

IMP 2025
RESEARCH
REPORT

SHAPING THE FUTURE NOW

About the kaleidoscope visuals

The report's art direction transforms scientific data into a visual experience that invites readers to look closer.

A kaleidoscope creates rhythm from one fragment, drawn from research group diagrams, fluorescence microscopy, and model organisms, which is mirrored time and again to produce predictable cycles of symmetry, like petals around a center, triangular wedges, or rotating star patterns.

You will see this repetition of geometric shapes and colors throughout the report.

Download all kaleidoscope designs
as mobile and desktop wallpapers:

www.imp.ac.at/downloads



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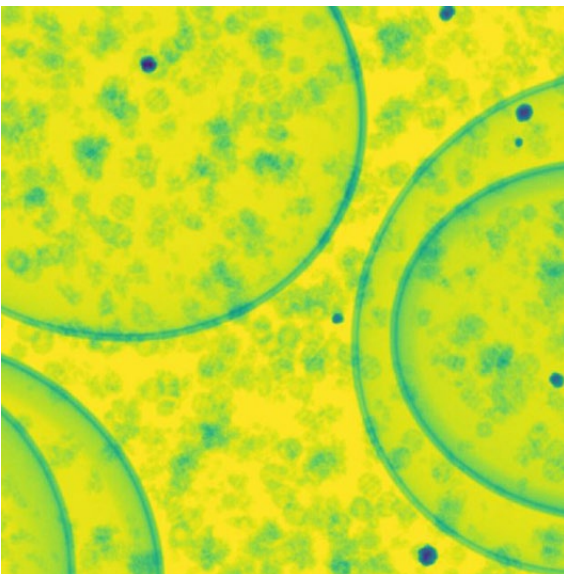
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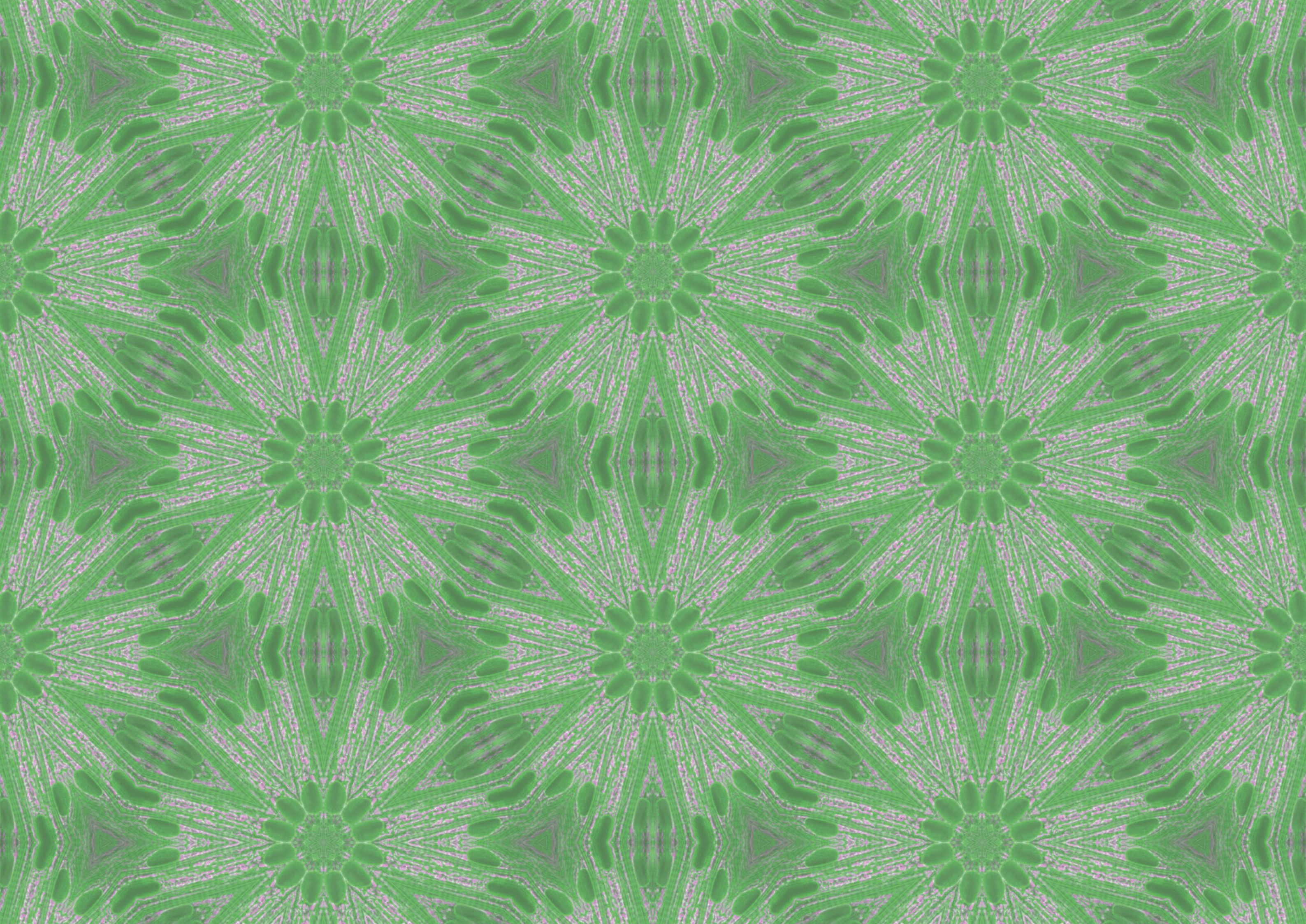
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Discovery does not happen in isolation. Every breakthrough at the IMP is made possible by organizations that believe that fundamental research matters—and that choose to invest in curiosity, talent, and long-term scientific vision.

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Test your knowledge of the institute's science, history, and community, or flip back through the IMP Research Report and Facilities & Community to track down the answers.

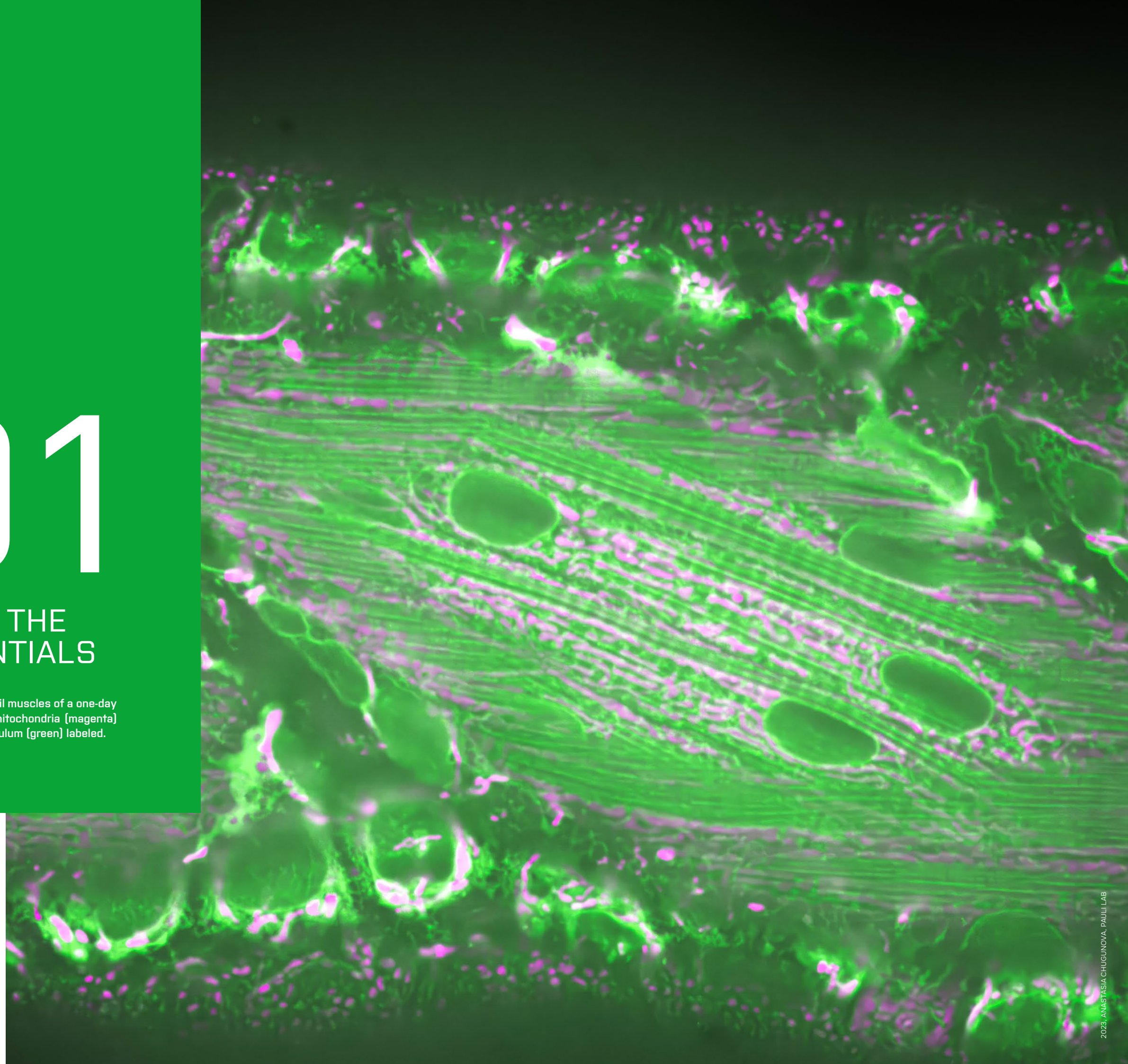
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01

IMP: THE ESSENTIALS

Section through the tail muscles of a one-day zebrafish larva with mitochondria (magenta) and endoplasmic reticulum (green) labeled.



What's special about this report?

A reflection of the IMP's 40 years, a comprehensive inventory of milestones passed and challenges met: this would be a traditional research report; but this is not what you are holding in your hands.

What you are holding in your hands is the endpoint of a year-long process that connected people. People at the IMP, at IMBA, in services shared by these two, and other organizations. Peers, stakeholders, partners. In short, people who care about the IMP and its mission.

This report targets the many people who truly care about the IMP—and they were actively involved in creating it. Seen here are Michaela Pagani, Shenzhi Chen, Alexander Stark, and Nikola Tesla (external).

When this project was started, the defined goal was to avoid creating a traditional research report that some external readers flick through once and then discard. This report targets the many people who truly care about the IMP—and they were actively involved in creating it.

Lists and supportive data were largely moved online—you will find them via QR codes. This freed up space. Space that was given to magazine-style stories, suggested by the community through surveys and actions on campus. A journalist, tasked with finding an outsider's perspective on the campus, started by attending a social hour to soak up some of the campus spirit. This was the starting point of an intense effort to capture diverse and fresh views on the IMP, IMBA, and everything in between. Interviews she conducted involved colleagues from all trades and backgrounds, from directors to participants of the 40-year anniversary symposium. Themes under the heading of "40 years of finding out" were captured.

Feedback on these magazine-style stories and other elements of the report was collected in several stages and in diverse focus groups. The photography that goes with the stories centers on people, and just like the stories themselves, it was developed through a series of consultations and photo sessions with plenty of input from the community.

The journey that led to this publication drew from many people and was at least as important as the final product. Collaborative, determined, fun. A process that reflects the essence of this campus: the people who imbue it with life.



What has made the IMP work?

IMP Directors Harald Isemann and Jan-Michael Peters on 40 years of curiosity, the importance of trust and freedom in research, and how the institute is preparing for a data-intensive future.

The IMP at 40. First thing that comes to mind?

Harald Isemann: (laughing) Wow. That old?!?

Jan-Michael Peters: It's been a history of discoveries driven by the freedom to pursue curiosity-driven research without major limitations. People can pursue projects that are important and long-lasting.

Harald Isemann: And what's grown out of and around the IMP over those 40 years is impressive. From 70 to 80 pioneers on campus in the late 1980s, we now have almost 3000 people on site. At the start, Vienna wasn't recognized as a hub for molecular biology. The IMP was founded in an old industrial area, far from established research centers, which posed significant challenges but created an opportunity to build a scientific community from the ground up.

The IMP has 40 years of alumni now. How is the institute connecting with them?

Jan-Michael Peters: The Vienna BioCenter academic training team launched an integrated platform for alumni from IMP, IMBA, GMI, and Max Perutz Labs. Within nine months of the March launch, the platform had grown to nearly 1000 members from around the globe.

Four decades is a long time. How do you sustain that?

Jan-Michael Peters: Successful research needs first-class infrastructure and strong funding, but ultimately it needs the right people. Scientists who are creative, curious, rigorous, ambitious, fearless, yet at the same time realistic about which projects are feasible. It's all about people.

Harald Isemann: Many scientists come here for the collaborative environment. For example, Senior Group Leader Andrea Pauli turned down an offer from MIT to join the IMP, drawn by the institute's spirit and innovative environment. Group Leader Francisco Balzarotti, a physicist from Stefan Hell's lab at Max Planck Institute for Multidisciplinary Sciences, chose the IMP to develop novel microscopy techniques in collaboration with biologists. Between 15 and 20 percent of our publications involve collaborations between at least two IMP research groups, and that has increased over the past five years.

Jan-Michael Peters: Yes, how well these people work together matters. The institutional setup here allows scientists to focus most of their time on scientific discovery. That requires excellent infrastructure, maintenance, service facilities, equipment, and talented support staff.

What kind of research does that setup allow?

Jan-Michael Peters: Science is about realizing how many things you don't know and having the freedom to pursue that unknown. Former Group Leader David Keays spent more than a decade searching for magnetoreception in animals. Despite uncertain outcomes, the IMP provided dedicated infrastructure, including a room shielded from external magnetic fields and high-end microscopy techniques. This research recently resulted in a breakthrough publication in the journal *Science* that provides insight into the fundamentals of magnetic sensing.

110+

publications with contributions
from IMP scientists in 2025



ANNA STÖCHER

IMP Directors Harald Isemann and Jan-Michael Peters

The IMP is constantly changing. What does that look like?

Jan-Michael Peters: We're building infrastructure to support future research. Together with IMBA, we recruited IMBA-IMP Fellow Sven Klumpe to establish a cryo-electron tomography facility. This technology visualizes individual molecules inside cells and tissues in three dimensions and will enable important research projects across the Vienna BioCenter.

Harald Isemann: Actively recruiting new research groups is the most important investment we can make in the institute's long-term future since the incoming groups will define our scientific direction for years to come. And what gives us confidence is that even as we do that, our output hasn't slipped. We've had over 110 publications with IMP contributions this year, above our usual average despite not being at full capacity. That tells us the existing teams are as strong as ever.

So where does the IMP go from here?

Harald Isemann: As machine learning and robotics become integral to research, the structure of research groups is evolving and groups will operate quite differently in the coming years. To support this, the IMP has already taken steps to give principal investigators the infrastructure they need to adapt. For example, we recently renewed and expanded our High-Performance Computing Cluster, which now provides 3600 CPU cores, 64 NVIDIA B200 GPUs, and four high-memory nodes with six terabytes of RAM each. It's operated in partnership with other institutions on campus.

Jan-Michael Peters: Beyond those investments in high-performance computing, microscopy, and sequencing technologies, a key focus will be enhancing scientific productivity through the intelligent application of machine learning tools. These technologies will empower researchers to analyze complex data more efficiently and accelerate discovery. Having said that, the curiosity, creativity, critical thinking, and intuition of our scientists will always remain the IMP's biggest strength. ●

The IMP in its 41st year

Twelve research groups and one joint IMP/IMBA research group, world-class experts in scientific and other services, outstanding infrastructure: all these things shape the IMP, and they are all firmly aligned with a shared passion for discovery and commitment to excellence.

The Research Institute of Molecular Pathology (IMP) is a leading basic research center in the molecular life sciences. Its 12 research groups and one joint IMP/IMBA research group with scientists from 40 countries address fundamental questions in molecular biology.

Funded primarily by Boehringer Ingelheim and with unconstrained academic freedom, the IMP is the ideal environment for curiosity-driven biomedical research. As part of the Vienna BioCenter, the IMP is embedded in one of Europe's biggest life science hubs with almost 3000 people working on life science research, education, and business.

Forty years after its foundation in 1985, scientists at the IMP continue to address important problems in research areas including molecular and cellular biology; structural biology and biochemistry; gene expression and chromosome biology; stem cell biology and development; and immunology and cancer.

In pursuit of their research goals, scientists at the IMP employ the latest methods and equipment in molecular genetics, imaging, biochemistry, and structural biology on an array of model systems. This is achieved with the help of state-of-the-art core facilities.

The IMP performs innovative research at the highest level, demonstrated by many achievements. In a typical year, IMP scientists publish 60 to 90 papers in international peer review journals—an average that was exceeded in 2025.

