Andrea Barta lab

Current position
Head of research and development, ADN Institut, Barcelona, Spain

Role/responsibilities
Developing consumer-facing products for precision medicine and genetic diagnostics using next-generation sequencing and microarray technologies.

What led you to your current position?
I was looking for a job that could combine research, which is one of my passions, and my bioinformatics background in projects and products in a clinical setting.

What was the best thing about doing your PhD?
The wide range of nationalities that you could find in the PhD program. Having the opportunity to meet people from many different cultural backgrounds was a very enriching experience that allowed me to witness how people can approach a problem from different perspectives.

What did you learn during your PhD studies that prepared you for your current position?
In a single word, troubleshooting. During your PhD studies you have to overcome many challenges, and in most of them you have to find the solution by yourself. This helps you enormously to face and solve new challenges in your everyday work.

What do you like about being in industry?
That projects usually are short term with very well-defined goals. And moreover, in my current position it is also rewarding to see how our findings impact and improve people's quality of life.

What advice would you give to future PhD students?
Be open to possibilities. The PhD program prepares you with many soft skills that are very valuable to a wide range of positions. In my opinion, you just have to find something that you feel passionate about and go for it.

The Josephinum houses the collections of the Medical University of Vienna and is a site of dialogue, teaching and research.

Viennese Modernism

With a population of nearly 2 million, the Austrian capital of Vienna has repeatedly been named the number-one most livable city in the world. Complete with all the advantages of a multicultural, big city, Vienna is also one of the greenest cities in Europe, surrounded by the Wienerwald (Vienna Woods), and with many parks, green spaces and over 160 km of biking paths and hiking trails in and around the city. Vineyards and rolling hills are just a short train ride away and offer spectacular views across the city and the Danube.

Rich in history and culture, the city is brimming with incredible museums, theaters, art galleries and music venues. Vienna is the undisputed cultural center of Austria and one of the world capitals of music. It is renowned for its stunning Baroque and Art Nouveau architecture and vibrant arts scene. Vienna also has a celebrated restaurant scene and exciting nightlife.

The Viennese Coffeehouse: A Laboratory

Sprinkled throughout Vienna are academic institutions of a special kind — Viennese coffeehouses, beloved for their relaxed and quaint environments, as well as their exquisite coffee. According to legend, the first such establishment opened with an inventory of Turkish coffee beans, part of the booty from the Siege of Vienna in 1683. Scientists, artists and philosophers (Sigmund Freud, Ernst Mach, Ludwig Wittgenstein, Gustav Mahler and many others) turned the coffeehouse into a sort of second living room during Fin-de-siècle Vienna. This melting pot of minds played an influential part in the evolution of Viennese Modernism (Wiener Moderne): an explosion of creativity in arts, design and architecture as well as analytical thinking in the late 1800s and early 1900s.

Nurturing Innovation: Vienna as an Intellectual Hub for the Life Sciences

The University of Vienna and Medical University of Vienna, both stakeholders of the Max Perutz Labs, are two of Europe's largest and most significant universities. Throughout the city, more than 40,000 people are employed at over 600 companies, research institutions and organizations dedicated to the life sciences. Vienna hosts more than 200,000 students, as well as numerous global organizations, contributing to the city's large international community and status as a place of international dialogue. Drawing on its universities, pioneering research institutions, and a thriving ecosystem of startups and established companies, Vienna has become a magnet for researchers and entrepreneurs, seeking to revolutionize healthcare and biotechnology. Besides this innovative spirit, many scientists are attracted by the high living standards, affordable housing, excellent healthcare and childcare, and general safety in Vienna.


ESPRESSO
YOURSELF

“There is so much inspiring art around Vienna beyond conventional museums. To keep up to date with art events, such as gallery openings, shows and performances, I recommend esel.at. My highlight is the ImPulsTanz — Vienna International Dance Festival every summer. It creates an incredibly vibrant and inspiring atmosphere across the city. One can participate or watch workshops, enjoy food, drinks and sunshine, or just dance the night away.”

— Christiane Hütter, PhD student

“I love hiking and the outdoors. What I really like about Vienna is that you don’t have to leave the city to spend time in nature. My family and I enjoy hiking in the Lobau floodplain near the Danube River. It’s often referred to as the ‘jungle of the Viennese’ since it’s part of the Donau–Auen National Park that protects one of the last floodplains in Europe. The best thing is that you can even reach it by public transport.”

— Elif Karagöz, group leader

View across Vienna and the Danube river from the vineyards.

“Vienna has been kind to me so far. Being my first venture abroad, I got quite a lot of guidance from people here and I luckily managed to make a few friends along the way. One of my favorite things about Vienna is that it is international enough to provide culinary experiences from around the world. My favorite restaurant is actually Ethiopian! Vienna has a lot to both see and do, so on days when I’m not pipetting, I have plenty of options to explore.”

— Kavya Shetty, PhD student

“One of my favorite summer activities in Vienna is visiting the ‘Heurige’ (wine tavern) on Kahlenberg. The views of the city and the delicious local food make for an unforgettable experience. I like a cold ‘Spritzer’ and a platter of traditional Viennese delicacies such as spicy sausages, Speck (smoked ham), a variety of cheeses and different kinds of spreads — it’s the perfect way to spend a lazy summer afternoon and appreciate the beauty of Vienna.”

— Gerald Raffl, PhD student

Located in the heart of Vienna, the MuseumsQuartier (MQ) is one of the largest districts for contemporary art and culture in the world.

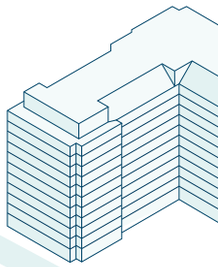
“I moved to Vienna two years ago and am still exploring the city. There are a lot of great things to discover all year round. In winter I enjoy ice skating at the Wiener Eistraum in front of city hall, and in summer nothing beats spending a day at Copa Beach on the Danube or at the Arbeiterstrandbad public pool, when I want a quieter space.”

— Jose Julián Valenzuela, postdoc

“I guess you could call me a movie aficionado. My most impressive cinema experience in Vienna so far was the Viennale — Vienna International Film Festival. Favorite cinema? The Filmcasino, not only because of its unique retro ambiance but also its wide selection of movies, including new releases, classics and thematic series. It can be challenging for a non-German speaker sometimes, but many cinemas show movies with English subtitles. I am looking forward to visiting one of the open-air cinemas in summer.”

— Grzegorz Ścibisz, PhD student

Vienna BioCenter Campus



5
Research institutes

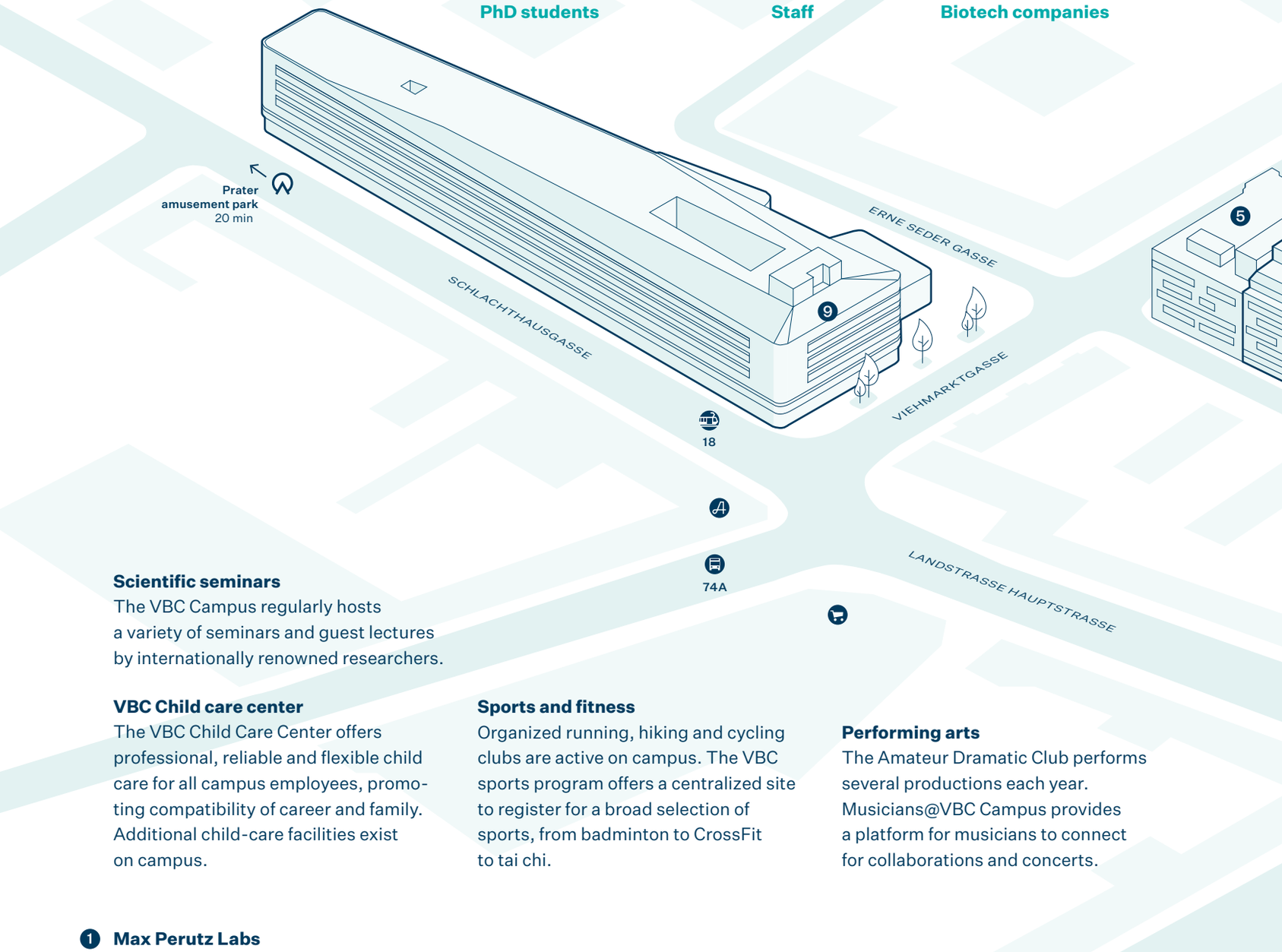
145
Research groups

2,269
Scientists

395
PhD students

2,893
Staff

39
Biotech companies



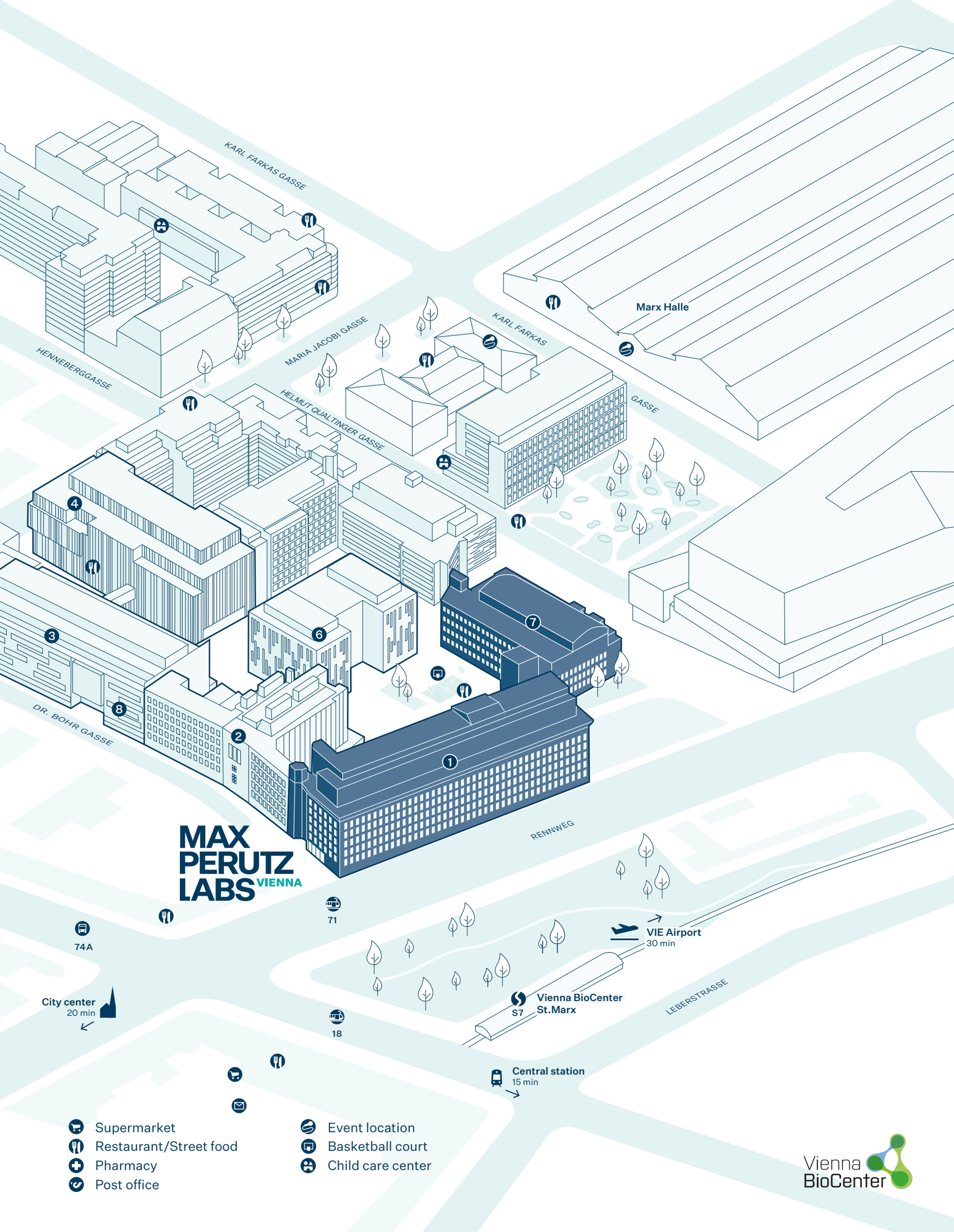
Scientific seminars
The VBC Campus regularly hosts a variety of seminars and guest lectures by internationally renowned researchers.

VBC Child care center
The VBC Child Care Center offers professional, reliable and flexible child care for all campus employees, promoting compatibility of career and family. Additional child-care facilities exist on campus.

Sports and fitness
Organized running, hiking and cycling clubs are active on campus. The VBC sports program offers a centralized site to register for a broad selection of sports, from badminton to CrossFit to tai chi.

Performing arts
The Amateur Dramatic Club performs several productions each year. Musicians@VBC Campus provides a platform for musicians to connect for collaborations and concerts.

1. **Max Perutz Labs**
2. **VBC Core facilities**
3. **GMI** Gregor Mendel Institute of Molecular Plant Biology
   IMBA Institute of Molecular Biotechnology
4. **IMP** Research Institute of Molecular Pathology
5. **VBC 2** Building
6. **VBC 3** Building
7. **VBC 5** Building **Max Perutz Labs**
8. **Vienna Open Lab**
9. **University of Vienna Biology Building (UBB)**


KARL FARKAS GASSE
HENNEBERGGASSE
MARIA JACOBI GASSE
HELMUT QUALTINGER GASSE
KARL FARKAS GASSE
Marx Halle
DR. BOHR GASSE
RENNWEG
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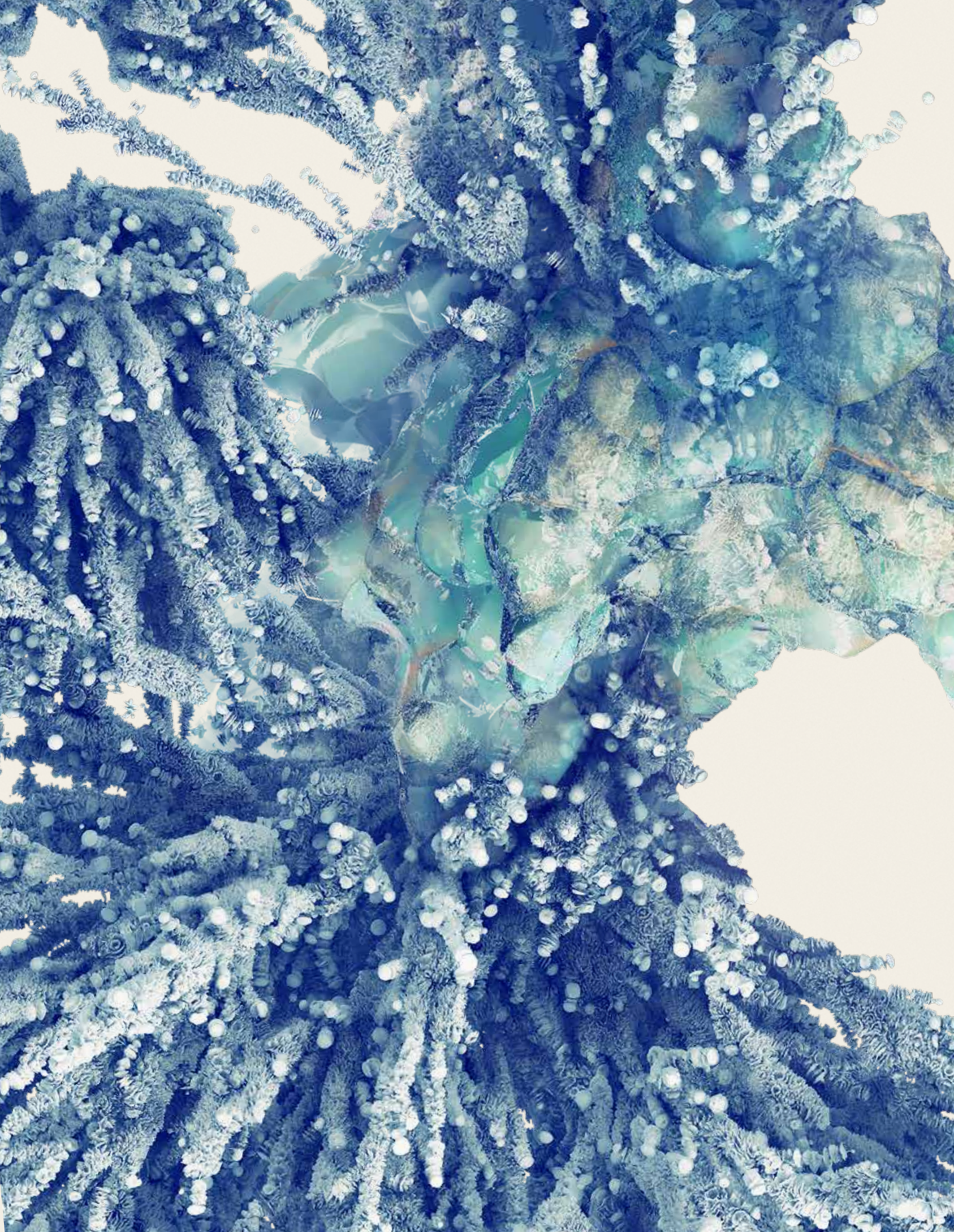
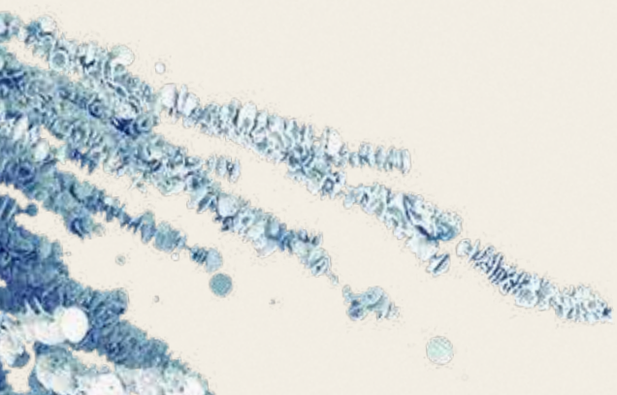
Central station
15 min
Supermarket
Restaurant/Street food
Pharmacy
Post office
Event location
Basketball court
Child care center
Vienna BioCenter