An impressive number of grants and awards have been given to IMP scientists: as of early 2026, more than two-thirds of IMP faculty members were recipients of at least one ERC grant (a total of 25 ERC grants were awarded from 2007 to 2025); all seven Senior Group Leaders are elected EMBO members; and five Wittgenstein Awards have been presented to IMP scientists. Emeritus Director Kim Nasmyth was awarded a Breakthrough Prize for work largely done at the IMP; IMP alumna Angelika Amon was presented with the same honor for her work at MIT.

The IMP's international scope is reflected by the many outstanding scientists who visit and give lectures or seminars at the IMP every week, as well as the high-level attendance of symposia and conferences that are hosted at the IMP and other Vienna BioCenter institutes. In turn, IMP faculty enjoy great interest in their work and present ongoing research at conferences and visits to academic institutions worldwide.

To mark its 40 year anniversary, the IMP hosted a symposium that drew alumni from different periods since its founding. Many of them recalled the pioneering spirit and foresight of the earliest members, and the gradual transition as the campus grew and increased in size, influence, and complexity. Condensed into a cheerful crowd, the symposium showed that, thanks to the people who shape the institute, the IMP can afford to look to the future with optimism.

THE IMP IN 2025

252
people

40
countries

12
research groups
+ 1 joint IMBA/IMP
research group

100+
publications

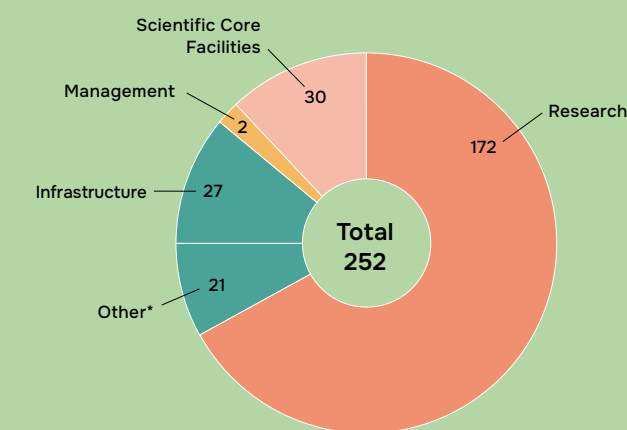
25
ERC grants*

5
Wittgenstein
Awards

* Source: <https://erc.europa.eu/projects-statistics>

STAFF BY FUNCTION

IMP's achievements are powered by a diverse, international team of scientists, technical experts, and professional support staff.

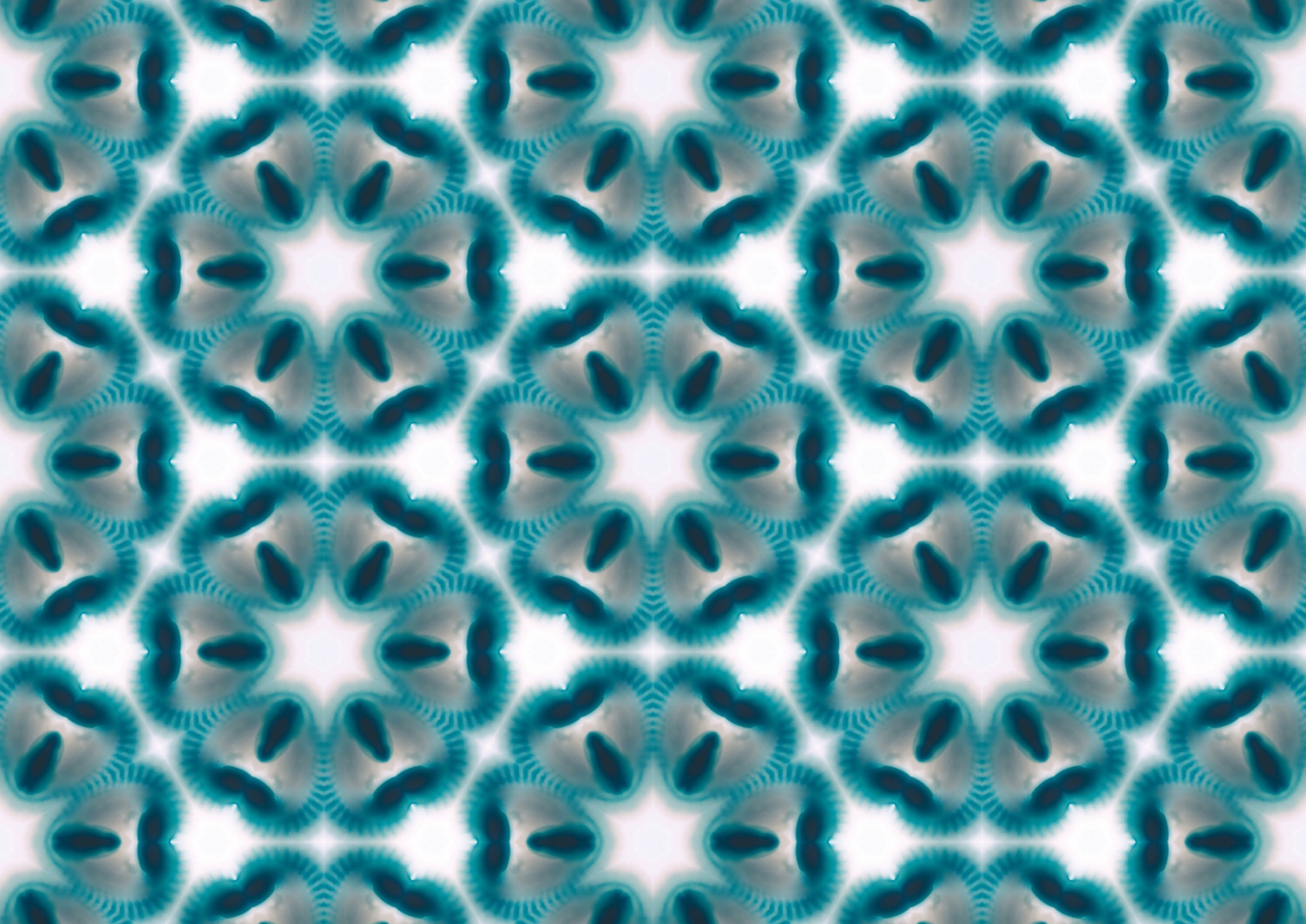


*Cafeteria, Communications, Ethics & Biosafety, Project Management Office, Scientific Training Unit

Data as of 31 December 2025



Curious?
Take a closer look at the IMP.



02

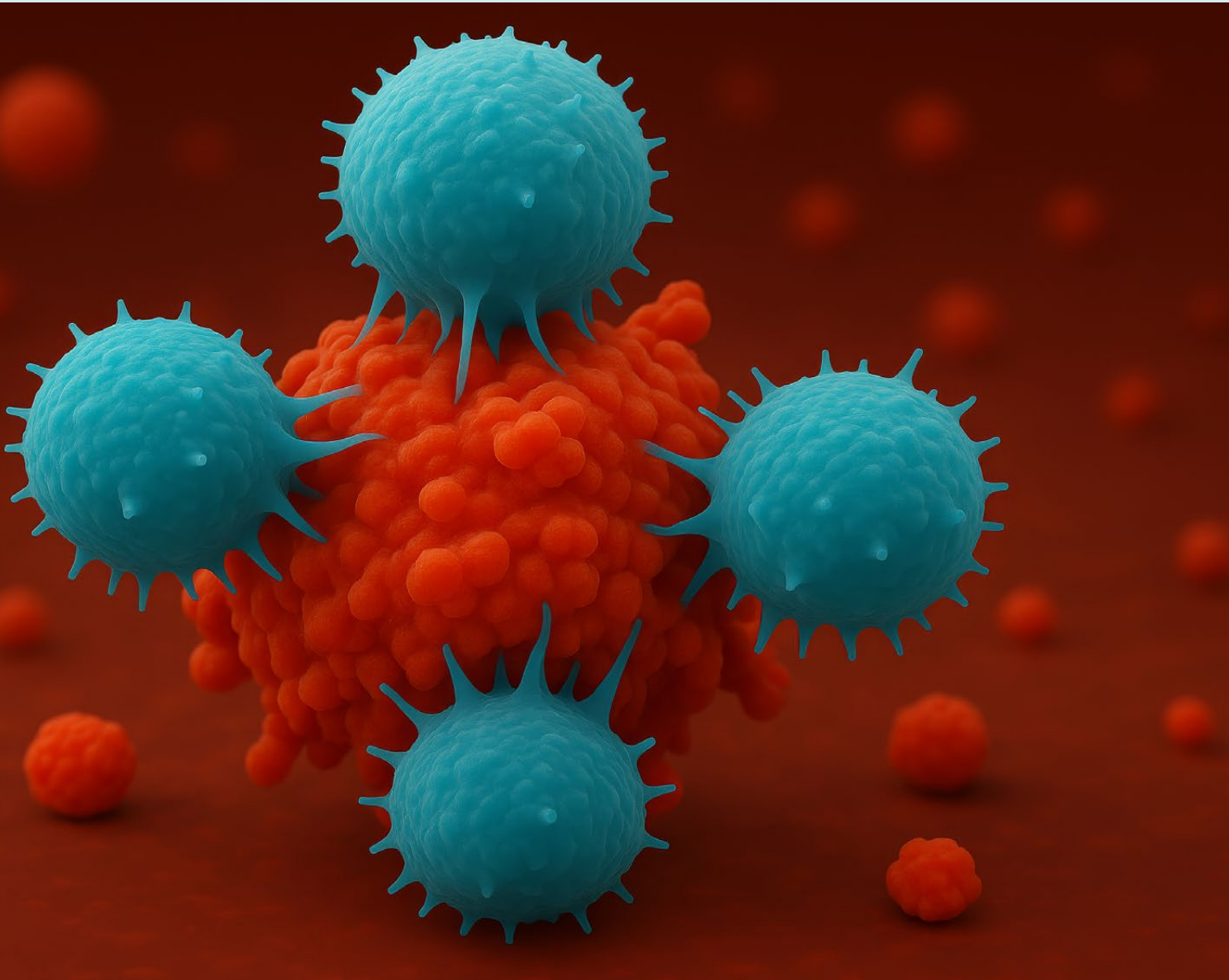
THE QUESTIONS WE CHASE

Transgenic mouse embryo (E11.5) carrying a lacZ-reporter gene with a synthetic enhancer designed to be active in the limb.



Five rules for working at speed

A key paper on immune regulation succeeded because opportunity, collaboration, and persistence aligned at exactly the right moments.



Regulatory T cells (Treg cells) keep the immune system from causing excessive inflammation or attacking the body’s own tissues. AI-generated 3D illustration of a cancer cell (red) being attacked by immune cells (blue).

When a project moves quickly, the typical roadmap doesn’t always apply. Christina Jäger, a PhD student in the van der Veecken lab at the IMP, completed her project on the immune protein Foxp3 in just 2.5 years, from first experiment to publication in the journal *Science Immunology*. The pace revealed five lessons that apply when momentum builds.

RULE 1:
When opportunity knocks, jump on it

The opportunity arrived at exactly the right time. By October 2022, the Busslinger lab had developed a new experimental model that enables inducible protein degradation with great efficiency. “They had established this model,” explains Group Leader Joris van der Veecken, “and we had been interested in working on Foxp3, an important regulator of immune responses, for a very long time. We got extremely lucky that this tool was now available for us.”

That head start was crucial. The new inducible degradation system worked in experiments on the first try, and Jäger could run her first pilot experiments just nine months after the project started. Looking back, the team recognizes how valuable it was to have this model available from the start. “At the time, we were excited, of course, but seeing how challenging it can be to develop new experimental models, we should have been even more excited,” Jäger says.

“At the time, we were excited, of course, but seeing how challenging it can be to develop new experimental models, we should have been even more excited.”

Christina Jäger

The lesson is about recognizing opportunity when it appears. “A lot of it is timing,” says van der Veecken. “When a great tool becomes available, you just have to go for it.”

RULE 2:
When experiments work, don’t slow down

The project moved forward quickly. First proof-of-principle results were not a stopping point but a signal to accelerate. “If your experimental system works, you directly run with it and move to the next stage,” she explains. “If experiment results are promising, we repeat it and go from there.”

“A lot of it is timing. When a great tool becomes available, you just have to go for it.”

Joris van der Veecken

Jäger is, by van der Veecken’s account, a very organized planner. Her approach was to focus on coordinating multiple experiments in parallel with the help of her colleagues. “The pace was very high, but this also kept it very exciting,” van der Veecken says. “Sometimes a project can drag on for years, and it’s hard to keep that same level of energy and enthusiasm.”

RULE 3:
When your friend is ten meters away, ask

The experiment that provided the paper’s key finding started with a collaboration just down the hall. Jäger wanted to test whether Foxp3 degradation would affect tumor-infiltrating Treg cells differently than those in healthy tissue, but at that time no one in the van der Veecken lab had experience with tumor models. A friend and fellow PhD student from the Obenauf lab, Guillem Estivill, worked nearby. “We came up with the idea just a few weeks before starting the experiment,” Jäger says. “Since all expertise was already in place, I simply reached out to the Obenauf lab to discuss setting up the model.”

Estivill and Senior Group Leader Anna Obenauf provided the tumor cells and training. From initial idea to first tumor cell experiments took just three weeks, fast for this type of experiment. For Jäger, the significance was clear. “Since the tumor model ended up being the crucial experiment in our paper, this was a really important collaboration.” The tumor model gave very clear visual results. The size of the lymph nodes was a key indicator: giant lymph nodes meant the inflammation was uncontrolled, while normal-sized lymph nodes meant the Treg cells were suppressing the anti-tumor immune response. Seeing these effects, van der Veecken knew immediately that the system was working. This collaboration provided one of the study’s central results.

2.5

years from first experiment to publication in the journal *Science Immunology* for a study of Foxp3

RULE 4:
When rejection comes, keep collecting data

The journal *Nature* rejected them. Then *Nature Immunology*. Then *Science*. Then *Science Immunology* offered something unexpected: they declined the paper but invited a resubmission if certain experiments were added. It was a sign that they liked the work but wanted to see more data before moving forward.

So the team kept going. “We focused on collecting more data to make the story more stable, including additional inflammation experiments,” Jäger says. This involved further experiments and repetitions to strengthen the core findings.

The publication journey began with the initial submission in May 2024 and continued through October. When the manuscript status finally changed to “in revision,” Jäger remembers the moment clearly. “It was exciting because that was the first real sign that the paper had a chance of being published.”

“The pace was very high, but this also kept it very exciting. Sometimes a project can drag on for years, and it’s hard to keep that same level of energy and enthusiasm.”

Joris van der Veeken



Christina Jäger, a PhD student in the van der Veeken lab at the IMP.

RULE 5:
When the Nobel Committee recognizes your field, share the news

“It’s great to see the field getting this kind of attention.”

Christina Jäger

The 2025 Nobel Prize in Physiology or Medicine recognized discoveries about immune tolerance and regulatory T cells. Not just the field Jäger works in, but the exact protein she studies: Foxp3, the master regulator. The scientific background document for the Nobel Prize even referenced the lab’s recent work.

For the van der Veeken lab’s first publication, having the Nobel Committee recognize the field has been very encouraging for the lab’s research direction, and has also helped communicate the significance to people outside the field. “You can show them that the questions we’re asking in the lab are considered fundamentally important,” says Jäger. “It’s great to see the field getting this kind of attention.” ●

PUBLICATION

Jäger C., Dimitrova P., Sun Q., Tennebroek J., Marchiori W., Jaritz M., Rauschmeier R., Estivill G., Obenauf A., Busslinger M., & van der Veeken J. “Inducible protein degradation reveals inflammation-dependent function of the Treg cell lineage-defining transcription factor Foxp3.” *Science Immunology*, DOI: 10.1126/sciimmunol.adr7057

ACKNOWLEDGMENTS

Research projects are teamwork involving authors and others. The work leading to this paper is no exception, with support drawn from and beyond the Vienna BioCenter. Focusing on local contributions, the authors would like to highlight Christian Theussl and Jacek Rodegar Wojciechowski at the IMP/IMBA Transgenic Service facility; staff of the IMP/IMBA shared Comparative Medicine facility; the IMP/IMBA/GMI BioOptics facility for help with flow cytometry and cell sorting; the VBCF Preclinical Phenotyping facility for help with osmotic pump implantation; and the VBCF Next Generation Sequencing facility for high-throughput sequencing and data preprocessing.

A friend and fellow PhD student from the Obenauf lab, Guillem Estivill, worked nearby. “We came up with the idea just a few weeks before starting the experiment,” Jäger says. “Since all expertise was already in place, I simply reached out to the Obenauf lab to discuss setting up the model.”



ANNA STANESCU

Understanding Foxp3 and Treg cells

Regulatory T cells (Treg cells) keep the immune system from causing excessive inflammation or attacking the body’s own tissues. They do this by suppressing immune responses once a threat has passed. The transcription factor Foxp3 defines these cells and has long been thought to be essential for their identity and function, until a recent 2025 paper from the lab of Joris van der Veeken in the journal *Science Immunology* showed that this is not always the case.