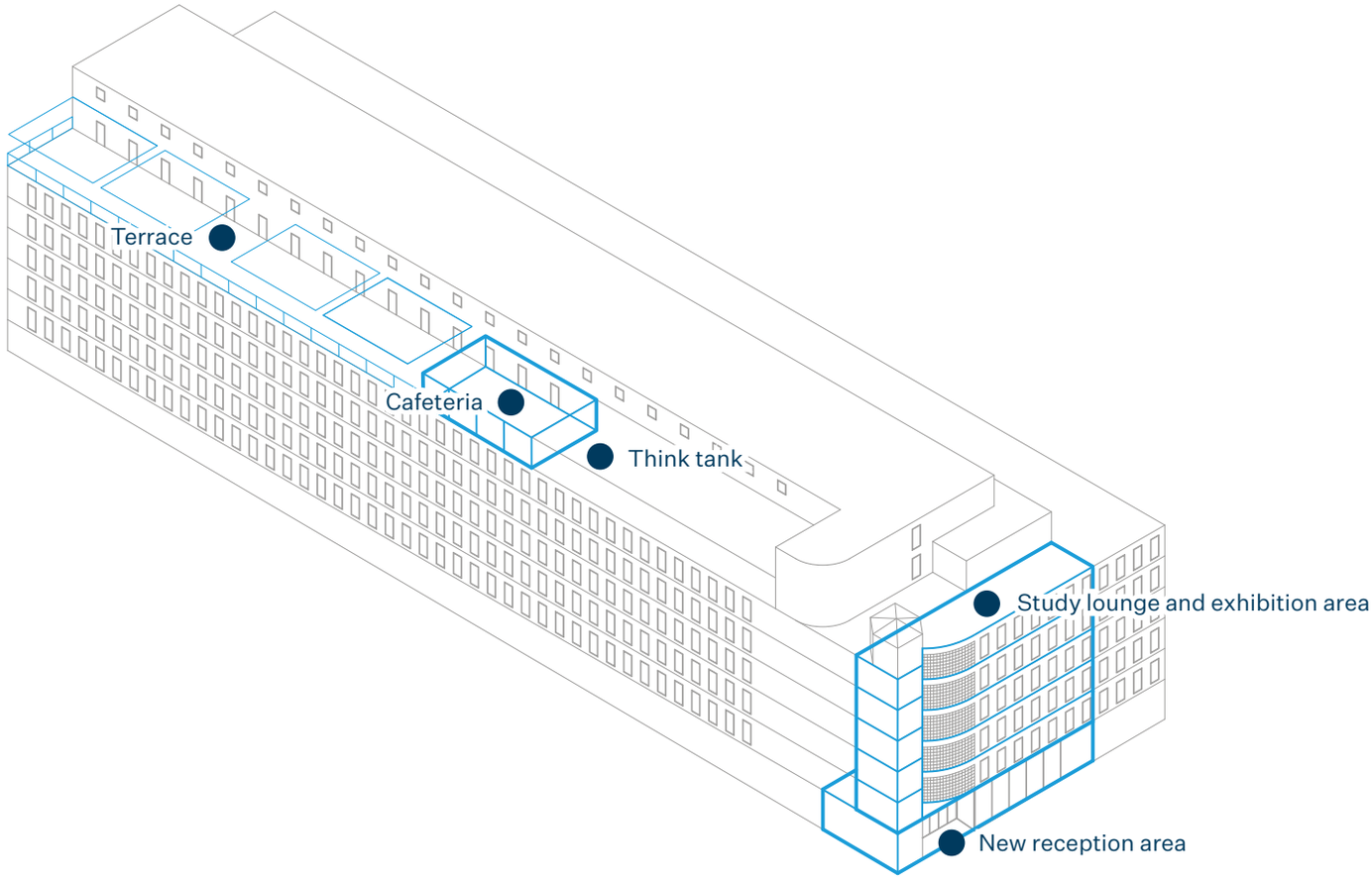
The architecture of a research institute is more than just a matter of aesthetics; it directly influences how scientists interact with each other. A well-designed institute can encourage spontaneous discussions and collaboration among scientists from different fields, leading to innovative approaches to complex problems.




MAX
PERUTZ
LABS VIENNA
"In science,
truth always wins."

Reshaping the Perutz

In the past four years, several changes to the institute's original architecture have transformed both the look and functionality of the Perutz. A new glass facade and open reception area generate a modern, welcoming atmosphere when entering the institute. On the top floor, communal areas offer scientists a comfortable setting for collaborative discussions. These amenities include a new study lounge for students, a think tank, an exhibition area featuring Max Perutz's biography and, most notably, a new cafeteria and revamped terrace with sweeping views to the southeast.



"First impressions count. When thinking about how to redesign the entrance, we had a simple idea in mind: to tell everybody working here, as soon as they step into the Perutz, 'You're important to us. Enjoy the science.' That's what we aimed for, plain and simple."

— Alwin Köhler, scientific director

"In science, truth always wins."

— Max Perutz

New Reception Area and Student Lounge

The newly designed areas within the institute honor the legacy of Max Perutz. In the reception area, you'll find a representation of hemoglobin's interaction with oxygen, inspired by Max Perutz's 1967 structural model. In the student lounge, we show Max Perutz alongside an earlier hemoglobin molecule from 1959. Perutz stated that, unlike in philosophy and economics, where debates continue for generations, in science nature always tells us what is right, and that answer is final.

Coffee Culture

"Experience had taught me that laboratories often fail because their scientists never talk to each other."

— Max Perutz

Understanding the value of interdisciplinary exchange at a time when it was not yet widely embraced by the research community, Max Perutz disrupted the status quo when he established a top-floor cafeteria at the LMB at Cambridge to encourage open exchange and collaboration among researchers.

The "Max Bar" cafeteria on the rooftop of the Max Perutz Labs was established in the very same spirit. It quickly became a popular spot for conversations among Perutz scientists and colleagues from the broader Vienna BioCenter Campus.

The Max Bar was equipped with a modern Faema E61 espresso machine, which was originally introduced a year before Max Perutz received the Nobel Prize in 1962. Now an all-time classic, back then the machine revolutionized coffee-making by introducing a new mechanism for brewing espresso.

An International Community

With 400 individuals representing 50 nationalities and different backgrounds, the scientists, students and staff at the Perutz form a multicultural community.* Diversity, equity and inclusion are at the core of who we are. We recognize and respect the importance of diversity in fostering an inclusive culture in which all individuals, regardless of race, ethnicity, national origin, religion, social background, age, gender, sexual orientation or disability, feel safe and can thrive. We encourage everyone to play an active role in cultivating this environment. It is essential not only for the community, but also for science.

1	Armenia
2	Australia
232	Austria
1	Belarus
2	Belgium
3	Bosnia and Herzegovina
1	Brazil
2	Bulgaria
1	Canada
4	China
1	Columbia
1	Costa Rica
8	Croatia
1	Czech Republic
1	Ethiopia
3	France
28	Germany
4	Greece
1	Guatemala
2	Hungary
7	India
1	Iran
1	Ireland
19	Italy
2	Japan
1	Latvia
1	Lebanon
1	Lithuania
1	Mexico
1	Nepal
1	Netherlands
1	Peru
1	Philippines
3	Poland
1	Portugal
1	Romania
6	Russia
5	Serbia
1	Slovenia
9	Spain
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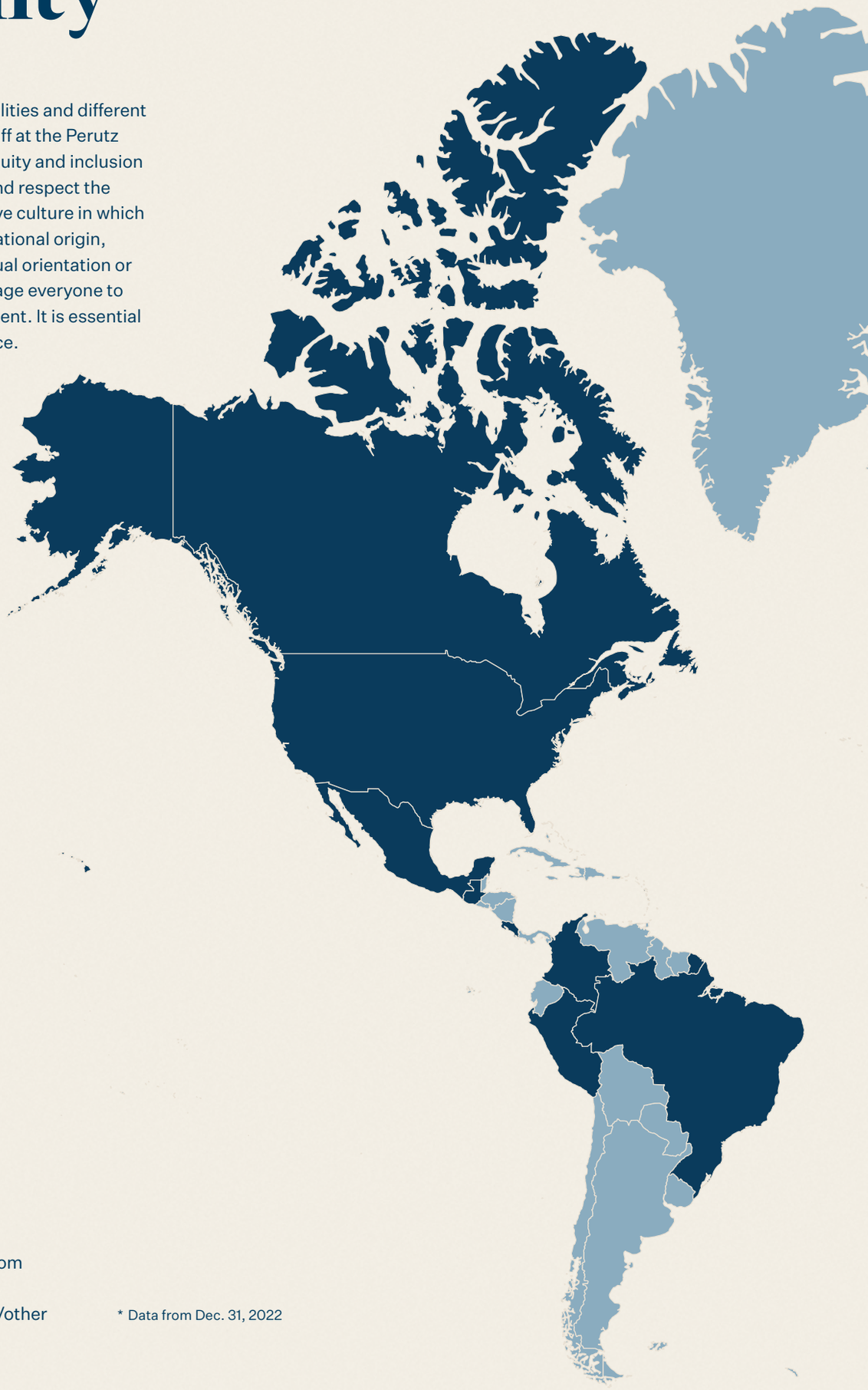
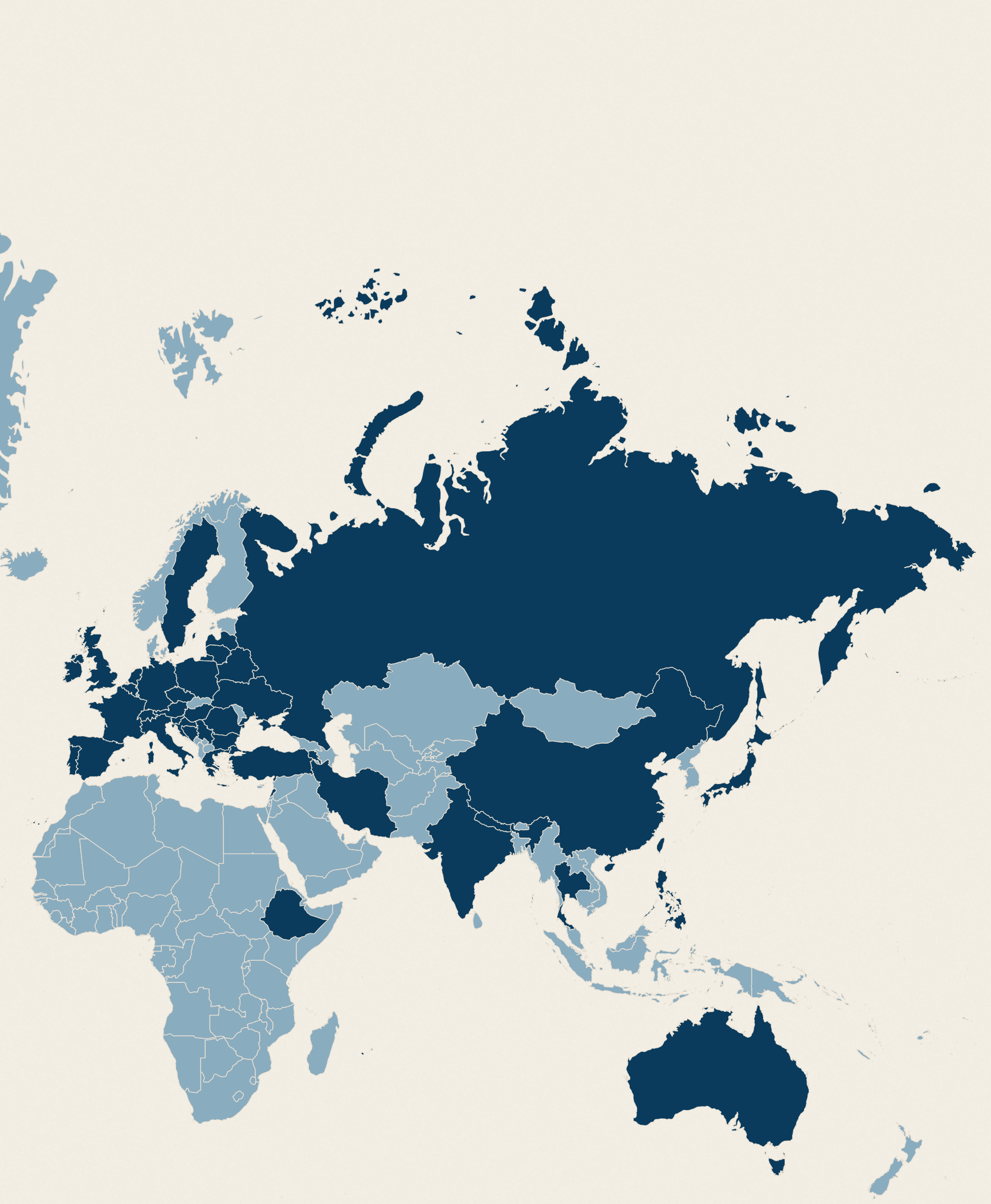
1	Taiwan
1	Thailand
3	Turkey
5	Ukraine
3	United Kingdom
6	United States
9	Not specified/other



* Data from Dec. 31, 2022



Celebrating (at) the Perutz

Social events are a regular part of life at the Perutz and provide the perfect opportunity for scientific exchange and connecting with peers. A highlight each year is Max Perutz Day, celebrating the inspiring life of the institute's namesake. The event also gives newly appointed group leaders the opportunity to introduce themselves and present their past and future research.

Celebrating Max Perutz Day on the terrace, June 2023

Alpine Christmas village on the terrace — chestnuts roasting on an open fire ...

Christmas 2022

Local vendors offering authentic Austrian specialties


$d = \frac{n\lambda}{\sin(\theta)}$

Knowledge Through Street Art

Painted across the 500 m^2 facade of the Max Perutz Labs, in bold shades of red, yellow and black, is a mural depicting hemoglobin crystals; a diffraction image from Max Perutz's X-ray crystallographic experiments; an equation describing the mathematical relationship between the positions of the diffracted X-rays and the arrangement of atoms in a crystal; and Max Perutz himself.

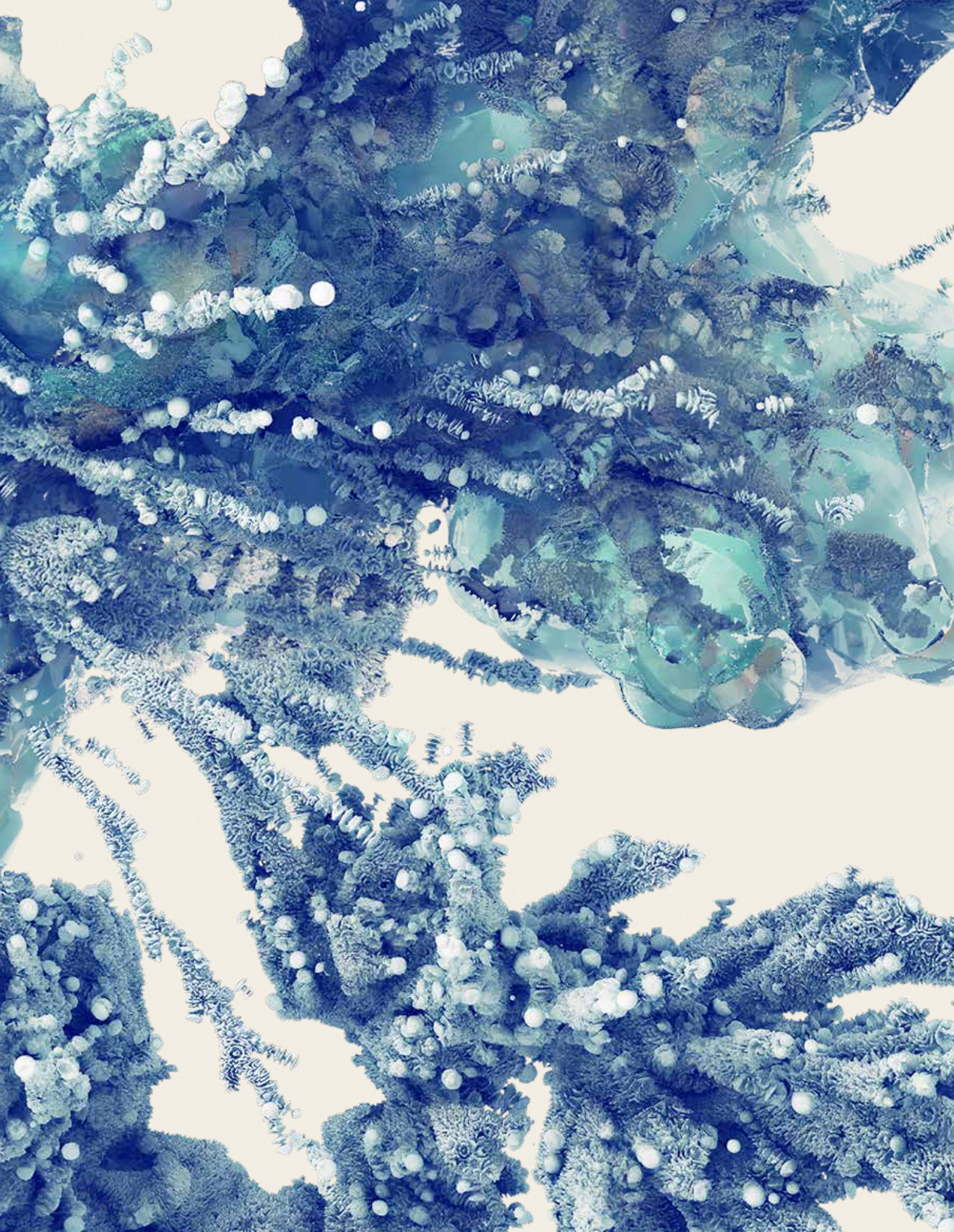
The mural is a product of a scientific outreach project, WIENERWISSEN, initiated by Thomas Juffmann, a group leader at the Perutz. The initiative aims to explore new ways of communicating about science to the public through art — specifically, disseminating Viennese science to Vienna.