Using a technique that allows precise, temporary breakdown of proteins, the scientists were able to remove Foxp3 from mature Treg cells without affecting their development. They found that in healthy, non-inflamed conditions, Treg cells can survive and function even without Foxp3. However, during inflammation, such as infection, autoimmunity, or within tumors, Foxp3 becomes critical for Treg cell survival and suppressive activity.

A systemic depletion of Foxp3 removes the protein from every Treg cell. While the protein was absent in all T cells, the effect was largely limited to Treg cells inside tumors, where inflammation is present. This reduced the immune suppression specifically in the tumor environment, leading to a strong anti-tumor immune response. Importantly, this boost in immunity did not trigger widespread inflammation or autoimmune side effects in healthy tissues.

The findings suggest that Foxp3 is a context-dependent regulator: essential during immune activation, but not during immune calm. Targeting Foxp3 in active tumor settings could therefore provide a more precise and potentially safer approach to cancer immunotherapy by enhancing immune attacks on cancer while preserving immune balance elsewhere.

Spotlight on research

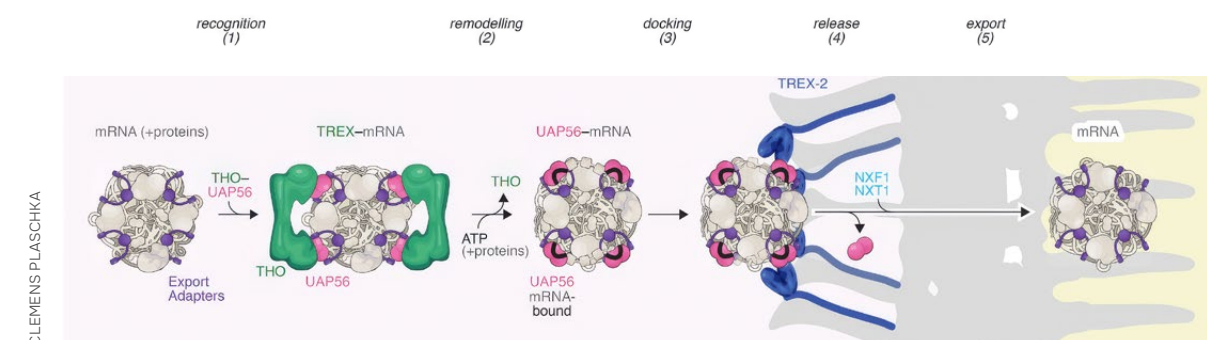
In 2025, IMP scientists published more than 100 research papers. Across these publications, IMP researchers explored questions spanning genome organization, development, immunity, regeneration, cancer, and cellular mechanisms.

IMP & IMBA

Putting the pieces together: mRNA export from the nucleus

Cellular information is stored in DNA and put into action by proteins. However, between the two lies a third molecule, the crucial carrier of this information—messenger RNA (mRNA). To help build proteins in the cytoplasm, mRNA must first get out of the DNA-storing nucleus. Although the factors involved in getting mRNA “out” have been discovered over the past 30 years, how these factors orchestrate this export process had been unclear.

In 2025, the Plaschka lab at the IMP, in collaboration with the Brennecke lab at IMBA, put these decades-old puzzle pieces together, unveiling the big-picture view of the mRNA nuclear export pathway. Combining structural, biochemical, and cellular approaches, they revealed that the mRNA-clamping protein UAP56 directs mRNAs through multiple remodeling events, culminating with the docking of mRNAs at the nuclear pore complex to begin export.

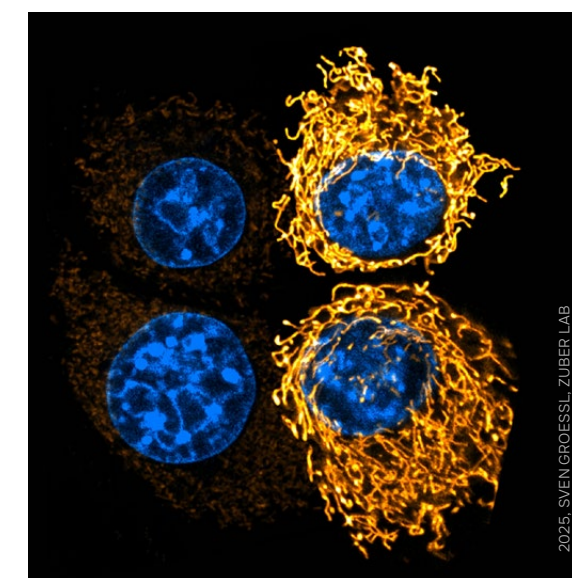


IMP & IMBA

Boosting protein research with new mass spectrometry technology

Cross-linking mass spectrometry allows scientists to freeze-frame and study protein interactions. However, this approach is limited by its sensitivity—many important interactions are too rare or too weak to detect because their signals are easily drowned by more abundant peptides.

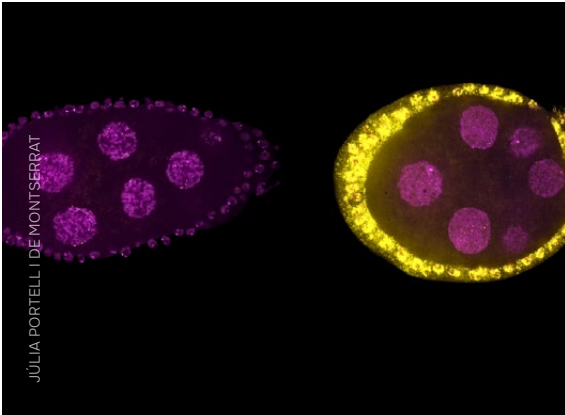
Using the new Orbitrap Astral mass spectrometer, researchers at the Proteomics Tech Hub developed an improved protocol able to identify 40 percent more crosslinks from the same samples, allowing scientists to identify and explore protein connections to an unprecedented level, detecting previously unseen surface interactions and even rare connections buried deep within the proteins themselves.



How cancer turns sour into power

Cancer cells are masters of survival. Inside a tumor, they face a hostile environment where nutrients are scarce, oxygen is limited, and waste products accumulate—conditions that would kill most healthy cells. Yet, cancer cells manage to keep growing by reprogramming their metabolism, drawing energy from any resource at hand.

Using innovative CRISPR-based genetic screens in tumor models, the Zuber lab discovered that acidosis—souring owing to the build-up of metabolic byproducts—acts as a master switch in energy metabolism. By triggering mitochondrial fusion and boosting energy production, acidosis promotes stress resilience, enabling cancer cells to thrive where normal cells perish.



IMP & IMBA **The beginning of the end: how PIWI proteins protect animal genomes**

“Jumping genes” can severely harm animal genomes when uncontrolled. To defend against these genes, animal cells use small RNAs—piRNAs—and PIWI proteins. How these RNAs and PIWI proteins begin genome defense and how this is regulated has remained a key unresolved question.

Researchers in the labs of Clemens Plaschka at the IMP and Julius Brennecke at IMBA uncovered the first steps of the PIWI-piRNA pathway. Combining AlphaFold-based modeling of protein-protein interactions with genetics, biochemistry, and cell biology, the team identified a sequence of events by which silencing begins once a PIWI-piRNA protein complex engages with a transposon sequence. Specifically, the team identified Piwi’s main interactors in the nucleus and the cytoplasm, which mediate Piwi’s different functions in the two cellular compartments. These molecular interactions are highly conserved from sponges to flies and humans, highlighting their crucial and evolutionary ancient role in protecting the genome.

Inside the cell’s quality-control hub: unveiling the architecture of UBR4

To keep cells fit, quality control systems detect misfolded, damaged, or misplaced proteins and swiftly remove them before they can cause harm. Essential to this process is URB4, a protein that detects ubiquitin-“tagged” proteins and processes them for degradation. However, how URB4 performs this function was poorly understood.

Scientists in Tim Clausen’s lab captured the first snapshot of URB4 working together with its cofactors KCMF1 and CALM1. Using cryo-electron microscopy, the team showed that these proteins form a giant ring-shaped complex that serves as a hub where faulty proteins are brought in, inspected, and processed for degradation. They also showed that URB4 identifies damaged proteins through a combinatorial code that includes signals from other ubiquitin ligases. This overlap establishes coordinated degradation pathways that target unassembled orphan proteins and safeguard the cellular proteome, a function linked to aneuploidy and tumor biology.



DANIEL BEN GRABARCZYK



IMP & IMBA **Making diagnostics simpler, cheaper, and open-source**

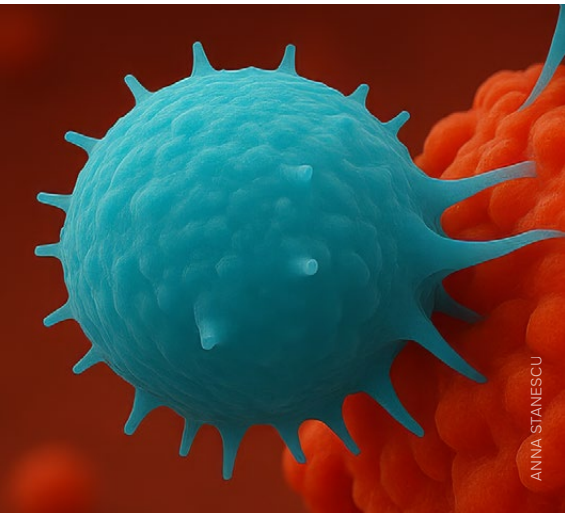
Access to reliable molecular diagnostics in low- and middle-income countries is often limited by high costs and complicated logistics. Scientists from the Pauli lab at the IMP and the Brennecke lab at IMBA, together with collaborators in Ghana, presented a powerful alternative: a fully open-source, freeze-dried diagnostic assay based on RT-LAMP technology. This colorimetric assay is especially useful for rapid, inexpensive pathogen detection in resource-limited settings.

The open-source nature of reagents, including the heat-stable, home-made enzymes that can be produced by diagnostics labs themselves, expands its applicability to low-resource areas worldwide. As a proof-of-concept, the freeze-dried RT-LAMP reaction mixes were tested in Ghana in 2025 and delivered diagnostic performance on par with assays run in Vienna.

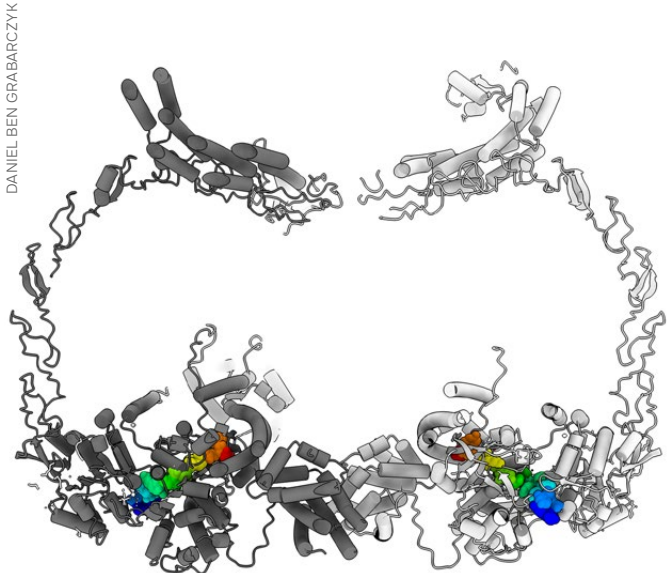
Releasing the brakes on the immune system

When the immune system is triggered—by infection, injury, or cancer, for example—it launches a coordinated defense to eliminate the threat. But an immune response that goes unchecked can do more harm than good. Regulatory T cells (Treg cells) act as the immune system’s brakes, suppressing other immune cells to prevent excessive inflammation and autoimmune reactions. This function is mediated by the transcription factor Foxp3.

Using a new method to temporarily control Foxp3’s degradation, scientists in the labs of Joris Van der Veeke, Anna Obenauf, and Meinrad Busslinger found that Foxp3 is essential only during inflammation, when Tregs are activated. The team also discovered that breaking down Foxp3 triggers a strong immune response against tumors, providing a potential new therapeutic strategy to improve cancer immunotherapy.



ANNA STANESCU

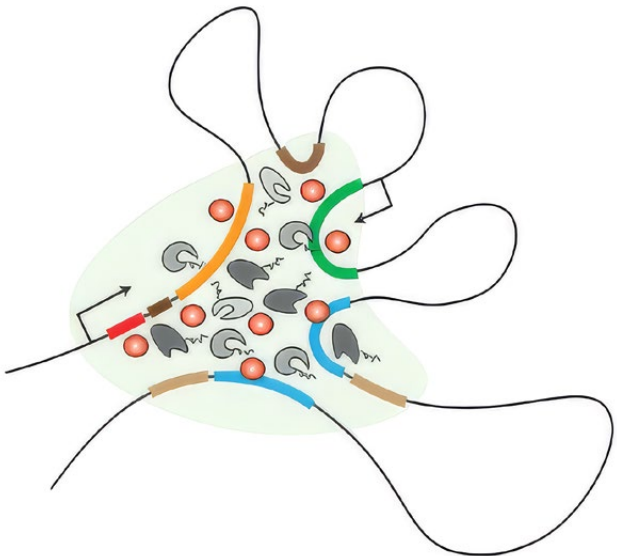


DANIEL BEN GRABARCZYK

ZNFX1 compacts and tags RNA to keep immunity in check

Organisms from plants and bacteria to humans have developed intricate defense systems to detect viral invaders and shut them down. However, if these systems are not tightly regulated, the immune system can overreact and attack the host, leading to autoimmune disease. While the protein ZNFX1 is key to keeping this delicate balance, its molecular function was unclear.

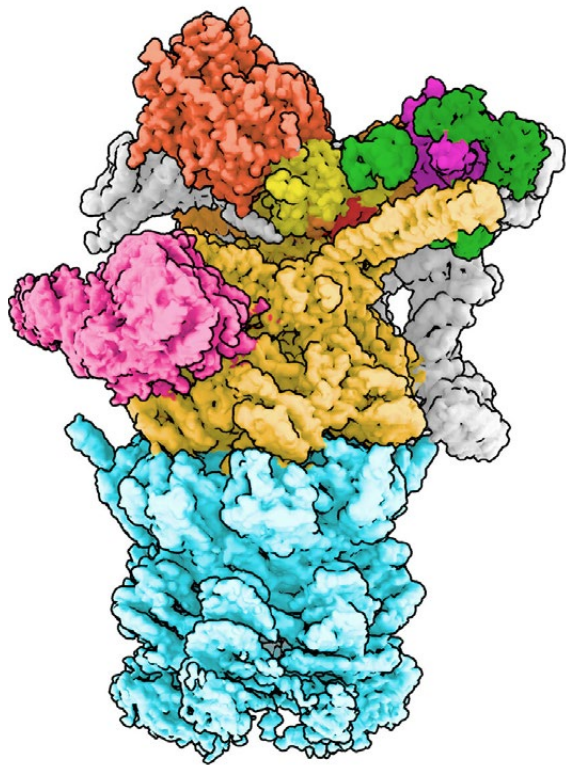
Researchers in Tim Clausen’s lab combined structural biology, enzymology, and cell biology to study ZNFX1 in detail. They discovered that ZNFX1 binds to long RNAs and then performs a highly unusual reaction: it compacts these RNAs into condensates and attaches ubiquitin both to the RNA and to itself. By extending ubiquitin signaling to RNA, ZNFX1 helps regulate the production of viral and immune proteins, allowing cells to fight infection while avoiding harmful autoimmune responses.



How human antibodies get better at fighting infections

Antibodies are essential to adaptive immunity, recognizing and neutralizing pathogens. After an initial response, B cells improve and diversify their antibodies to refine their response against a certain antigen. This antibody maturation depends on two independent processes—somatic hypermutation and class switch recombination—that take place very closely within the same genetic sequence while seemingly not affecting each other.

Prior to the lab’s move to King’s College London, researchers led by Rushad Pavri studied how these two processes can occur at the same time and discovered that the DNA can form a flexible structure that accommodates both processes. The team studied three-way interactions between DNA regions and showed that this structure is independent of the molecular motor cohesin, challenging previous models of antibody maturation.



How cells decide on the life or death of a protein

Every eukaryotic cell needs a waste disposal system to stay healthy and function properly. Damaged and unwanted proteins are tagged with ubiquitin and transported to the proteasome for degradation. Scientists have long known that ubiquitin tags can be arranged in different shapes, but how the proteasome reads and interprets these messages was unknown.

Researchers at the cryo-Electron Microscopy Technology Platform led by David Haselbach provided the first high-resolution view of the human proteasome, revealing how it reads ubiquitin signals to determine the life or death of a protein. Using cryo-electron microscopy, the team built a 3D model of the human proteasome and how it interacts with ubiquitin chains. They showed that this interaction is more complex than expected, ensuring accurate proofreading so that only the right proteins are degraded.