"The mural not only reflects Max Perutz's science, but also Max Perutz as a person. We have tried to capture his life story, which was characterized by an incredible amount of perseverance."

— Käthe Schönle, artist

WIENERWISSEN wall murals serve as an invitation to learn about an equation, to find inspiration in stories about both science and scientists, and to engage in discussions about how science and technology shape our lives. "The Max Perutz mural is a bold statement that science has a place in all areas of society. We hope it will create dialogue and inspire new ways of thinking" says Scientific Director Alwin Köhler.

The artist duo Käthe Schönle and Sebastian Schager collaborated with WIENERWISSEN to develop the Max Perutz mural, which was completed in November 2022. It is the first project of the young initiative, and can be spotted easily when entering Vienna via Rennweg.



As scientists, we recognize our responsibility toward society. We apply our expertise to address pressing global issues, including the COVID-19 pandemic and climate change. By communicating the importance of basic research through a variety of initiatives and outreach events, the Perutz is fostering a crucial dialogue between researchers and the public.

Vienna COVID-19 Detection Initiative

2020 will be remembered for a long list of challenging events. It will also be remembered as a year that showcased the remarkable pace at which science can move. In less than a year, we have gone from zero knowledge of a new infectious pneumonia to efficient testing protocols and promising new therapeutics and vaccines — accomplishment unparalleled in history. The Vienna COVID-19 Detection Initiative (VCDI) was launched in March 2020 with the goal of developing fast and reliable tests against SARS-CoV-2. The VCDI allowed the largely uninterrupted operation of scientific activities at the Perutz and Vienna BioCenter during the pandemic, and its services and protocols were extended to the wider public.

The VCDI was initially formed from a broad alliance of researchers in Vienna (21 institutes and numerous volunteers) and later consolidated into a dedicated, self-contained laboratory at the Max Perutz Labs, which ran the operation together with the Vienna BioCenter Core Facilities, the IMP (Research Institute of Molecular Pathology), the IMBA/GMI (Institute of Molecular Biotechnology/Gregor Mendel Institute of Molecular Plant Biology), and the Centre for Microbiology and Environmental Systems Science at the University of Vienna. The VCDI acquired emergency funding from the Federal Ministry of Education, Science and Research (BMBWF) and the Vienna Science and Technology Fund (WWTF).

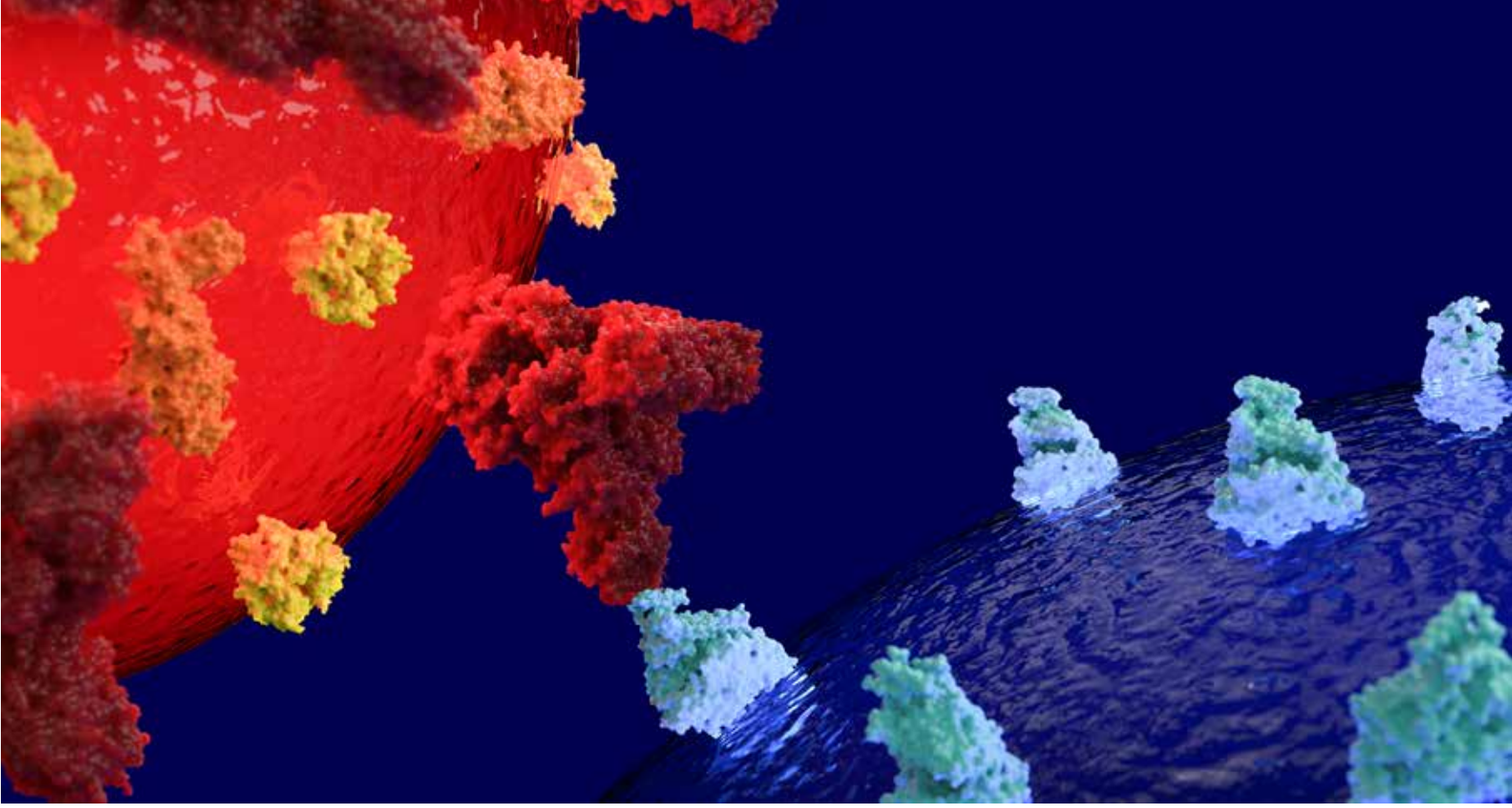
The VCDI developed mass-applicable, certified testing methods, which were adopted by other monitoring projects in Austria (e.g., “Alles gurgelt” in Vienna) and Germany. Over 17 months of operation, the VCDI delivered 300,000 tests and helped prevent the uncontrolled spread of the virus.

At its peak, the service performed 3,000 tests daily, reassuring staff, boosting morale and fostering community cohesion. The efforts of VCDI researchers have resulted in a long list of achievements. These include:

- Gargling as a simple method for sample collection
- Optimized pooling procedures
- Cost-effective, high-throughput PCR and LAMP assays for sensitive RNA detection
- Innovative methods for mutation analysis (SARSseq)
- Strategies for the surveillance of demographic hotspots
- Sharing standard operating procedures with collaborators worldwide
- Public outreach with accurate, up-to-date, and evidence-based information

In particular, the VCDI and its partners conducted vigilant surveillance of SARS-CoV-2 within nursing homes, with the objective of protecting the elderly population, known to be particularly vulnerable to the virus. Nearly 1,000 staff members were subjected to biweekly SARS-CoV-2 testing, with rapid results turnaround. This initiative effectively detected asymptomatic carriers of the virus, who could have unknowingly transmitted it to the residents.

SARS-CoV-2 in children often shows milder or no symptoms compared with adults. At the onset of the pandemic, the role of children and schools in virus spread was unclear. In response, the VCDI launched a monitoring project in Austrian schools. A comprehensive SARS-CoV-2 surveillance system was implemented in 250 Austrian schools, involving around 14,000 students and 1,200 teachers. This generated high-



quality data for tracking trends, detecting outbreaks, assessing COVID-19 impact and evaluating school preventive measures by the government.

Employee monitoring allowed the Max Perutz Labs and research institutions at the Vienna BioCenter to keep scientific operations running while prioritizing the health and well-being of its employees and the wider community.

Alongside these initiatives, the VCDI published timely research findings, provided guidance to the Austrian government, and established a website that served as a comprehensive, science-backed resource on the coronavirus and COVID-19. This platform and other activities addressed critical questions during a period when misinformation, deliberately crafted and disseminated, was prevalent both in Austria and globally.

The VCDI showcases the commitment of scientists to addressing global societal challenges — through collaboration across boundaries, by using basic research to tackle applied questions, and through dissemination of evidence-based information that guides political decision making.

“We established a high-throughput testing pipeline under extreme time constraints,” said Alwin Köhler, who launched the initiative. “It was like constructing an airplane while it was already in flight, with evolving blueprints. I’m immensely proud of the VCDI researchers’ dedication, energy and innovative spirit. Looking back, I’m truly amazed by what the VCDI accomplished — against all odds.”