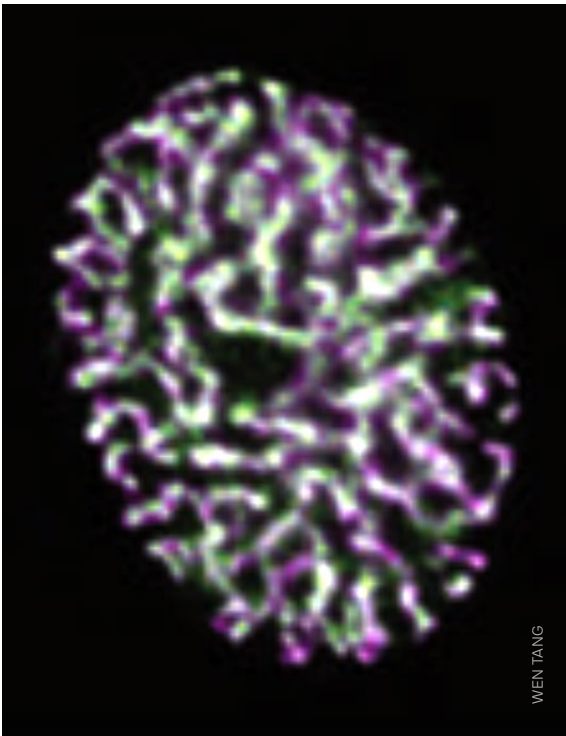
Watch how the human 26S proteasome interacts with a K48-linked tetra-ubiquitin chain.



Unprecedented protein quantification in single cells using advanced proteomics

Single-cell proteomics enables the study of protein expression and function at the level of individual cells. By revealing details that are not detectable in bulk analysis, the field is transforming how scientists study proteins and their impact on cellular behavior.

Researchers at the Proteomics Tech Hub led by Karl Mechtler, in collaboration with Thermo Fisher Scientific and Nicolas Rivron’s lab at IMBA, developed a new workflow that can quantify up to 5300 proteins in a single cell at unprecedented accuracy. The researchers performed single-cell proteomics on blastoids—stem cell-based models of the early human embryo—and were able to detect significant differences in protein expression among cells in the same lineage.



Beyond loops: cohesin links DNA architecture and epigenetics

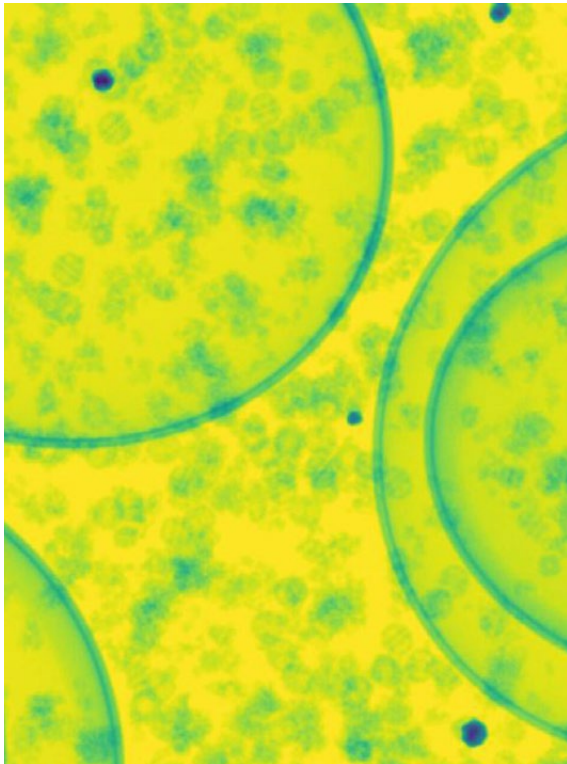
A single human cell stores two meters of DNA tightly packed in the nucleus. During the cell’s “daily life,” the molecular motor cohesin rearranges the DNA’s structure to facilitate gene expression. At the same time, epigenetic modifications in chromatin histone proteins mark DNA regions for silencing or activation. Together, both factors fine-tune gene expression and influence cell function. However, how cohesin interacts with histones was poorly understood.

Using a combination of biochemistry, microscopy, and genomic tools, scientists in Jan-Michael Peter’s lab showed that cohesin interacts with the epigenetic reader Phf2, positioning it at specific DNA sites and carrying it along chromatin. Their findings suggest that cohesin complexes may transport cargo along the DNA, revealing a new and unexpected role for this essential molecular motor.

FakET: new method advances electron microscopy with AI simulations

Cryogenic Electron Tomography (cryo-ET) enables structural biologists to capture high-resolution images of the structures inside the cell, offering a close-up view of biological processes at the near-atomic level. Despite its breakthroughs, several challenges make it difficult to identify microscopic particles within cryo-ET images.

To tackle this issue, scientists at the IMP’s Cryo-EM Technology Platform developed FakET, a data-driven method that produces fake cryo-ET images to train AI-based analysis software. Using this software, scientists can streamline particle identification in cryo-ET images, providing faster and more accurate data analysis to enable new biological insights.



Watch how FakET is transforming cryo EM particle identification with AI-driven simulation.



Explore more than 100 publications from 2025.

The image as a map

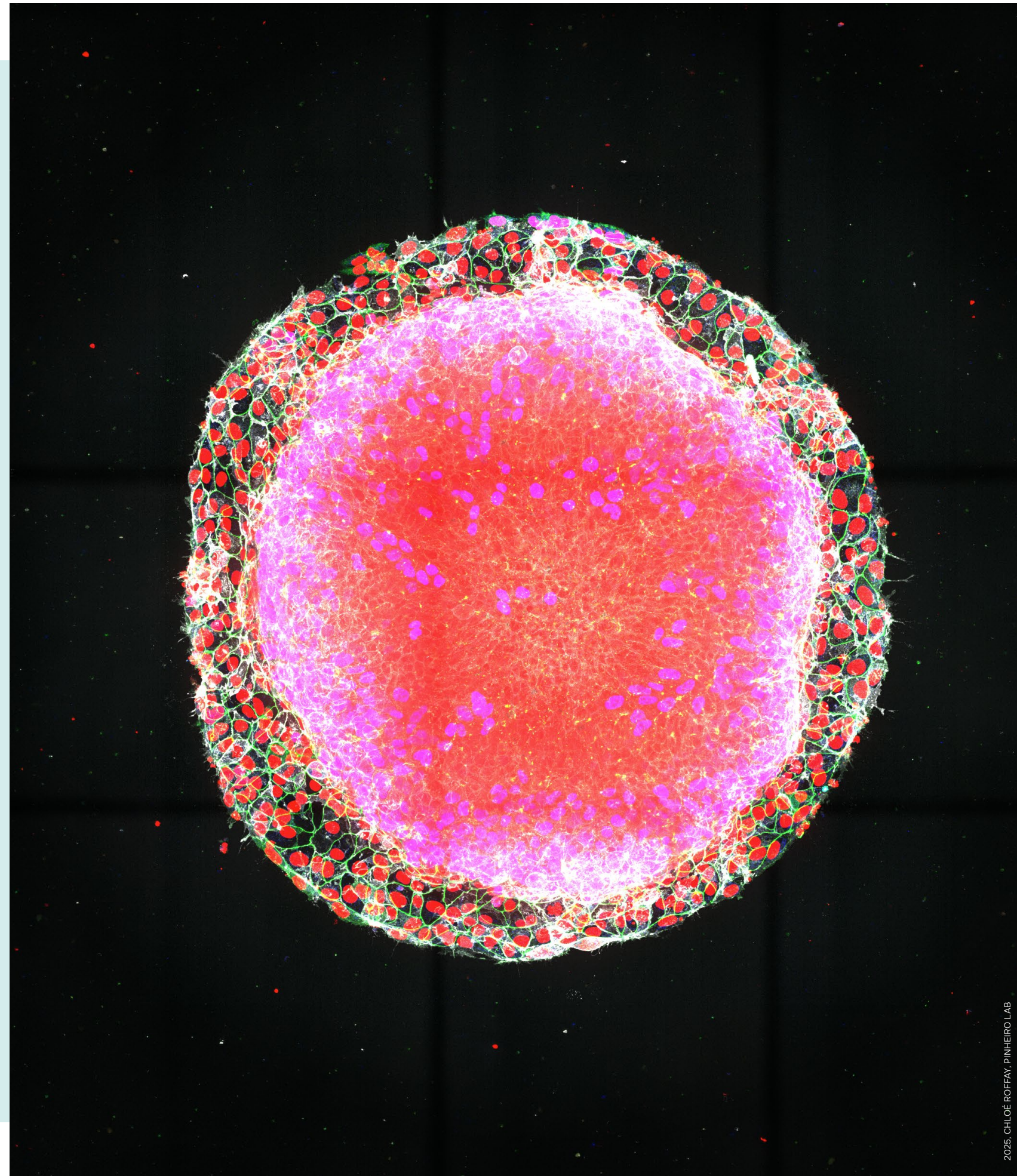
Sometimes a single image can show you exactly where a question will take you.

In science, an image can be more than a record of what happened. It can be a guide to what comes next: which question to ask, which path to follow, where the work is heading. This year, IMP postdocs and PhD students were called upon to share an image that mattered to them, one that captured a key result or communicated the direction of their research. The result is a glimpse of science in motion, seen through the eyes of the researchers driving it forward.

When cells begin to find their way

Chloé Roffay, Postdoctoral Researcher in the Pinheiro lab, works on one of the most fundamental events in development. “Gastrulation is an essential step of life,” she says. It is the process by which an embryo’s cells first take on distinct identities and physically reorganize into the earliest outline of a body, and understanding exactly how that happens is what her research is about. To study it, Roffay works with a lab-grown model called a gastruloid disc, built from human embryonic stem cells and designed to mimic the gastrulation process. The model is induced with a signaling protein called BMP4 and observed over 48 hours.

The image she shared is a portrait of that process in action. Four markers tell the story: a DNA stain called DAPI (red) reveals the nuclei of all the cells, while three specific proteins track the cells’ identity and shape. ZO1 (green) marks the boundaries facing the outside of the structure; BRA (blue) identifies the cells committing to becoming mesoderm, one of the three primary tissue layers that will eventually give rise to muscle, bone, or connective tissue; and E-cadherin (gray) marks the adhesion protein that holds cells together as they reorganize. “Our work aims to understand how fate and form occur,” Roffay says. Her image captures the exact moment those decisions are made, giving us the shape of things to come. ●



The IMP by group

In 2025, scientists at the IMP worked together in twelve research groups and one joint IMP/IMBA research group that often collaborated across labs or even institutes to address scientific questions.

Curiosity, a passion for discovery, academic freedom, and a commitment to excellence: the IMP's research groups bring together scientists at all career levels and draw from a range of colleagues in support roles. Close ties with the faculty of partner institutions such as IMBA and the GMI, as well as the wider Vienna BioCenter, ensure that the IMP's research groups thrive in a stimulating environment.



Advanced light microscopy and biophysics | BALZAROTTI LAB

The first light microscopes transformed cell biology by allowing scientists to see what happens inside cells. However, even today's most advanced instruments struggle to capture many essential processes—how RNAs are packaged, how protein complexes move, how organelles shift shape—because they unfold at scales far below conventional resolution limits.

The Balzarotti lab is an interdisciplinary team combining expertise in physics, engineering, mathematics, and biology. It builds new instruments and designs the optical and computational methods that power them. The researchers' work builds on MINFLUX, a super-resolution microscopy technique that allows scientists to pinpoint and track individual molecules in living cells with nanometer precision.

Current projects

Smarter MINFLUX microscopes: seeing molecules with fewer photons: The Balzarotti team is developing next-generation MINFLUX microscopy, a technique that pinpoints single molecules with sub-nanometric precision. Their latest advances—new beam shapes, refined mathematical models, and diverse detection strategies—dramatically boost performance, enabling longer and faster tracking of molecular dynamics.

Combinatorial DNA-PAINT multiplexing: barcoding molecules for large-scale nanoscale imaging: Studying cellular architecture often requires imaging many targets simultaneously, but fluorescence microscopy is usually limited to a handful of colors. DNA-PAINT circumvents this, using short, transiently binding DNA strands as programmable “colors,” but traditionally needs one imaging round per target—which is slow and potentially damaging.

The Balzarotti lab's combinatorial DNA-PAINT multiplexing assigns each target a DNA barcode rather than a single sequence. This allows many molecular species to be mapped at nanometer resolution in a single experiment, vastly expanding the biological questions that can be tackled.

Visualizing native mRNA structure in cells: RNA is one of the most important yet least imaged biomolecules. Conventional methods can only capture coarse features such as end-to-end distances. By combining DNA-PAINT with MINFLUX and new combinatorial labeling strategies, the Balzarotti lab can image native mRNA particles in the nucleus and cytoplasm with nanometer resolution. These approaches reveal how mRNAs are packaged, how their structures depend on splicing, and how they interact with protein partners—opening a new window into RNA biology.

LAB MEMBERS

Karina Arellano Ayala, Santiago Federico Barrera Boada, Jakub Dokulil, Alba Gomez Segalas, Juan Augusto Maya, Alessandro Passera, Lennart Piotraschke, Simon Roschger, Matthias Teuschl, Erjia Wang, Paul Weizl



Francisco Balzarotti | Group Leader



▶ How can light-based methods provide maximal information on biological processes? Francisco Balzarotti will tell you more.



Molecular mechanisms of targeted protein degradation | CLAUSEN LAB

Proteins are the fundamental building blocks of life, performing essential cellular functions ranging from building structures to processing nutrients and transporting molecules within the cell. However, damaged, unwanted, or mislocalized proteins can have devastating effects for the cell, and getting rid of them is essential to ensure cellular fitness. For this, proteins are labeled with “degradation tags” that mark them for breakdown by specialized cellular machines.

The Clausen lab studies the molecular mechanisms governing targeted protein degradation, integrating structural biology, biochemistry, and cell biology to obtain a comprehensive picture of the cellular guardians maintaining protein homeostasis. Its research provides insights with implications for infection biology, immunity, and protein homeostasis in health and disease.

Current projects

Inducible protein degradation through BacPROTACs: While studying protein degradation in bacteria, the Clausen lab discovered arginine phosphorylation as a new degradation signal, and used it to develop BacPROTACs, a system that enables targeted protein degradation in bacteria. The team is advancing this approach to selectively eliminate essential bacterial proteins—an innovation that could lay the groundwork for a new generation of antibiotics.

E3 ligases as guardians of the cell: Ubiquitin—one of the main protein degradation markers—plays a double role in immune response, helping eliminate pathogen proteins but also degrading unneeded host proteins to keep the immune response in check. The Clausen lab uses an integrative structural biology approach to dissect the function of E3

ubiquitin ligases, a group of enzymes that recognize and mark aberrant proteins for degradation. Its findings provide insights into how protein turnover maintains balance in the innate immune system, while at the same time counteracting proteotoxic stress.

Keeping muscle proteins in shape: Muscle contraction relies on myosin, a molecular motor that drives the sliding of muscle fibers. The Clausen lab investigates how cells maintain myosin in a properly folded, functional state to preserve muscle performance. Using *C. elegans* as a model organism, the team studies how disease-associated mutations trigger myosin aggregation, ultimately causing muscle dysfunction and premature aging, and explores strategies to prevent these harmful effects.

LAB MEMBERS

Elias Adriaenssens, Lillie Eve Bell, Luiza Deszcz, Anna Dosa, Victoria Faas, Andreea Alexandra Gheorghita, Rebeca Gogova, Daniel Ben Grabarczyk, Juliane Kley, Eliska Kohoutkova, Konstantina Kravvariti, Robert Kurzbauer, Julia Leodolter, Moritz Mayr, Anton Meinhart, Prajnadipta Panda, Vanessa Reznikow, Adriana Savova, Moritz Helmut Wallnöfer, Annie Weston, Thomas Lloyd Williams



Tim Clausen | Senior Group Leader



Discover how the Clausen lab is investigating molecular mechanisms of protein quality control.



Functional genomics of the innate immune system | GAIDT LAB

To evade host defenses and exploit host cells, pathogens such as viruses deploy virulence factors, also known as effectors, that disrupt key immune pathways. In response, the innate immune system has evolved Effector-Triggered Immunity (ETI)—a sensing mechanism that detects the activities of these virulence factors and initiates inflammation. ETI works, for example, by monitoring cellular processes commonly targeted by pathogens and activating inflammatory responses when these processes are perturbed.

The Gaidt lab investigates the molecular mechanisms driving ETI in mammals, with the goal of understanding how the innate immune system detects pathogens and initiates inflammation. Using functional genomics in cell, mouse, and pathogen models, the team identifies the genetic and molecular components that mediate host-pathogen interactions, innate immune sensing, and immune homeostasis. This research may ultimately inform the development of therapeutic strategies to fine-tune immune responses.

Current projects

Effector-Triggered Immunity in mammals: ETI is well known from plants and bacteria, which rely on this mechanism in the absence of adaptive immunity. The Gaidt lab recently discovered a mammalian ETI pathway, showing that mouse and human cells can detect pathogen effector activities in unexpected ways. As this represents a novel—and still largely unexplored—mode of immune sensing in mammals, the lab is now focused on uncovering its molecular logic and its broader role in early pathogen detection and inflammatory signaling.

Self vs non-self recognition by the innate immune system: Distinguishing between self and foreign molecules is a fundamental challenge for the innate immune system. Errors in this process can result in autoinflammation or an inability to detect infections. The Gaidt lab studies how innate immune receptors recognize molecular signatures of pathogens, with a particular focus on nucleic acid sensing. Its work seeks to uncover how innate sensors discriminate between viral and host DNA and how downstream signaling pathways shape immune outcomes.

LAB MEMBERS

Monika Anna Bazyl, Nanette Nathalie Becht, Silvana Gligoric, David Hollaus, Markus Jaritz, Paul Clemens Kirchgatterer, Saskia Kowald, Luisa Krumwiede, Andreas Postl, Patrick Andreas Ringl, Karina Schindler-Schumitsch, Emina Selimovic, Erika Valeri



Moritz Gaidt | Group Leader



How does the innate immune system recognize pathogens and induce inflammation? Moritz Gaidt will tell you more.



Structural dynamics of protein degradation |

CRYO-ELECTRON MICROSCOPY TECHNOLOGY PLATFORM

To maintain cellular health, damaged or misfolded proteins must be efficiently removed. These unwanted proteins are tagged with ubiquitin and sent to the proteasome—the cell’s main recycling center—for degradation. Far from being a static machine, the proteasome is a modular and adaptable machine that can adjust its structure and activity to meet the cell’s needs.

The cryo-Electron Microscopy (cryo-EM) Technology Platform, led by David Haselbach, seeks opportunities to feed its technology into collaborations with other groups, and itself studies the architecture and regulation of the proteasome to understand how protein degradation shapes its structure and function. By integrating cryo-EM, cryo-electron tomography (cryo-ET), and genetics, the team explores how the proteasome recognizes and responds to different ubiquitin signals and how proteasome function regulates other cellular processes to maintain protein homeostasis.

Current projects

Ubiquitin chain formation and recognition: Ubiquitin tagging is a complex molecular language, with distinct ubiquitin chain types conveying specific cellular instructions—from targeting proteins for degradation to mediating signaling pathways. The cryo-EM Technology Platform studies the structure of ubiquitin chains and the proteins that recognize them to determine how ubiquitin chains are built and how cells use ubiquitin codes to regulate diverse processes.

Subcellular localization and compartmentalization of Ubiquitin–Proteasome System (UPS) components: The various UPS components can act in different cellular compartments depending on the cell’s needs. To fine-tune

gene expression, UPS components enter the nucleus, where they quickly process transcription factors. In immune cells, additionally, UPS components act at the endoplasmic reticulum, where they process pathogen antigens recognized at the cell surface. The cryo-EM Technology Platform investigates how UPS components are trafficked within the cell and how spatial organization fine-tunes their function to support various cellular processes.

Specialized UPS function in gametogenesis: Removing unwanted proteins is essential during gametogenesis. The proteasome adapts its structure and function to support the formation of sperm, but is also essential to oocyte arrest—the decades-long “pausing” of oocyte development essential to fertility. The cryo-EM Technology Platform studies how UPS supports these processes that are key to forming new life.

LAB MEMBERS

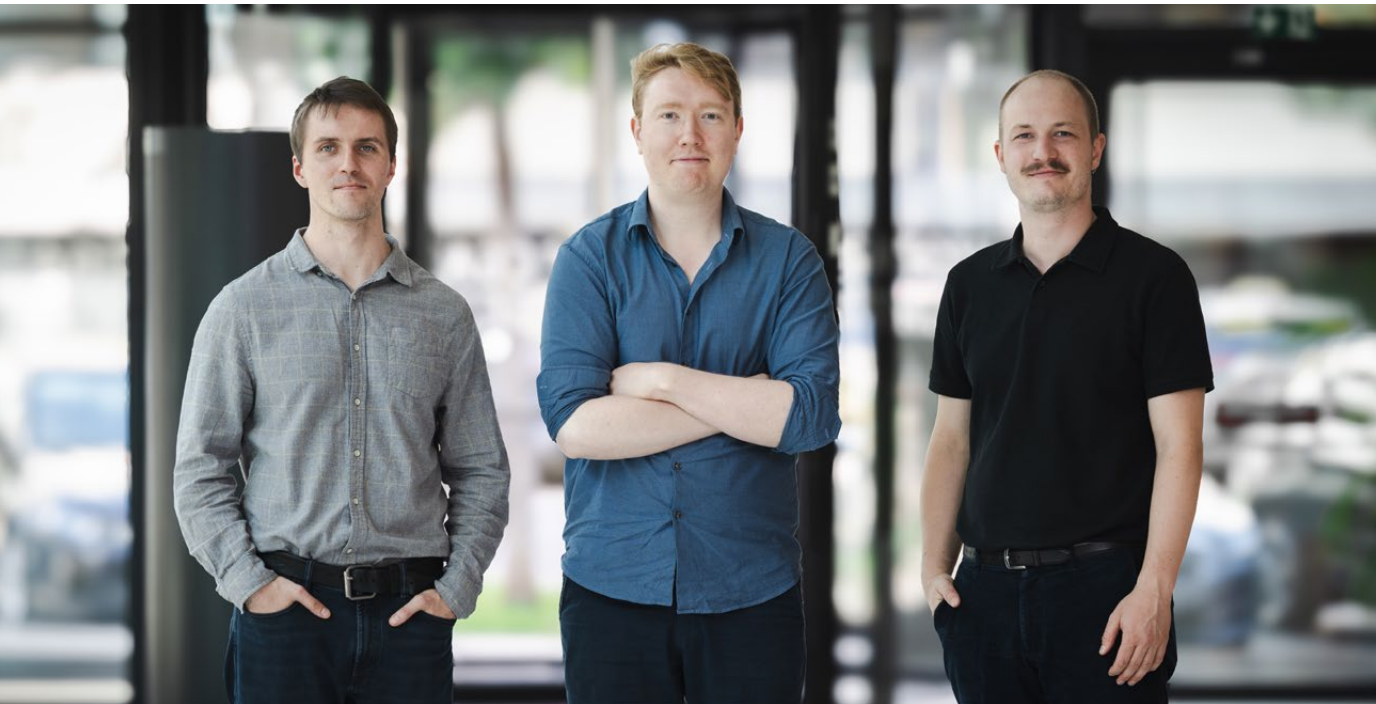
Sascha Josef Amann, Hanna Leonie Brunner, Irina Grishkovskaya, Lorenz Emanuel Grundmann, Zuzana Hodakova, Luis Leon King, Hannah Knaut, Selena Margherita Prantner, Rebecca Soliwoda, Michal Strzala



David Haselbach | Technology Platform Head



▶ How are molecular machines designed to fulfil their productive function? How is the failure of such machines prevented? David Haselbach will tell you more.



In situ structural biology laboratory | KLUMPE LAB

Transposable elements, or “jumping genes,” are mobile genetic parasites capable of copying and inserting themselves throughout the genome. While their activity poses a major threat to genome stability, the molecular mechanisms and cell biological processes that enable transposon activity often remain elusive.

To address this gap, the Klumpe lab uses cryo-electron tomography (cryo-ET)—a cutting-edge imaging technique for generating three dimensional reconstructions of rapidly frozen biological samples with an electron beam at molecular resolution. Structural information gained by cryo-ET is then used to reconstruct three-dimensional models that provide key insights into how structure influences biological function. By combining cryo-electron tomography with biochemistry and genetic tools in the fruit fly *Drosophila melanogaster*, the team seeks to reveal the cell biology of transposon activity in the germline.

Current projects

Structural biology of the *D. melanogaster* LTRome: LTR retrotransposons (LTRs)—a class of transposable elements closely related to retroviruses—represent an important threat to genome stability. In *Drosophila* germline cells, these elements are normally silenced, but when reactivated, they offer a unique opportunity to study transposon biology in

action. The Klumpe lab uses cryo-ET to visualize active LTRs within germline cells, uncovering how they move, replicate, and interact with host defenses—insights that may inform understanding of similar elements in genomes across the tree of life, including us humans.

Technology development for cryo-FIB milling and in situ cryo-ET: High-quality sample preparation is essential to guarantee successful cryo-electron tomography. To prepare samples for cryo-ET, scientists use a “cell slicing” method called cryo-focused ion beam milling (cryo-FIB). Sven Klumpe has developed innovative methods to improve sample quality when using cryo-FIB, increasing the throughput and success rate of cryo-ET and expanding the spectrum of samples amenable to in situ cryo-ET. His team continues to develop new methodological improvements for sample preparation, aiming to make cryo-ET more accessible to other scientists and to facilitate biological discoveries.

LAB MEMBERS

Artem Kushner



Sven Klumpe | IMP-IMBA Fellow



Discover how the Klumpe lab develops and applies technologies for in situ structural biology and transposons.



Mechanism-based combination therapies for metastatic cancer | OBENAUF LAB

One of the greatest challenges in treating cancer is posed by its adaptability. Tumor cells evolve to survive—rewiring their signaling pathways, reshaping their microenvironment, and even manipulating the immune system to their advantage. Each treatment or immune attack is a selective pressure, favoring the emergence of resistant cell populations that continue to grow, spread, and drive relapses after therapy. Understanding how these resilient cancer cells arise, and uncovering their molecular strategies for survival, is essential in order to develop more durable and effective treatments.

The Obenauf lab investigates how cancer cells acquire resistance to therapies and evade immune destruction using advanced human and murine models and approaches, which include lineage tracing, functional genetic, and pharmacological screens, as well as a wide array of molecular and biochemical techniques. Mechanistically, the team focuses on the molecular and cellular adaptations that allow tumors to persist despite targeted treatments or immune attacks, with the goal of identifying new therapeutic vulnerabilities.

Current projects

Cancer-cell intrinsic adaptations: To study the molecular mechanisms behind the adaptation of tumors to therapeutic pressures, the Obenauf lab developed CaTCHseq, a powerful platform that integrates lineage barcoding with single-cell RNA sequencing to trace how resistance emerges over time. Using CaTCHseq, the team can observe in real time how drug tolerance and metastasis develop, uncovering molecular pathways that could be exploited to prevent or reverse resistance.

Tumor-instructed immune regulation: Cancer cells not only evade immune destruction—they can actively reprogram the immune system to protect themselves. In recent years, the Obenauf lab studied a multitude of immune escape mechanisms and discovered that tumors disrupt inflammatory hubs within the tumor microenvironment, where immune cells are activated to attack cancer. Building on this finding, the team studies how tumors modulate the balance between immune targeting and immune suppression, revealing how cancer can hijack immune regulation to ensure its survival.

LAB MEMBERS

Tobias Beschauer, Shona Mary Cronin, Anaïs Elewaut, Guillem Estivill i Caparrós, Jörg Fallmann, Johanna Fitz, Lisa-Maria Frasz, Jakob Grünewald, Valentina Heilmayer, Shannon Huang, Verena Kern, Andri Konstantinou, Danko Atanasova Kozareva, Izabela Krecioch, Sofia Moysiadou, Lisa Muskovich, Elisabeth Pottendorfer, Antonia Maria Riedl, Martin Schönlein, Sarah Schwarz, Tanja Schwickert, Kateryna Serbina, Jingyi Shen, Milica Vulin, Eva-Maria Wiedemann, Lisa Wybrantz, Patrick Zelger



Anna Obenauf | Senior Group Leader



Discover how the Obenauf lab is investigating molecular mechanisms of immune-evasion and therapy resistance.



Molecular mechanisms of fertilization and embryogenesis | PAULI LAB

The beginning of life is one of nature's most fascinating and mysterious biological processes. During fertilization, sperm and egg come together to form an embryo that will eventually give rise to a complex organism. While we understand the broad steps of this process, the molecular details that drive the transition from a dormant egg to a developing embryo remain largely unknown.

The Pauli lab uses mainly fish models to study the molecular events enabling fertilization, early embryonic development, and dormancy. Combining genetics, in vivo and in vitro assays, biochemistry, and structural biology, the team investigates how sperm and egg establish contact, how this relates to cell fusion, and how some species can pause embryonic development to ensure reproductive success. The team's research could inform new strategies to improve reproductive medicine and reveal general principles of cellular regulation in health and disease.

Current projects

The molecular mechanism of vertebrate sperm-egg interaction and fusion: In 2024, the Pauli lab combined AI-based protein structure prediction with experimental approaches to identify a protein complex that facilitates the first interaction between sperm and egg—the essential “kiss of life.” The team is now further studying the fertilization process, focusing on the molecular mechanism by which the sperm enters the egg. It is also expanding its research into new animal models to gain a comprehensive understanding of fertilization across species.

Control of developmentally programmed and environmentally triggered dormancy: Cellular dormancy is a widespread

yet poorly understood biological phenomenon. A prime example is the egg—a cell capable of storing large amounts of macromolecules in a dormant state until fertilization occurs. Apart from the egg, certain species, such as rodents, marsupials, bears, and killifish, can also pause embryonic development under environmental stress until conditions improve. This dormant state—also called diapause—is reversible and essential to ensure reproductive success. The Pauli lab investigates the molecular players controlling how embryos enter, maintain, and exit dormancy, aiming to uncover conserved dormancy mechanisms that may explain how other cells—such as T cells or cancer cells—enter and exit similar dormant states.

LAB MEMBERS

Alek Adrianne Andresan, Tobias Ber, Theresa Beunings, Anastasia Chugunova, Victoria Eugenia Deneke, Romane Fauconnier, Olivia Füßl, Ida Marie Astad Jentoft, Phylcia Kidd, Ezra Wojtyla Levy, Laura Lorenzo Orts, Muriel Gudula Mirus, Amena Nabih Mostafa, Karin Panser, Carina Pribitzer, Lucie Kaya Esther Reinecke, Josef Röhsner, Sebastian Ruppert, Isabelle Fabienne Schütz, Johannes Peter Suwita, Auwal Ibrahim Tanko, Vivien Vogt, Theresa Ursula Zeisner



Andrea Pauli | Senior Group Leader



▶ What are the molecular mechanisms that drive fertilisation and embryonic development? Andrea Pauli will tell you more.



How cohesin regulates the genome by loop extrusion | PETERS LAB

Inside every cell's nucleus, long DNA molecules must be compactly organized yet accessible for gene expression, replication, and repair. The molecular motor cohesin plays a central role in this process by pulling DNA strands into loops—a mechanism known as loop extrusion. This dynamic structuring is crucial for gene regulation, recombination, and DNA repair, and errors in this process and other cohesin functions can lead to cancer or birth defects.

The Peters lab investigates how cohesin shapes and regulates genome architecture. Using advanced microscopy, genomics, and biochemistry, the team explores how cohesin activity is regulated and how cohesin collaborates with other proteins involved in maintaining chromosome structure.

Current projects

How cohesin functions as a molecular motor: Cohesin can reel DNA into loops. The Peters lab studies this process in molecular detail to understand the mechanism that cohesin uses to perform this function.

How cohesin's loop extrusion activity is regulated: The loops formed by cohesin need to be located in specific positions in the genome and must have the right sizes and lifetimes to fulfil their functions in gene regulation, recombination, and DNA repair. Cohesin-mediated loop extrusion is therefore tightly controlled in space and time. The Peters lab investigates these regulatory mechanisms and the proteins that mediate them.

Interactions between loop extrusion and chromatin states: DNA is not a free-flowing fiber; it is tightly wrapped around

histone proteins to form chromatin. Chemical modifications in histone proteins can make DNA more or less accessible for gene expression. The Peters lab investigates the interactions between different chromatin states and cohesin-mediated loop extrusion to elucidate how these two layers of genome regulation influence each other.

Cohesin-topoisomerase interactions: Topoisomerases are enzymes that resolve DNA twists and tangles by making temporary breaks in the DNA. The Peters lab explores whether topoisomerases and cohesin cooperate and how their combined activity folds the DNA into the right shape.

LAB MEMBERS

Emilia Zoe Chlosta, Lorenzo Costantino, Iain Finley Davidson, Sabrina Michaela Horn, Gabriele Litos, Eric Maurer, Kota Nagasaka, Mariia Popova, Navaneeth Srinivasan, Roman Stocsits, Hiromi Tagoh, Wen Tang, Palina Trus, Petra van der Lelij, Gordana Wutz



Jan-Michael Peters | Scientific Director



▶ How can one cell divide into two identical daughter cells in a way that ensures the genome is precisely copied and partitioned? Jan-Michael Peters will tell you more.



Mechanics and signaling dynamics in embryogenesis | PINHEIRO LAB

Embryonic development involves a complex and dynamic choreography whereby cells sense and respond to chemical, as well as physical, cues to decide their fate and organize into the right shape (i.e. morphogenesis). Gastrulation is a milestone in this journey during which the three germ layers—ectoderm, mesoderm, and endoderm—and the body axis are established. Extensive work has focused on identifying the signaling pathways and gene regulatory networks driving germ layer specification during gastrulation. However, how these genetic networks control the mechanical forces encoding tissue shape, and how these forces interplay with the molecular fate specification programs, is still unknown.