VCDI Coordinator
Alwin Köhler

Supervisory Board
Johannes Zuber
Michael Wagner
Harald Isemann
Daniele Soroldoni
Alwin Köhler

VCDI Testing Pipeline
Daniele Soroldoni (chief scientific officer)
Johanna Trupke (head of laboratory)

School Testing Project
Michael Wagner (coordinator)

Nursing Home Surveillance
Johannes Zuber (coordinator)

Assay innovation — RT-LAMP
Julius Brennecke & Andrea Pauli

Assay innovation — NGS
Ulrich Elling, Luisa Cochella & Alex Stark

And the countless other employees and volunteers who have dedicated their time and energy to the VCDI

Members of Climate@MaxPerutzLabs (from left to right): Jeroen Dobbelaere, Dunja Rokvic, Lilian Nehlin and Nikola Winter

Inspiring Change for the Climate

A grassroots initiative established in 2019 by a group of students, postdocs, technicians and administrative staff, Climate@MaxPerutzLabs has evaluated the environmental impact of research at the Perutz, prompting discussions within the Perutz and with its stakeholders about how to create a more sustainable institute. Focusing on gathering data, raising awareness and initiating pilot studies, the group seeks to inspire action among researchers to reduce waste, cut emissions from international travel and to increase energy efficiency in their labs. They have also initiated numerous collaborative projects at the Vienna BioCenter and with climate initiatives at other universities.

Vienna BioCenter Climate Lecture Series
The Climate@MaxPerutzLabs group launched the Vienna BioCenter Climate Lecture Series to gain insights from peers, raise local awareness and establish a network of environmental experts from academia and industry. Collaboration is seen as crucial in addressing the climate challenge, and one of the lectures led to discussions with two suppliers about the life cycle of products used at the Perutz. As a result, the companies calculated the footprint of their products for the institute, providing a basis for fact-based decisions on sustainability. With over 20 speakers and more than 1,500 participants, the climate lecture series has become an integral part of the campus lecture program.

Sustainability Award 2022
In 2022, the Climate@MaxPerutzLabs initiative was honored with the Sustainability Award from the Austrian Federal Ministry of Education, Science and Research, as well as the Federal Ministry of Climate Action, Environment, Energy, Mobility, Innovation and Technology. This prestigious award acknowledges outstanding and sustainable projects within Austrian universities and higher education institutions. The Climate@MaxPerutzLabs project, titled "From molecule to climate — sustainability in basic research in molecular biology," secured the first prize in the "structural embedding" category.

"My flight to this conference released 0.76t CO_2. <2t CO_2 /year/person would be required to prevent a global temperature rise of 2°C. Traveling accounts for ~50% of a life scientist's CO_2 footprint."

The Paradox of the Life Sciences
A handwritten note attached to Nikola Winter's conference poster set things in motion: "My flight to this conference released 0.76t CO_2. <2t CO_2 /year/person would be required to prevent a global temperature rise of 2°C. Traveling accounts for ~50% of a life scientist's CO_2 footprint."

This note prompted intense discussions among scientists at the conference and led to an invitation by EMBO Reports to write a commentary. Published in February 2023 by Winter and fellow members of the initiative, "The paradox of the life sciences" sheds light on the conflicting nature of research — seeking to preserve and improve life on earth while causing greenhouse gas emissions. Embracing sustainable research practices should not be viewed as an extra burden or obstacle to scientific excellence and success. Instead, it should be an inherent aspect of research, much like adhering to health and safety regulations and ethical standards.

Nikola Winter, Raphaël Marchand, Christian Lehmann, Lilian Nehlin, Riccardo Trapannone, Dunja Rokvić, and Jeroen Dobbelaere. (2023). The paradox of the life sciences: How to address climate change in the lab. EMBO reports e56683.

https://doi.org/10.15252/embr.202256683

A Traveling Exhibition

Breathing at High Altitude

Nobel Prize winner. Pioneer of molecular biology. Founder of the Laboratory of Molecular Biology (LMB) in Cambridge. A mountaineer and researcher after whom a glacier in the Antarctic was named.

Despite his remarkable accomplishments, the tale of this accomplished scientist — Max Perutz — remains relatively unknown to many. To shed light on the life and work of this extraordinary figure, in 2022 Alwin Köhler initiated an exhibition and science outreach endeavor entitled “Breathing at High Altitude.”

Max Perutz’s life work was dedicated to elucidating the structure of hemoglobin, the protein vital for oxygen transport. Collaborating with Georgina Ferry, a prominent science writer and Perutz’s biographer, the multimedia exhibition interweaves Perutz’s personal journey and scientific achievements, housed in a pavilion modeled after a hemoglobin-containing red blood cell.

The exhibition, which drew over 5,000 visitors, made its debut in the courtyard of the historic central building of the University of Vienna and was accompanied by a series of public engagements. Tom Leonard, group leader at the Perutz, held a public lecture, sharing insights into Perutz’s inquisitive nature, scientific approach and relentless pursuit of a fundamental scientific question.

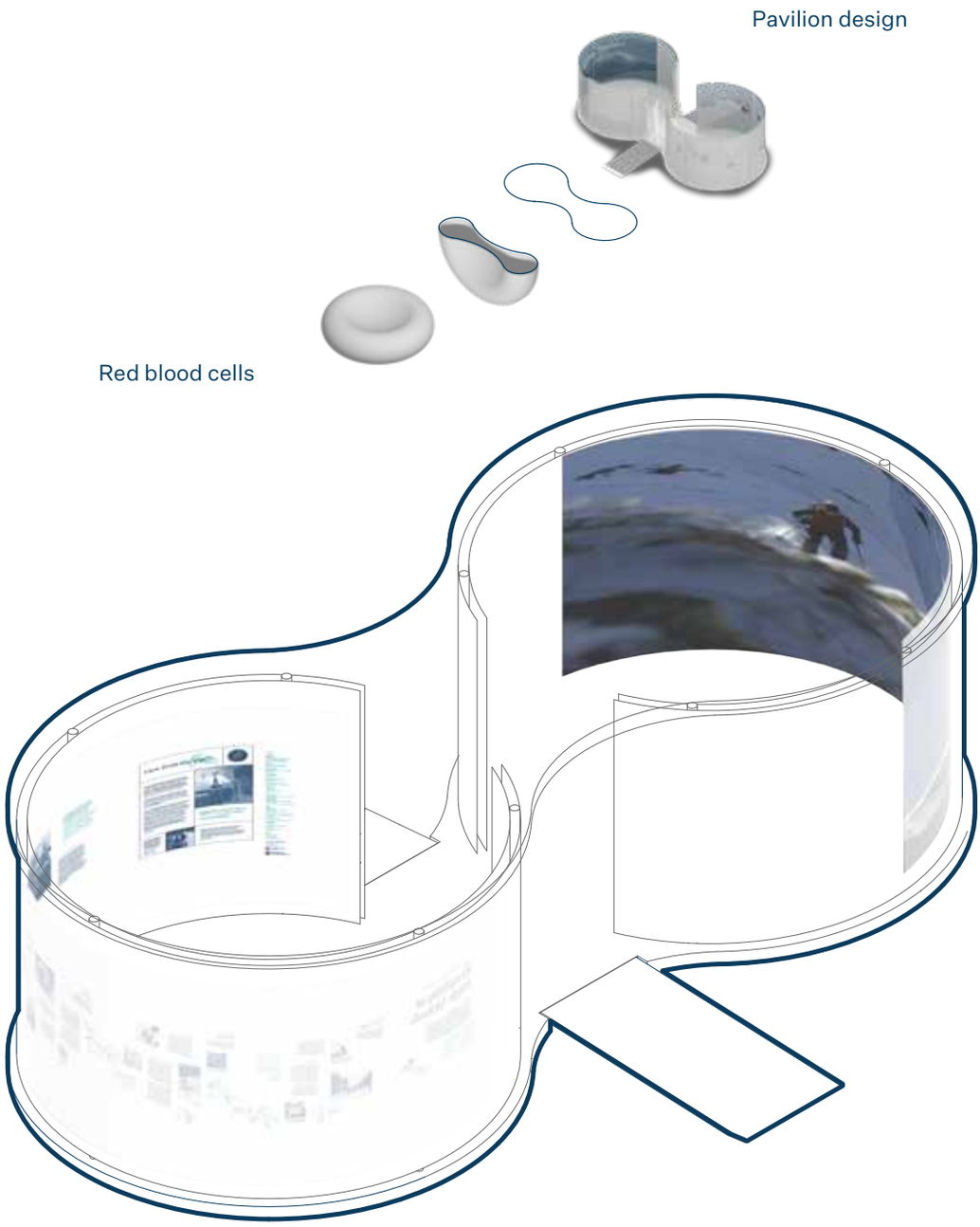
Max Perutz with his first high-resolution model of hemoglobin (1968).

Georgina Ferry (left) presented the recently translated German edition of “Max Perutz and the Secret of Life” (“Max Perutz und das Geheimnis des Lebens”) at the Austrian Academy of Sciences, with actor Cornelius Obonya (right) offering selected readings from the book.

Perutz’s life story juxtaposes the time, patience and perseverance required not only for scaling great heights in mountaineering, but also for advancing the boundaries of human knowledge and understanding.

Inspired by Red Blood Cells

The biomorphic design of the exhibition pavilion by buero bauer imitates the cross-sectional shape of an erythrocyte, which is typically biconcave. This unique shape enhances gas exchange efficiency and flexibility for navigating narrow capillaries. Unlike most cells, erythrocytes lack a nucleus and many organelles, but they are packed with hemoglobin, enabling them to excel at their primary function of transporting oxygen and carbon dioxide throughout the body.



The Life and Work of Max F. Perutz

Vienna-born chemist Max F. Perutz scaled the heights of scientific achievement, winning the Nobel Prize in chemistry in 1962. His work revealed the intricate mechanism of the "breathing molecule," hemoglobin, which transports oxygen throughout the body to keep us alive. His attitude to life, which he attributed to his experiences climbing mountains as a young man, illustrates the effort and determination that characterize successful scientists, and the euphoria that rewards success on reaching the top.