The Pinheiro lab investigates the molecular and biophysical mechanisms allowing cells to self-organize during gastrulation, focusing on the interplay between signaling, cell fate, and mechanics in vertebrate gastrulation. The team employs a quantitative imaging-based approach and comparative embryology to identify the general principles driving gastrulation in vertebrates, from fish (zebrafish and medaka embryos) to humans (stem cell-based models of gastrulation).

Current projects

Decoding the role of signaling dynamics in encoding biological form: To form a specific shape, embryonic cells need to integrate different complex chemical and mechanical signals. Using minimal in vitro assays amenable for quantitative imaging and morphometric analysis, the Pinheiro

lab is investigating how cells decode different features of signaling—concentration vs. duration—to instruct the mechanical properties of the mesoderm during fish gastrulation.

Uncovering the mechanisms linking cell fate and shape in a model of human gastrulation: The amnion is a thin, avascular membrane that surrounds and protects the forming embryo. Despite its crucial function, how the amnion's structure is built is poorly understood. Using advanced computational imaging analysis, force measurements, and theoretical modeling, the Pinheiro lab is exploring how the distinct morphology and tissue architectures of the extraembryonic amnion arise during human gastrulation.

LAB MEMBERS

Guilherme Bastos Ventura, Lena Bohaumilitsky, Lizbeth Airais Bolanos Castro, Mathilde Ducornet, Anna Christina Hubner, Sarah Jay, Tara Elizabeth McAteer, Umi Mohammad, Magdalena Novak, Andres Gordo Ortiz, Chloe Anne Mira Roffay



Diana Pinheiro | Group Leader



▶ Which biophysical mechanisms underlie the formation of embryonic pattern and shape? Diana Pinheiro will tell you more.



Mechanisms of mRNA processing and export | PLASCHKA LAB

Messenger RNA (mRNA) carries the essential genetic blueprint from DNA to the site of protein synthesis. However, more than 60 years after the discovery of mRNA, the molecular mechanisms that make one functional mRNA in the nucleus and export it to the cytoplasm remain poorly understood. These events are orchestrated by a series of complex molecular machines, whose precise modes of action, regulation, and quality control remain largely enigmatic.

The Plaschka group aims to uncover how key molecular machines act on human mRNA to ensure the accurate and efficient interpretation of the genome. By combining structural, biochemical, imaging, and genetic approaches, the team provides fundamental insights into the mechanisms of gene expression in the human cell nucleus.

Current projects

RNA splicing: Most human genes contain introns, which must be removed through RNA splicing to make functional mRNA. This reaction is catalyzed by the spliceosome, an enzyme comprised of more than 100 proteins and five RNAs. How these proteins and RNAs come together for splicing, and how splicing errors are detected and resolved, remains unclear. To address these questions, the Plaschka lab investigates the structure and function of endogenous spliceosomes.

RNA packaging: During RNA processing, nascent mRNA is packaged by proteins into an mRNA ribonucleoprotein complex (mRNPs). Packaging is important to both direct the mRNA toward export, to mark passed quality control, and to protect the mRNA on its journey from the nucleus to the cytoplasm. Current insights from the Plaschka reveal how

cell-essential and highly conserved members of the transcription-export complex help recognize and prepare an mRNP for its nuclear export.

RNA nuclear export: The packaged mRNP must export from the nucleus to the cytoplasm for protein production. This requires passing through the nuclear pore complex (NPC), the gatekeeper between nucleus and cytoplasm. However, how an mRNP exports through the NPC is unknown. Recent work from the Plaschka group has revealed how an mRNP can engage with the NPC, through the essential TREX-2 complex. The team is now establishing a generalizable, mechanistic framework for the packaging and export of human mRNA.

LAB MEMBERS

Farja Isabel Ayala Muñoz, Vytaute Boreikaite, Rupert William Faraway, Laura Fin, Jean-Marc Raffaello Matteo Furlano, Max Graf, Constanze Barbara Gremmelmaier, Ulrich Hohmann, Viktorija Karalkeviciute, Grigor Lepir, Leonie Opitz, Alexander William Phillips, Daria Riabov Bassat, Patricia Bianca Rothe, Kevin Sabath, Matthias Kopano Vorländer



Clemens Plaschka | Senior Group Leader



▶ How do molecular machines prepare messenger RNA for leaving the nucleus? Clemens Plaschka will tell you more.



Understanding transcriptional regulation | STARK LAB

All cells in an organism share the same genetic information but take on dramatically different shapes and functions. During development, cells adopt specific identities by activating distinct gene expression programs that control when, where, and how strongly genes are expressed. This differential gene expression depends on genomic regulatory DNA sequences and transcription factor proteins that turn genes on or off. While the general principles of gene expression are known, much about how regulatory sequences work, and how transcription factors interact with other proteins to fine-tune gene activity, remains to be discovered.

The Stark lab studies the molecular mechanisms that control transcription in enhancer and promoter regions in the DNA. Using an integrative approach bridging “wet lab” experimental work, computational AI-mediated analyses, as well as synthetic biology, the scientists combine genome-wide functional assays, bioinformatics, biochemistry, and mass-spectrometry. In doing so, the team identifies transcription factors and cofactors and explores their interactions and mechanisms. In recent years, the team predicted and created synthetic regulatory sequences that either activate or repress gene expression, expanding our understanding of the molecular grammar of gene regulation.

Current projects

Regulatory compatibilities in transcription control: Even though all genes are transcribed by the same core cellular machinery, different genes require distinct sets of regulatory transcription factors and cofactors. The Stark lab studies the regulatory logic of these differential requirements, focusing on how it arises from distinct enhancer and promoter classes.

Modeling enhancer activities with neural networks: To predict how DNA sequences regulate genes, the Stark lab developed DeepSTARR, a neural network that models enhancer activity. This tool enables the team to identify novel enhancers, understand their function, and even design synthetic enhancers to precisely modulate gene expression in specific cell lines and tissues.

Pathogen effectors as molecular tools to modulate cell biology: In a collaborative effort, the team has collected a large library of effector open-reading frames (eORFs) from diverse human pathogens to determine by functional genomics screening how the eORFs modulate diverse aspects of human cell biology. The researchers have identified and characterized many novel eORFs with different exciting functions.

LAB MEMBERS

Katharina Bergauer, Myrto Chatziangelou, Shenzhi Chen, Monika Heinzl, Sebastian Kleinfencher, Franziska Katharina Lorbeer, Vincent Loubiere, Nikolaus Mandlbürger, Sachin Mishra, Ken Murakami, Filip Nemcko, Tomas Pachano, Michaela Pagani, Matus Vojtek



Alexander Stark | Senior Group Leader



▶ How is gene regulation and therefore the development of our bodies encoded in our DNA sequence? Alexander Stark will tell you more.



T cell differentiation and function | VAN DER VEEKEN LAB

T cells are the main effectors of the adaptive immune response, tasked with quickly targeting and eliminating pathogens and tumors once activated. Once the threat is cleared, a subset known as regulatory T cells (Tregs) ensures immune balance by restraining excessive T cell activity—preventing harmful outcomes such as allergies and autoimmune diseases.

The van der Veeken lab studies how Treg cells perform their essential immunosuppressive role, focusing on the gene expression networks that define and control Treg function. By engineering immune cells in mouse models, the team dissects the molecular mechanisms that govern T cell responses in health and disease, aiming to inform new therapeutic approaches that restore or fine-tune immune balance.

Current projects

The role of FOXP3 in Treg activity: FOXP3 is a master transcription factor critical for Treg identity and function—mutations in this gene can lead to fatal autoimmune disorders. However, how FOXP3 confers suppressive capacity to Tregs and orchestrates their gene expression programs remains poorly understood. The van der Veeken lab develops advanced animal models to study how FOXP3 activity—and its loss—influences gene expression in Tregs and affects immune regulation. The team aims to dissect FOXP3’s function and to shed light on how other factors such as tissue context can influence Treg activity.

The many roles of RORγT: The hormone receptor RORγT lies at the center of key immune processes—from shaping T cell development in the thymus to building lymphoid tissues and maintaining tolerance to gut microbiota. But how does one nuclear receptor control such a wide range of functions? The van der Veeken lab uses targeted degradation models to investigate RORγT’s role across different immune cell types, aiming to uncover the distinct molecular pathways this receptor governs to keep the immune system balanced and resilient.

LAB MEMBERS

Po-Han Chou, Sandra Thu Tra Dang, Polina Dimitrova, Maura Hofmann, Christina Jäger, Elisa Marchiori, Rene Rauschmeier, Kateryna Serbina, Qiong Sun



Joris van der Veeken | Group Leader



▶ What are the mechanisms that direct T cell differentiation and function? Joris van der Veeken will tell you more.



Finding and understanding cancer dependencies | ZUBER LAB

Targeted therapies have transformed cancer treatment, but most tumors respond only temporarily before developing resistance. Fulfilling the promise of precision oncology requires expanding the set of actionable targets, identifying biomarkers that predict responses, and designing rational drug combinations that prevent tumor adaptation.

The Zuber lab develops and applies innovative genetic tools—including CRISPR/Cas9, RNA interference, and degron systems—to uncover context-specific tumor dependencies, understand their molecular functions, and evaluate their therapeutic potential in disease-relevant in vivo models.

Current projects

Probing tumor dependencies and combinatorial targets in vivo: Cell culture-based studies miss many cancer vulnerabilities because they fail to replicate the nutrient conditions, immune interactions, and microenvironmental cues of real tumors. The Zuber lab has developed precise CRISPR-based dropout screens in advanced mouse models to capture these factors. This approach reveals how tumors adapt metabolically—such as relying on mitochondrial energy production under acidic stress—to escape targeted therapies. By mapping these compensatory pathways, the team identifies rational combination strategies to improve cancer treatments and prevent tumor relapse.

Characterizing and targeting transcriptional dependencies: Cancer cells rely on transcription factors to maintain aberrant cellular states and adapt to therapeutic challenges. To understand and ultimately target these master regulators, the Zuber lab combines chemical-genetic protein degradation, time-resolved mRNA profiling, and reporter-based CRISPR screens to characterize pathways and co-factors controlling

the regulation and regulatory function of transcription factors. This deep molecular understanding will reveal new entry points for drug development.

Enhancing T cell-mediated anti-tumor immunity: Tumors evade immune attack by reducing their visibility to T cells or dampening T cell activity. Using CRISPR screens, the Zuber lab identifies cancer-cell pathways that limit immunogenicity and T cell-intrinsic regulators that constrain expansion or effector function. These findings guide the development of more effective immune-cell therapies. Through the DART2OS consortium, the team applies these principles to pediatric osteosarcoma, integrating single-cell genomics and personalized screens to identify patient-specific neoantigens and support individualized TCR-T cell approaches tailored to each tumor’s landscape.

LAB MEMBERS

Florian Andersch, Jonas Fridolin Bayerl, Michaela Fellner, Miriam Verena Fellner, Loran Geelen, Martin Gert Jäger, Robert Wolfgang Kalis, Romana Maerschalk, Martina Minnich, Olivia Juliette Neuhofer, Gabriel Pabst, Wolfgang Paster, Sophia Franziska Rampp, Emanuele Rovera, Bettina Sajtos, Mario Sanz, Markus Schäfer, Johannes Schmöllerl-Wolf, Fabian Ullrich, Martina Weißenböck, Jakub Zmajkovic



Johannes Zuber | Senior Group Leader



▶ Why are cancer cells immortal, what genes do they depend on, and how can we exploit cancer-specific vulnerabilities for cancer therapy? Johannes Zuber will tell you more.

Support Facilities

Researchers at the IMP are part of a supportive environment where world-class scientific facilities, infrastructure and administrative experts, and other colleagues all work toward enabling discovery.

Scientific facilities at the IMP and its partner institutes IMBA and GMI, as well as through the Vienna BioCenter Core Facilities (VBCF), offer all IMP researchers access to advanced equipment and expertise. Administrative and infrastructure services ensure smooth operations in all areas of a research institute. What unites all of these colleagues is their alignment with a shared goal: outstanding research in the molecular life sciences.

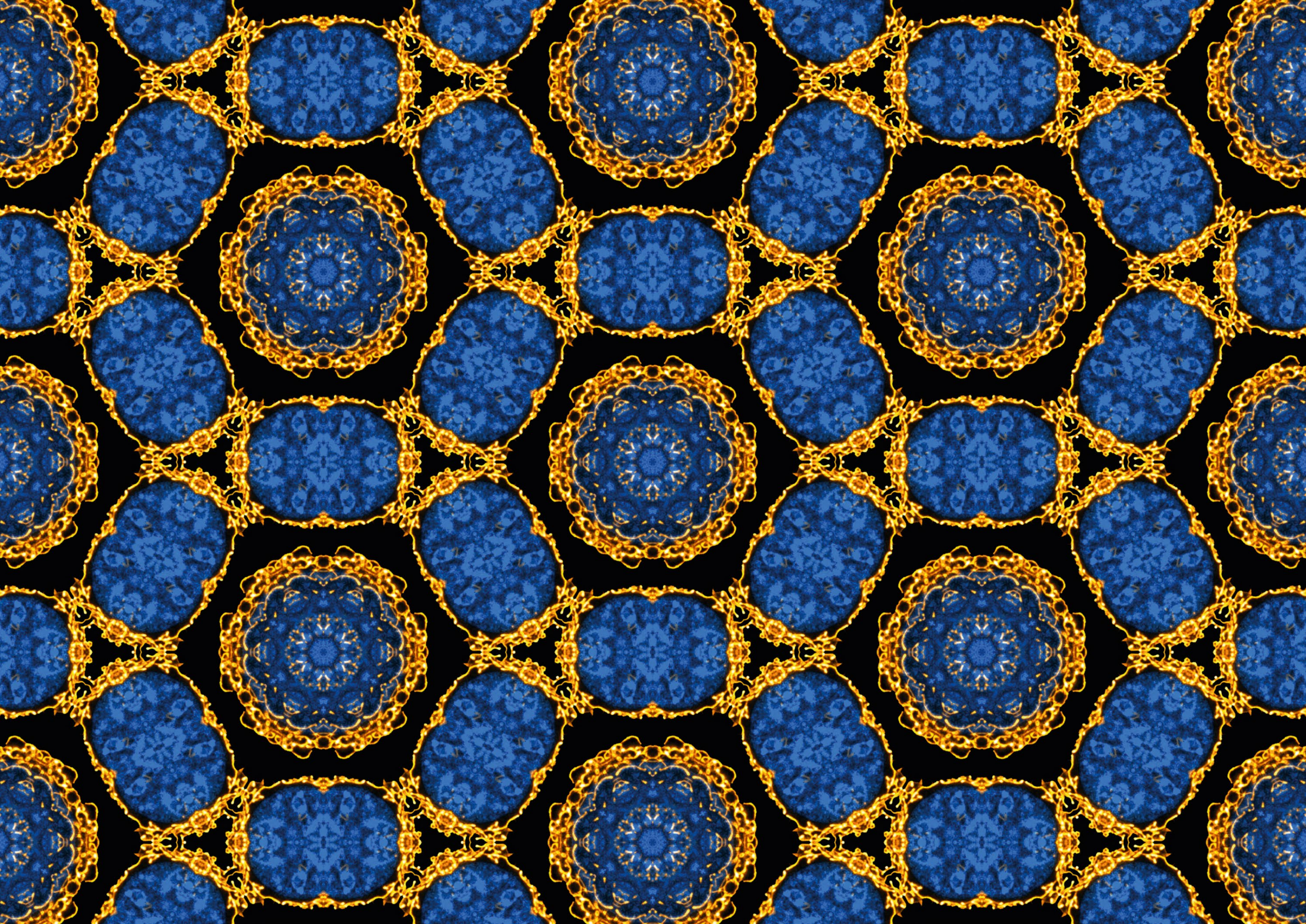
Experts in departments belonging to administration, infrastructure, and Scientific Core Facilities respond when their colleagues in research groups need support translating scientific intent into something that can be built, measured, analyzed, and sustained over time.

In Confessions of Core Facilities, we go backstage to hear from people who operate in that in-between space and who have a few things they wish research group members knew. Read the story in the Community and Facilities volume.



Services available to IMP research groups cover a broad range of methods, facilities, and expertise. Take a look.

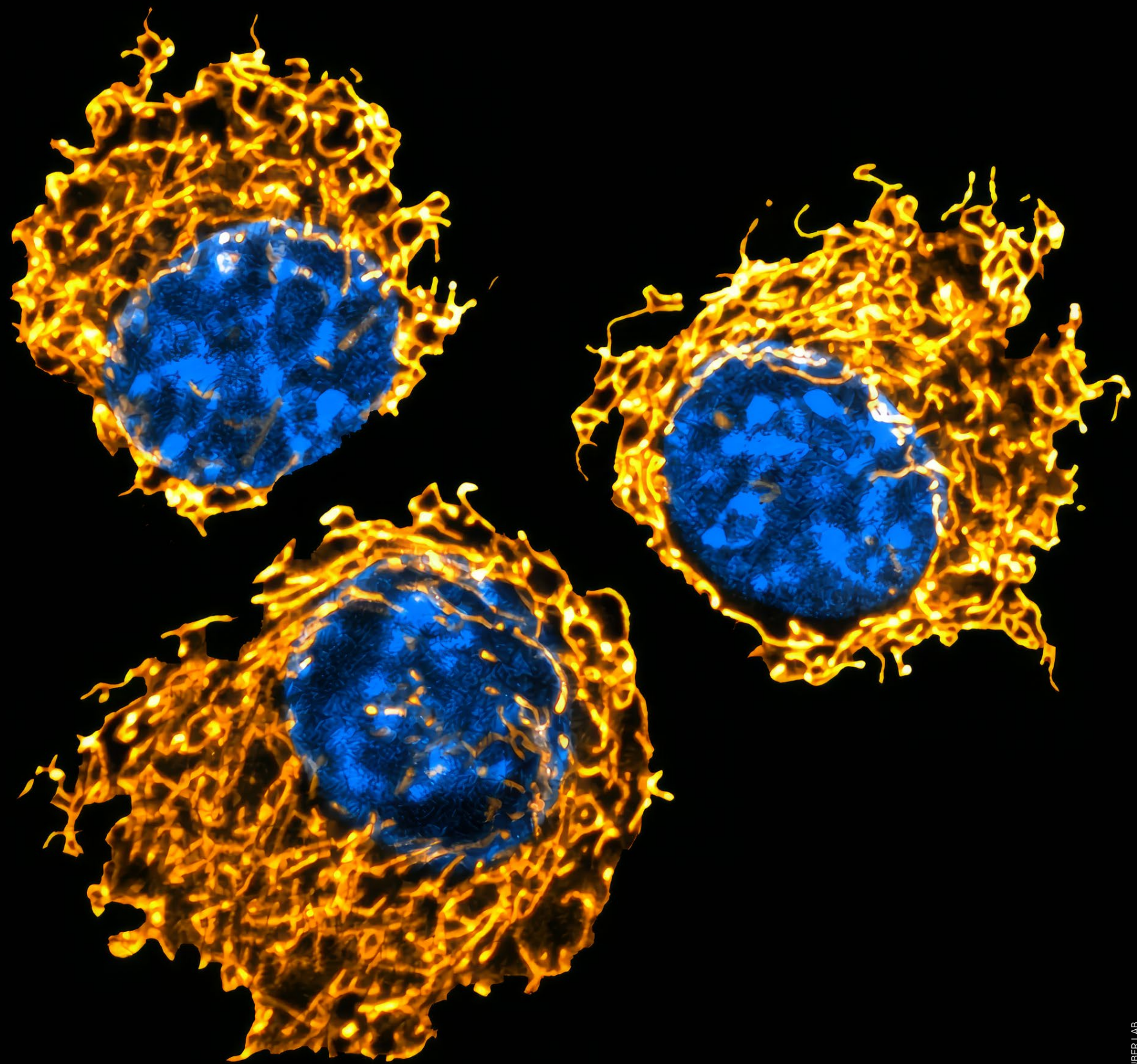
Molecular Biology Services is part of the support ecosystem behind research at the IMP. Seen here is Jiss John, Core Facility Scientist.



03

A LANDMARK YEAR

Acidosis triggers the fusion of mitochondria into elongated networks (stained yellow), which boosts energy production and renders cancer cells resilient to various stresses.



Close enough to collide

A conversation between neighboring labs turned complementary expertise into Anna Obenauf’s Steiner Award-winning research. 54

A week of code, a year of experiments

As a computational genomics researcher at the IMP, Jacob Schreiber set out to make machine learning as easy to use as any standard lab approach. 58

Community

Relationships make science travel. It includes researchers who arrive with new methods, scientists who bring life sciences into public view, and work that receives recognition beyond Vienna. This section looks at the IMP through the people and moments that link it to a broader scientific community.



BENEDEKT MANDL

Andrea Pauli, Senior Group Leader at the IMP, during filming for the ORF Österreich Bild documentary “Wien am Weg zur Weltklasse”. The 2025 program highlighted Vienna’s growing international profile in the life sciences and featured Pauli’s research on fertilization.

Close enough to collide

A conversation between neighboring labs turned complementary expertise into Anna Obenaus’s Steiner Award-winning research.

Stephan Rohr (chair of the Steiner Foundation) and Anna Obenaus at the Steiner Award ceremony in Bern, September 2025.



37

years between the first and most recent Steiner Award for an IMP scientist.

Anna Obenaus, Senior Group Leader at the IMP, had spent years studying why tumors that initially respond to treatment eventually stop working. Her office neighbor, Senior Group Leader Alexander Stark, had developed technologies to decode gene regulation. “When I realized what Alex had

“If you realize there’s really exciting biology in front of you that doesn’t relate 100 percent to what you proposed, you can follow it.”

Anna Obenaus

developed, it immediately became clear that these technologies could open entirely new ways to interrogate our melanoma model systems,” Obenaus says. “This is what the IMP is really about; it’s small enough that you get exposed to very different types of science.”

That convergence of expertise led to Decode-iTME, a project seeking to understand and reverse how tumors become resistant to therapy. In 2025, the work earned Obenaus the Dr. Josef Steiner Cancer Research Award. Given every two years and founded through the legacy of Swiss pharmacist Josef Steiner, it honors scientists whose work has led to fundamental advances in the understanding of cancer.

The award comes with five years of funding and a high degree of freedom to invest in conceptually ambitious projects. For Obenaus, this means pursuing work that builds on experimental systems and discoveries developed in her lab over many years, with the aim of understanding how gene-regulatory programs in cancer cells change as tumors evolve under treatment and reshape their surrounding immune environment.

Following the unexpected

To pursue these questions, the project will integrate complementary approaches developed across IMP labs. Genetic screening methods pioneered in the Zuber lab have been

applied in the Obenaus lab’s cancer models to systematically probe vulnerabilities of therapy-resistant tumor states. Technologies developed by the Stark lab add another dimension: the ability to decode the regulatory DNA elements that control gene expression during therapy resistance. Together, these approaches allow the Obenaus lab to link functional genetic screens with the regulatory programs that drive resistant cancer cell states.

Crucially, the Steiner Award will also give Obenaus the support needed to explore the unexpected. “What’s special about the Steiner Award is that if you realize there’s really exciting biology in front of you that doesn’t relate 100 percent to what you proposed, you can follow it,” she says. The five-year support also means she can hire experienced scientists for longer-term projects and tie together complex threads as projects evolve.

“This builds on many years of work where many other people have contributed,” Obenaus says. “My team members made this possible: the previous papers, the model systems established, the knowledge gained, the preliminary data.” It’s the kind of accumulated expertise that emerges when scientists work closely enough to collide, and have the freedom to follow where those discoveries lead. ●



Discover the grants and prizes that power the IMP’s research.

Connecting generations: the Steiner Award and the IMP

The Steiner Award’s history intersects at notable moments with the IMP. In 1988, Hartmut Beug, one of the institute’s first senior group leaders, received the distinction. His work on cell differentiation, growth control, and oncogenic transformation addressed core mechanisms of how normal cells become cancerous and led to the discovery of the epithelial-mesenchymal transition (EMT) during metastasis formation. The recognition marked an early international acknowledgment of both Beug’s research and the scientific caliber of the then young institute.

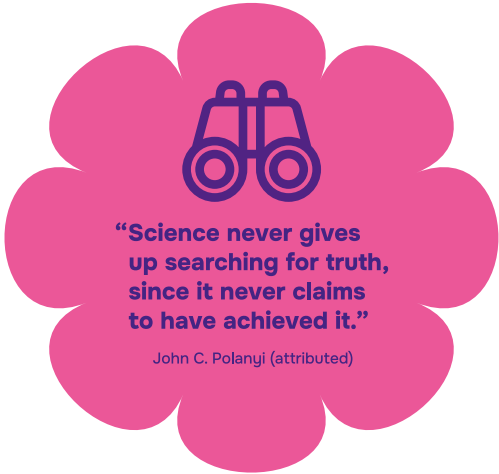
Several academic generations later, the 2025 award received by Anna Obenaus establishes a direct link between that formative period and the present. Obenaus’s research has provided key insights into how cancers evolve, metastasize, and develop resistance to therapy.

Viewed together, the awards won by Beug and Obenaus frame nearly 40 years of cancer research at the IMP. They illustrate how the Steiner Award has, at two distinct moments, recognized work emerging from the same institution while reflecting the changing scientific questions of the field, from foundational mechanisms of transformation to the dynamic evolution of cancer in patients.

Words worth repeating

The IMP community sent us the quotes they live by, borrowed from heroes, mentors, and some surprising places.

Sometimes a single sentence changes the way you think about your work. A phrase from a book, a line from a mentor, something overheard that simply stuck. When the IMP community was invited to share these words of wisdom, a collection that moves freely between famous voices and quiet ones was submitted—between rigorous empiricism and open-hearted idealism. It's a surprisingly honest portrait of how this community thinks, and what it chooses to hold onto.



"Science never gives up searching for truth, since it never claims to have achieved it."

John C. Polanyi (attributed)



"That's one of the great excitements of science: that always there is the unexpected, always there is something that no one thought of that completely revolutionizes our thoughts in this direction or that."

Isaac Asimov



"It is probably important to just tell you what the question was that the research was trying to answer because one should always start with a question before you are trying to say anything at all."

John Gurdo



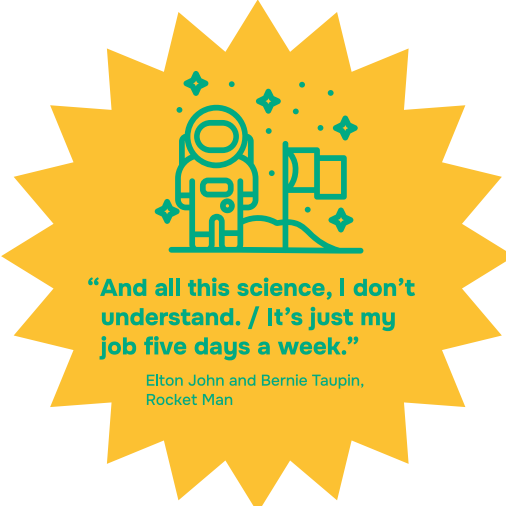
"If you're going to borrow wisdom, you could do a lot worse than this crowd."

Anonymous



"Go figure!"

Anonymous American



"And all this science, I don't understand. / It's just my job five days a week."

Elton John and Bernie Taupin, Rocket Man



"You may not be able to control the outcome of every interaction. But you can always choose to be kind."

Anonymous

"The best way to study a thing is to observe it as it comes into being from the beginning."

Aristotle

"You want to go where a question takes you, not where your training left you."

"In God we trust; all others must bring data."

W. Edwards Deming (attributed)

"Scientists can either be tree-shakers or jelly-makers."

Anonymous

"Every individual matters. Every individual has a role to play. Every individual makes a difference."

Jane Goodall

"The best investment you can make is in yourself."

Warren Buffett

"Knowing was a barrier which prevented learning."

Frank Herbert

"It's good to have fun in your life, but hard work is more important."

Anonymous

A week of code, a year of experiments

As the only purely computational researcher at the IMP, Jacob Schreiber set out to make machine learning as easy to use as any standard lab tool.



In 2024, computational scientist Jacob Schreiber came to the IMP for a year as a visiting scientist before starting his own lab in the United States.



Read the complete interview.

In 2024, computational scientist Jacob Schreiber came to the IMP for a year as a visiting scientist before starting his own lab in the United States. Now leading his research group, he looks back on what that year in Vienna made possible.

Your work sits at the intersection of computer science and biology. How did that play out at the IMP?

Jacob Schreiber: One of the key challenges in computational genomics is not so much scientific as it is engineering: researchers with a computational background can build and apply machine learning models, but for many experimental scientists, they're not yet easy to use. My goal was to make something any scientist could adopt without needing to know every technical detail.

A collaboration with the Gaidt lab captured exactly what I was trying to do. One of his students, Luisa Krumwiede, had spent over a year running experiments to characterize a biological process. Using the tools I'd developed, we reproduced her findings computationally in about a week, and the results aligned perfectly. It was clear evidence that these tools could genuinely empower researchers to explore data in new ways. Seeing Luisa use them independently afterward was particularly gratifying. By the end of my stay, three projects like this had turned into publications.

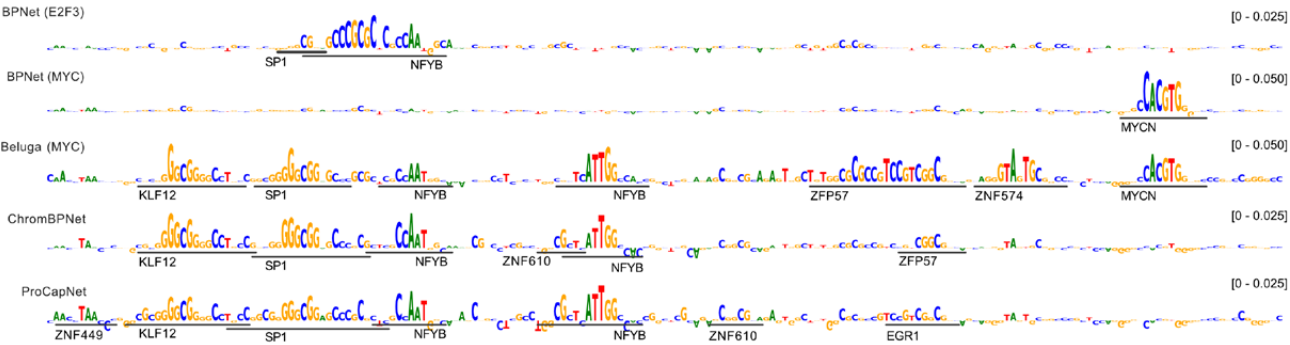
After a year of building these tools, what gives you confidence about computational biology's future here?

Jacob Schreiber: AI and computational approaches are clearly becoming integral to biology, and the IMP has recognized that early. The Stark lab is doing fantastic work on the computational side, and the establishment of the AITHYRA Institute is a very exciting step. Focusing explicitly on artificial intelligence as a pillar of research is exactly the right direction, and the scientists being brought in, particularly the new group leaders, are doing ambitious, forward-looking work.

How did a year at the IMP shape the kind of lab you're building now?

Jacob Schreiber: One thing I valued about the IMP was the honesty in feedback. Because the community is so tight-knit, it was easy to get straightforward critiques. That can be tough to hear, but it ultimately allowed everyone to do their best work. The collaborative culture runs deep. People are genuinely invested in each other's science, not just their own. It's a spirit and a culture I'm trying to carry into my own lab. ●

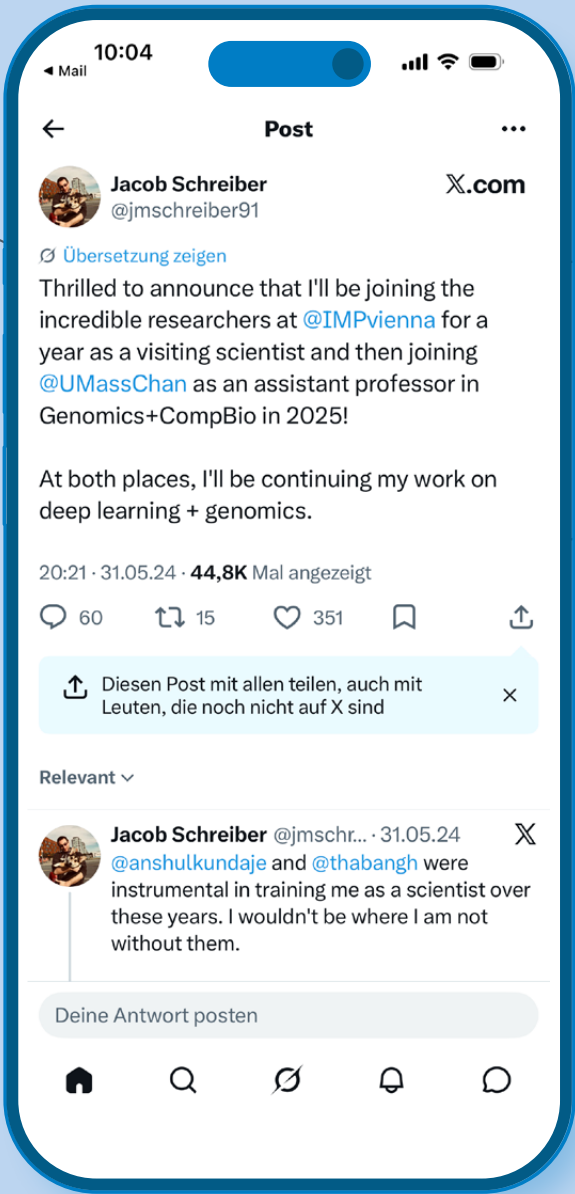
3 number of collaborative projects turned into publications during Jacob Schreiber's one-year visit to the IMP.