"As you approached the mountain ... you said to yourself: 'Good Lord, I shall never get up there!' ... Gradually and with absolute concentration you slowly made your way to the top ... the happiness with which the beauty filled you was compounded with the sense that your courage had paid off and that you had experienced a very great adventure."

— Max Perutz, in his unpublished memoir written in the month before his death in 2002

Historical view of Vienna's city center Opernring, 1914

1914–1937

Base Camp

Max was born in Vienna in 1914. He was the youngest of three children of Hugo and Dely Perutz, both descended from successful textile manufacturers. They lived in wealth and comfort in a spacious apartment in Jaurèsgasse.

Mountain Views

Max spent his vacations at his mother's beautiful villa in Reichenau, where he learned to climb in the nearby Rax mountains. Still in his teens, he made adventurous expeditions to the Alps, and he skied fast and confidently. He had been a sickly child, but the mountains gave him strength, and spending time at high altitude would always be essential to his well-being.

Max Perutz (right) and his friends Werner and Walter Weissel and Titi Höfft on the summit of Grosse Zinne in the Dolomites, Northern Italy.

"One has to imagine what will be lost to researching humanity if I do not concentrate on science and instead devote myself to a business career ... It would be very sad if the Nobel Prize had to be awarded to somebody not worthy of it."

— Letter from Max to Evelyn Baxter, Vienna, December 8, 1933

Chemistry and Cambridge

A teacher at the Theresianum inspired in him a love of chemical experiments, and he chose to study chemistry at the University of Vienna. He did well, but found the department old-fashioned in its approach, and so decided to go to England for his PhD. Thanks to an introduction from his professor Hermann Mark — and an allowance of £500 from his father — in 1936 he found a place in the crystallography laboratory of John Desmond Bernal at the University of Cambridge.

On the advice of a relative, the biochemist Felix Haurowitz in Prague, he chose to study the protein hemoglobin, which gives blood its red color. He soon had beautiful crystals to work with, but his choice carried risks. The field was new, the methods untried, and the outcome uncertain.

Max (center, with glasses) with his classmates in the organic chemistry laboratory at the University of Vienna in 1936

1938–1948

Detours

The annexation of Austria by Germany in 1938 threw Max's future into doubt. His family was Jewish, and his parents fled Vienna, leaving almost everything behind.

German troops received a joyous welcome when they marched into Vienna in March 1938

Max studied glacier flow on the Jungfraujoch, Switzerland, in 1948

Investigating Ice

With no means of supporting himself, Max accepted a summer job on an expedition to study glaciers on the Jungfraujoch in Switzerland: They needed a crystallographer who could ski. He thought it would be boring, but he and his colleagues made important new discoveries about glacier formation. He returned to the mountain a decade later to conduct studies of the rates of flow at different levels in the glacier, work seen as so important that a glacier in Antarctica has been named after him.

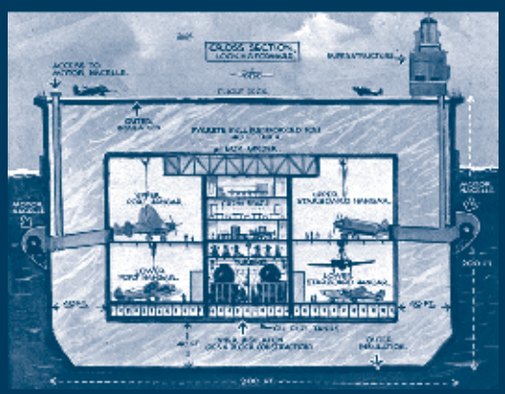
From Enemy Alien to British Citizen

The outbreak of the Second World War halted his scientific activities. In May 1940 he was arrested by the British police as an enemy alien, interned, and finally deported to a prisoner-of-war camp in Canada. Deprived of information, he feared he had been forgotten, a hardship worse than the intense cold. The efforts of his scientific friends saw him return to Cambridge the following January, a free man. Soon afterwards he met a fellow refugee, Gisela Peiser, and they were married in March 1942.

Thanks to his studies of ice, Max's PhD supervisor JD Bernal recruited him to a top-secret War Office project researching the far-fetched idea of making aircraft carriers out of reinforced ice — a project known as Habbakuk. No such vessel was ever made, but Max was issued a British passport so that he could go to the US to confer with American colleagues. It was a sign of his acceptance by the society he had chosen, and with Gisela also granted British citizenship, he was as happy as he had ever been.

"I think of you and my people and friends and I dream of all the marvellous things I shall do when I come back."

— Letter from Max to Anne Hartridge Camp L, Quebec, Canada, August 14, 1940



Project Habbakuk, ice aircraft carrier, 1943

On the way up to Jungfraujoch glacier, Switzerland, 1938

1945–1959

Ascent

After the war, Max returned to his research on hemoglobin. Understanding the three-dimensional structure formed by its more than 9000 atoms would be the key to explaining how it meets the body's need for oxygen.

Low-resolution model of myoglobin, 1957

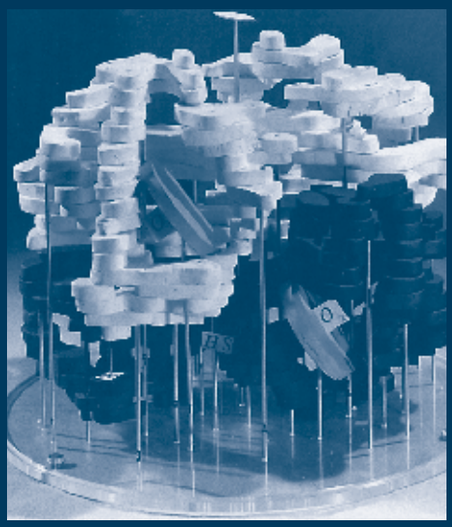
"If the myoglobin of a whale is like the haemoglobin of a horse ... these must have developed from a common primeval gene which provided the physiological basis for the development of higher animals, by making possible the storage and transportation of oxygen."

— Letter from Max to Harold Himsworth, October 1959

The Heavy Atom Breakthrough

As a student he had successfully taken X-ray photographs of horse haemoglobin crystals. These photographs showed a pattern of diffracted spots of different intensities, which encoded the arrangement of atoms in the crystal. Based on a painstaking and time-consuming analysis of the spots, in 1948 Max proposed a model of the way the protein chain folded in the molecule — only for it to be casually dismissed as incorrect by his own graduate student, Francis Crick.

X-ray photograph of horse hemoglobin crystals



Low-resolution model of hemoglobin, 1959

It was impossible to interpret the pattern without more information. In 1953 Max made the important discovery that he could obtain this extra information by growing hemoglobin crystals containing different heavy atoms, such as mercury. The differences between the patterns with and without mercury would provide the data he needed. But growing the crystals and analyzing the results was still very difficult.

In 1957 his junior colleague John Kendrew became the first to publish the structure of a protein using Max's heavy atom method. The protein was another oxygen-carrying molecule — myoglobin from the muscles of the sperm whale — which was a quarter of the size of horse hemoglobin.

The First Protein Structures

In 1959 Max finally had a structure for hemoglobin — 22 years after he took his first X-ray photograph. He was intrigued to see that each of the four chains that made up one molecule of horse hemoglobin looked very like the single chain of whale myoglobin. For the first time, X-ray crystallography had revealed evolutionary relationships at the level of individual molecules.

1959–2002

The Summit

Until 1947 Max had held no permanent position at the University of Cambridge. That year the UK's Medical Research Council (MRC) made him the head of a new Unit for Research on the Molecular Structure of Biological Systems. By the end of the 1950s not only had the unit produced the first protein structures, but its members James Watson and Francis Crick had also published the double helix structure of DNA.

Max's team outside "the hut" in Cambridge that housed his lab in the 1950s

The LMB — Nurturing Nobel Prize-Winners

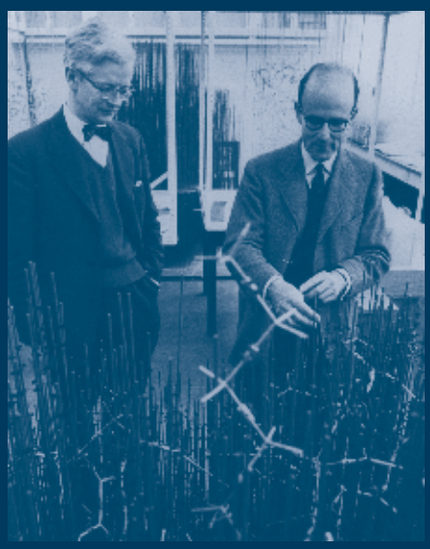
The MRC decided to found a separate institute in Cambridge, the MRC Laboratory of Molecular Biology (LMB), with Max as chairman. It was opened by the Queen in May 1962, and brought together leading scientists, including the Nobel Prize-winning protein chemist Fred Sanger. That autumn brought Nobel Prizes to Max and John Kendrew for their protein structures, and to James Watson and Francis Crick for the double helix of DNA. To date, nine further Nobel Prizes have been awarded for work conducted in the distinctively egalitarian research culture fostered by Max at the LMB.

"Unravelling the anatomy of the haemoglobin molecule may have needed much perseverance ... but comparatively little of the imaginative power which made the giants of the scientific revolution ... I stand in awe of the company which I am now supposed to join."

— Speech of thanks by Max following the Nobel banquet, 1962

The "Breathing Molecule"

Max continued to head a research team and was happiest in his lab. He discovered how the shape of the molecule changed between its oxygenated and deoxygenated state, "breathing" in response to the changing concentrations of oxygen and carbon dioxide. He looked at the genetic adaptations of hemoglobins in species from crocodiles to migrating geese, which enabled them to survive in variable levels of oxygen. And he studied the way mutations in the globin genes disrupt hemoglobin's function in people with diseases such as thalassemia and sickle cell disease, launching the whole field of molecular genetics.



Max F. Perutz and John Kendrew with high-resolution haemoglobin model

View From the Top

For Max, science was a vocation. Its aim was to increase human understanding and well-being, as well as being of value for its own sake. He loved art, music and other products of human culture, and always perceived scientific discovery as equivalent to these acts of creation.

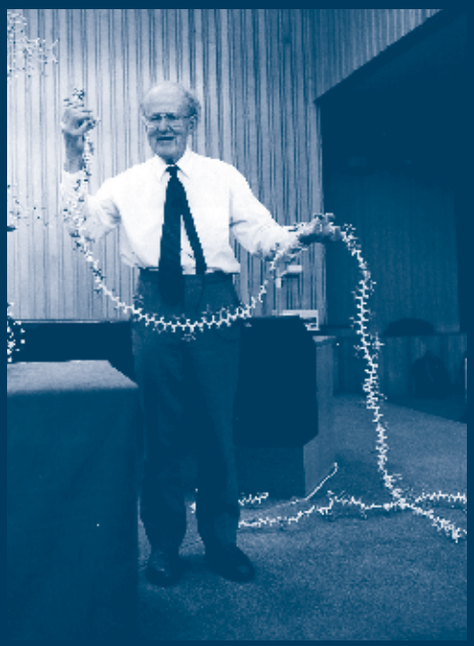
His Nobel Prize made him a celebrity, and he used his fame to write a series of articles in literary magazines exploring the role of science in society. His cultural legacy is preserved in the books of collected essays he published.

Max acknowledged that the benefits of technological progress needed to be balanced against its risks, and was an outspoken opponent of nuclear weapons. As a member of the Pontifical Academy of Scientists, he argued that improving the health of women and children, and ensuring the survival of humanity, depended on universal access to contraception and policies to encourage its use. He also believed that scientists had a duty to champion human rights. Drawing on his own experience of wrongful detention, he personally campaigned against political imprisonment, torture and other forms of oppression.

He had no religious belief, but he respected the beliefs of others. His simple view of ethics was that "even if we do not believe in God, we should try to live as though we did." Max greets Pope John Paul II, 1983

"Imagination comes first both in artistic and scientific creation."

— Max F. Perutz, Is Science Necessary?: Essays on Science and Scientists, 1991



Biology today owes a debt to Max and other pioneers who demonstrated the value of exploring molecular structures. But his life also shows how to practice science with compassion and humility. "In science," he reflected, "truth always wins."

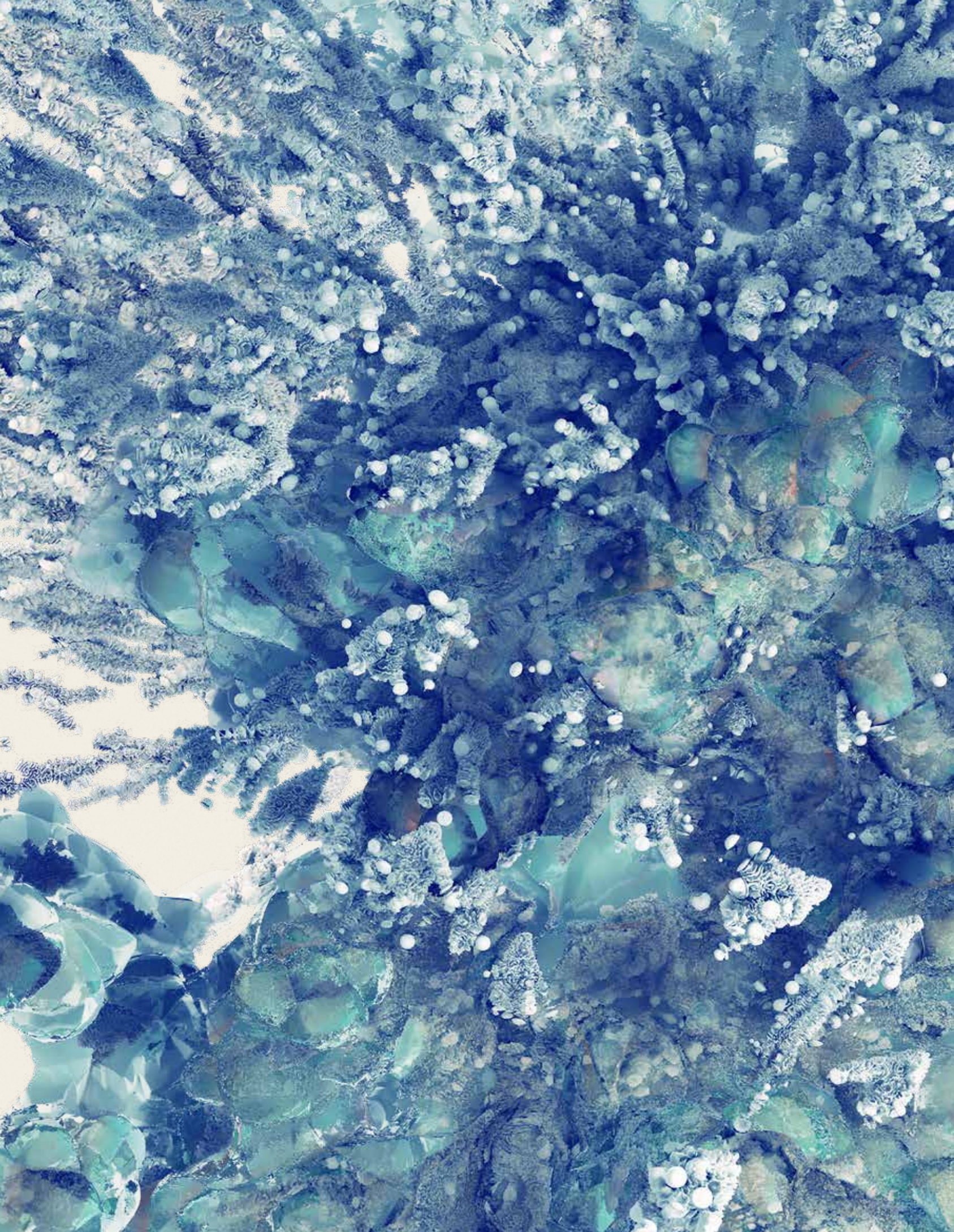
Breathing at High Altitude: The Film

Commissioned by the Max Perutz Labs, this short film parallels mountain climbing to the ambitions that drove Max Perutz in his quest to solve hemoglobin's structure. "Breathing at High Altitude" employs the metaphor of high-altitude respiration to convey the intricate molecular dynamics of hemoglobin. Set against the breathtaking Arlberg massif in the Austrian Alps, the film offers a visually stunning journey. Leading the way is Björn Heregger, an Austrian renowned for his mastery of extreme skiing. The film, directed by Harry Putz and buero bauer, made its debut at the scientific exhibition and was also featured at the Free Ride Film Festival.


“where the mind is without fear”
SCAN THE CODE – PLAY THE MOVIE – SCAN THE CODE – PLAY THE MOVIE –

"Science has an existentialist quality — it aims to answer questions about how the world works but, more importantly, it also creates new questions. Through my art, I want people to feel that deep human sense of wonder at the marvels of our world, and I want to challenge our ideas of how knowledge is formed and the nature of knowledge itself."

— Markos R. Kay



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Photos

p. 12	MedUni Wien/feelimage; Universität Wien/Johannes Hloch
p. 14	MRC LMB Visual Aids (L. Passmore); NYU Langone Health, Perlmutter Cancer Center (B. Neel); courtesy of C. Arrowsmith; Uwe Dettmar (I. Dikic)
p. 60	Hallbauer & Floretti
p. 74–76	Courtesy of A. Schoenenwald, Y. Marquez, D. Serwas
p. 77	Reiner Riedler
p. 78	Anastassiya Redko
p. 90	Gruppo Cimbali S.p.A.
p. 111; 118–123	Breathing at High Altitude exhibition. Many thanks to Vivien Perutz (Cambridge) for allowing us to reprint pictures that are owned by the Perutz family. MRC Laboratory of Molecular Biology, Fotografia Felici, WikiCommons, Österreichische Nationalbibliothek, Perutz Family, Illustrated London News/ Public Domain
p. 124–125	Breathing at High Altitude film. Harry Putz, buero bauer
All other images:	Max Kropitz and buero bauer for Max Perutz Labs Vienna

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Markos R. Kay

Markos R. Kay (MRK) is best known for the artificial-life video art experiment aDiatomea (2008), first exhibited at Ernst Haeckel's Phyletic Museum, the generative short film The Flow (2011), shown worldwide, and the series of particle simulation paintings Quantum Fluctuations (2016), now part of the Fidelity Art Collection. His art and design practice ranges from screen-based media to print and has been featured in museums, exhibitions, festivals and publications such as the ArtScience Museum, Museum of Contemporary Digital Art, Bill and Melinda Gates Foundation, Ars Electronica, National Geographic, Wired and VICE.

MRK has worked with various scientific, government and art organizations including: MIT, Belfast City, European Parliament, Howard Hughes Medical Institute, Simons Foundation, National Hemophilia Foundation, and Playgrounds Design Festival. He has also worked with commercial clients such as: Apple, Fox, Disney, Nike, Adidas, Maserati, Ford, MTV, Nvidia, BBC, Vimeo, Warner Bros and Channel 4.

In tandem with his art and professional practice, he has worked as lecturer of design and animation at Chelsea College of Art & Design and the University of Greenwich. Between 2016 to 2020 he was Pathway Leader of Animation Arts at the London College of Communication, University of the Arts London, where he collaborated with partners such as the Barbican, the Horniman Museum, Stanley Kubrick Archives, Imagine Science Films and others.

In 2016 MRK became disabled as a result of a chronic neuroimmune disease, confining him largely to his bed by 2019. Despite these challenges, he perseveres in his artistic endeavors through AI-based experiments and traditional analog drawings.


maxperutzlabs.ac.at
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