Schreiber uses deep learning models to understand where and why proteins bind to our genomes. Here, he uses feature attribution methods to show how different deep learning models (and the biology they predict) are driven by the binding of different proteins to the same genome sequence.

A visiting scientist in Vienna

Jacob Schreiber's year at the IMP, told through research, relocation, and the small rituals of settling in.



The DNA of memory

Artist and IMP alumnus Philipp Dexheimer used the remnants of current research to honor the scientist who laid the foundation for the IMP. 66

The PhD student next door

Three generations of scientists reveal why casual hallway conversations drive success. 68

40 years of finding out

2025 marked the IMP's 40th anniversary. History serves as the launchpad for what lies ahead. This research report on an anniversary year provided an opportunity to dive into the curiosity, determination, and pioneering spirit that has made the IMP the institute it is today—and that shapes the institute today as much as its journey into the future.



Taking a dive into the history of the IMP

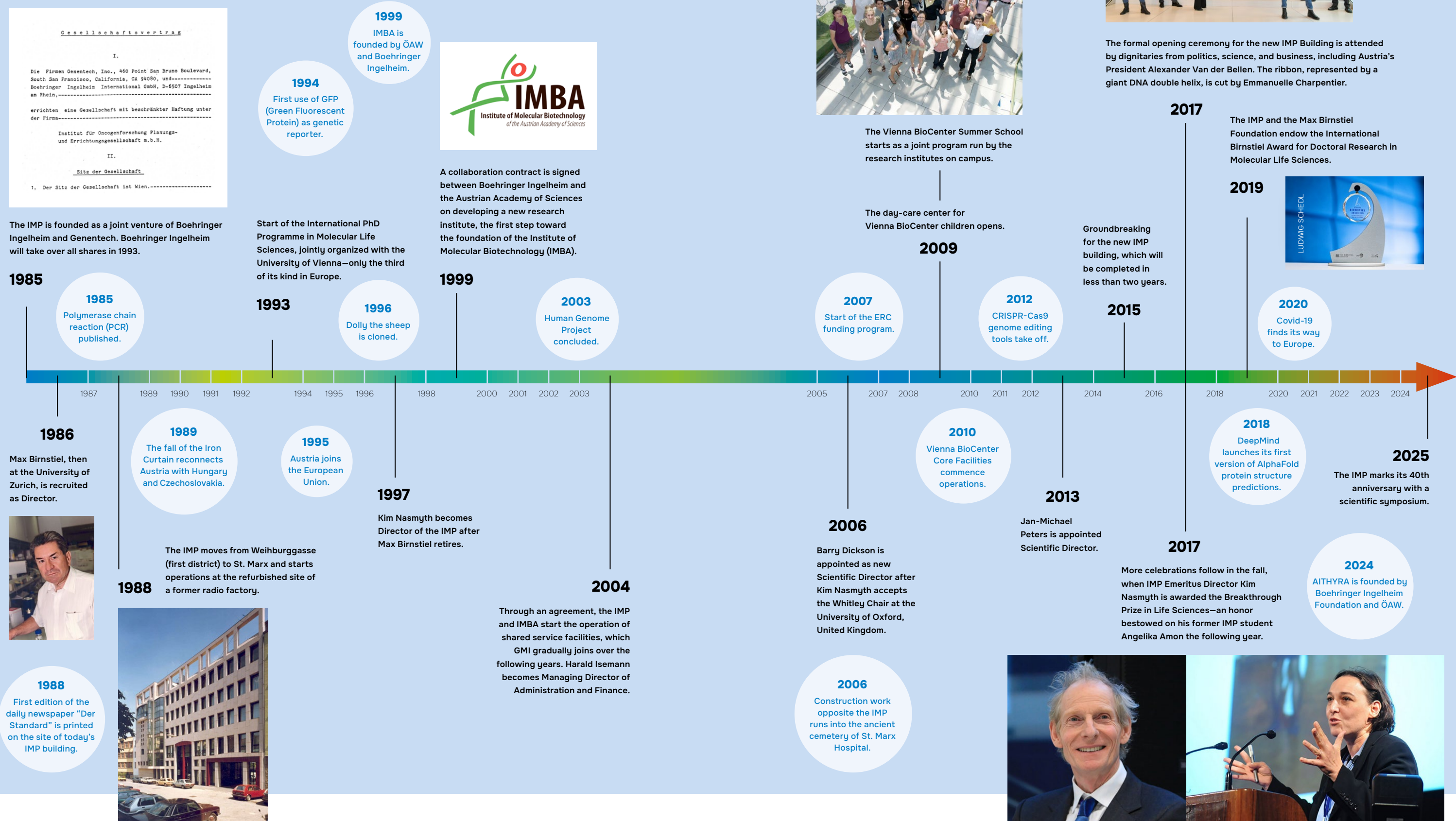
From PCR to CRISPR, from the fall of the Iron Curtain to the founding of AITHYRA, the past 40 years have reshaped biology and Europe alike. The IMP's anniversary is a chance to see those shifts side by side.

The IMP's story starts before the Human Genome Project and stretches into the age of AI-assisted biology. Forty years later, the institute stands as part of a larger narrative about how modern life science research was built.

The IMP was founded in the year PCR was published and when Europe was still divided. Four decades later, genome editing, AI-driven protein prediction, and a new generation of institutes define the landscape. This timeline follows the institute's growth against the backdrop of discoveries and turning points that reshaped biology.

The tiny people were introduced in 2016 as part of the relaunch of the IMP corporate design. Realistic miniature figures popular in the 1970s were set within a scientific landscape. The concept played with the contrast between familiar objects from everyday lab life and the tiny figures, creating scenes that felt both unexpected and relatable. A beaker filled with water, for example, could become a setting in which tiny diver figurines looked up at it. The concept was developed by Gerhard Bauer at Perndl+Co.

Our journey of discovery



The DNA of memory

Artist and IMP alumnus Philipp Dexheimer used the remnants of current research to honor the scientist who laid the foundation for the IMP.



Philipp Dexheimer turned more than 10,000 oligo tubes into a portrait of Max Birnstiel, the IMP's Founding Director whose vision shaped the Vienna BioCenter.

What nearly ended up in the autoclave bin became a work of art. In 2021, Philipp Dexheimer stood in Luisa Cochella's IMP lab, about to discard 2500 oligo tubes. "Don't you want to do something interesting with them?" Cochella asked. Four years later, those tubes, along with more than 10,000 further donated tubes, became a portrait of Max Birnstiel, the IMP's Founding Director whose vision shaped the Vienna BioCenter.

Birnstiel's influence on Dexheimer's life began long before this portrait. In 2014, Dexheimer saw a poster in Munich advertising the Vienna BioCenter Summer School. Attending that program led to a PhD in Cochella's lab at the IMP, and later a research position in the Clausen lab, also at IMP. Now working as an artist and visualization expert creating illustrations, videos, and art for scientists and institutes, Dexheimer can trace his career directly back to Birnstiel's decision to establish the IMP. "It's funny," he reflects, "how someone you don't know personally and their decisions in establishing an institute can have such a major impact on how your life unfolds."

The face nobody knew

In 2021, Dexheimer pitched the idea of turning the oligo tubes into a mosaic for the institute to Harald Isemann and Jan-Michael Peters, Managing Directors of the IMP, who supported the project. However, finding a subject that would resonate with the entire IMP community took time. Then in 2024, Adrian Bird, a first-generation IMP Senior Scientist and now IMP Scientific Advisory Board member, noted that Max Birnstiel wasn't represented anywhere in the institute he shaped. The choice became clear: a portrait of the Founding Director would finally give Birnstiel a presence at the IMP.

The decision proved apt when Dexheimer showed colleagues his mosaic in progress. Most didn't know whose face they were looking at. Everyone knew the name from the International Birnstiel Award for Doctoral Research in Molecular Life Sciences, an annual prize for PhD students, and from the institute's Max Birnstiel Lecture series featuring leading researchers, as well as the Talents for Future training program sponsored by the Birnstiel Foundation. But few knew the man himself or his scientific legacy.

"It's funny how someone you don't know personally and their decisions can have such a major impact on how your life unfolds."

Philipp Dexheimer

Max Birnstiel's legacy

As a scientist and research manager, Max Birnstiel was a lifelong advocate of egalitarian work culture, sharing knowledge and enabling future generations of scientists. The Max Birnstiel Foundation was created in 2017 in this spirit. It supports initiatives such as the Vienna BioCenter Summer School, the International Birnstiel Award for Doctoral Research in Molecular Life Sciences, and the Talents for Future training program to empower students from underprivileged backgrounds. Since 2009, the IMP has organized a distinguished lecture series to pay tribute to Max Birnstiel's legacy.



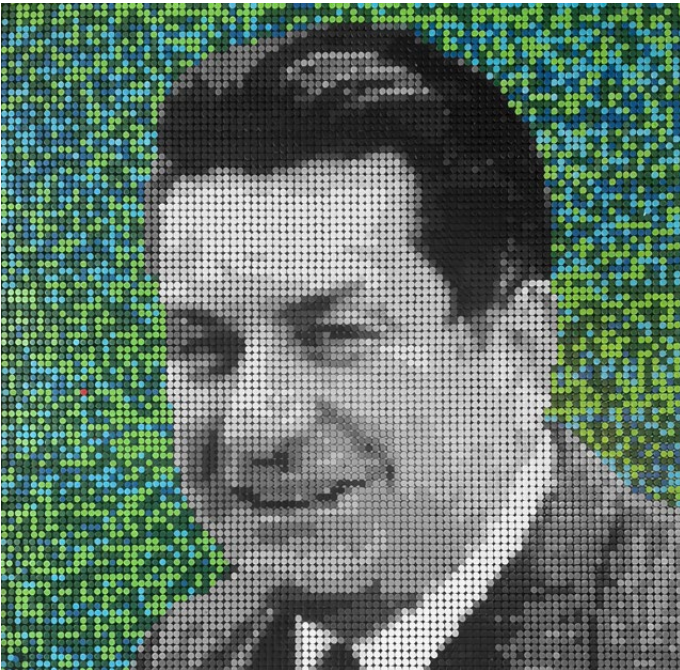
Building blocks of legacy

For five months, from June to October 2025, Dexheimer worked at his dinner table, matching thousands of colored tubes to the pattern he'd created for the mosaic. The background depicts the ribosomal DNA locus from *Xenopus* oocytes, the isolation of which was one of Max Birnstiel's most significant scientific achievements. This 1966 breakthrough revealed how genes responsible for ribosome production are organized and regulated. The four colors in the mosaic represent DNA's four bases. A single red oligo tube stands out: it contains the 5.8S rDNA sequence that Birnstiel described, echoing the red dot at the center of the IMP logo.

The mosaic reveals its meaning in layers. Up close, you see individual tubes, the everyday objects of molecular biology research. Step back, and they resolve into Birnstiel's face. But the mosaic's deeper significance lies in its materials. These tubes came from researchers working at the Vienna BioCenter today, whose experiments continue to build on the foundation laid by Birnstiel.

10,000

laboratory tubes donated by researchers to build a mosaic portrait of IMP Founding Director Max Birnstiel



A personal connection

That sense of shared identity starts with recognition. "It creates a more personal, emotional connection to the person who founded all of this," Dexheimer says. When he delivered the finished mosaic and returned home, his living room felt strangely empty. For five months, Max's 1.3-meter face had occupied his workspace and daily routine. "Max was gone, and I have to admit I felt a little sad." The portrait was revealed at the 40th anniversary symposium in November 2025. It now hangs at the institute, giving Birnstiel the presence he'd lacked and creating a visual reminder of the community's shared history. ●

In 2021, Philipp Dexheimer stood in Luisa Cochella's IMP lab, about to discard 2500 oligo tubes. "Don't you want to do something interesting with them?" Cochella asked.



The PhD student next door

Three generations of scientists reveal why casual hallway conversations drive success.

At the Research Institute of Molecular Pathology's 40th anniversary celebration in November 2025, three scientists from different periods gathered to discuss what makes the institute successful. Their answers converged on one factor: daily conversations with colleagues outside their immediate

research groups. From the institute's founding in 1985 to today, this culture of informal exchange has shaped careers, driven collaborations, and helped scientists overcome self-doubt.



By the sofas near Harry's Bar, researchers meet for coffee, talk science, and find the kind of everyday community Andrea Pauli remembered from her first one and a half years at the IMP.

Community as a foundation

What was the culture like for early PhD students at the IMP in the 1980s?

Giulio Superti-Furga was the IMP's first PhD student. Then Scientific Director of CeMM*, Research Center for Molecular Medicine of the Austrian Academy of Sciences, and Professor of Medical Systems Biology at the Medical University of Vienna, he remembers a different kind of scientific life. "Being a PhD student was a lifestyle. We were hanging out together all the time. We used to watch a soap opera [Falcon Crest] at five o'clock every day together, the students and the postdocs, before heading back to the labs. Actually, there was no difference between the students and postdocs—we were one community."

When the IMP moved into its first research building in 1988, a converted 1950s factory building for the Hornyphon electronics company, the surrounding area was what Superti-Furga describes as "industrial wasteland," a rough neighborhood 33 years after Soviet occupation ended. Despite the surroundings, researchers inside were building something new. "Everything was sort of exciting. Competitive. Pioneering," Superti-Furga recalls.

"There was no difference between the students and postdocs; we were one community."

Giulio Superti-Furga, CeMM*

*Giulio Superti-Furga, PhD, is the Founding Director of CeMM and served as its Scientific Director until the end of 2025.

5 o'clock

when the IMP's first generation of PhD students and postdocs would stop to watch the soap opera Falcon Crest together every day, before heading back to the labs



Before its adaptation for research, the future IMP site housed a 1950s factory building used by the Hornyphon electronics company.

Why she came back: the 1.5-year effect

Other institutes were courting you. Why return to Vienna?

Andrea Pauli, now a Senior Group Leader at the IMP, started her doctoral research at the institute in 2004 under Group Leader Barry Dickson (now Emeritus Scientific Director) and Kim Nasmyth, who was then both Group Leader and the IMP’s second Scientific Director (now Emeritus Scientific Director). When Nasmyth moved to Oxford in 2006, Pauli went with him, completing her PhD there. In 2015, when considering where to establish her own research group, she had offers from multiple top-tier institutions.

Jan-Michael Peters, the IMP’s Scientific Director, recalls that much larger and older institutions were actively recruiting her, including a major American one whose president called directly to make their case. “I got really nervous,” Peters recalls, “and I thought: she’ll never come to the IMP.” But Pauli’s decision came down to daily working life rather than a big name.

“I always compared it back to my time here at the IMP, which was only one and a half years as a graduate student,” Pauli explains. “But it was really very formative for me. Having this community spirit was so strong, and I had never felt this at any other place.”

“Who would be the people that I would interact with on a daily basis, who would be the people that I would hang out with, that I would have a coffee with, that I would discuss science with?” Pauli says. “I think it was very clear to me that the IMP was absolutely top.”

“Having this community spirit was so strong, and I had never felt this at any other place.”

Andrea Pauli, IMP

Peers as proof you belong

How do informal conversations with colleagues shape a scientist’s development?

Ida Jentoft, a postdoc who was a Birnstiel Award winner in 2023, visited the IMP four times in one year before joining. “I always left with this really strong feeling of motivation,” she says. “Everywhere you go here, there are people sitting with computers discussing science.”

But her advice for young scientists isn’t about finding a perfect environment; it’s about using the one you’re in.

“Engage with the people around you, especially people outside your field,” Jentoft suggests. “And it doesn’t really have to be a group leader or some bigshot professor coming to a conference, but also the PhD student next door, or a postdoc, or the person who gave a Monday Seminar you thought was cool.”

The magic happens in translation. “When you get to discuss your project with someone who doesn’t know it to that great detail, you get these curiosity-driven questions, and you also realize how much you know about what you’re working on and why it’s interesting. You kind of realize, ‘oh, actually, I do know a lot about what I’m doing.’”



Weekly social hours bring researchers from the IMP, IMBA, and the GMI together, creating the kind of peer network described by Ida Jentoft.

The formula that endures

Forty years separate the daily soap-opera breaks of the Superti-Furga generation from Jentoft’s computer-based discussions, but the formula remains unchanged: put smart people in small labs. Give them coffee. Let them talk to their neighbors. Some of them will leave only to return. Some of them will change biology. All of them will realize they know more than they think. ●

“When you get to discuss your project with someone who doesn’t know it to that great detail, you get these curiosity-driven questions, and you also realize how much you know about what you’re working on and why it’s interesting.”

Ida Jentoft, IMP

The shape of 40

Numbers that capture what has changed since 1985, and what the IMP has built in the process.

60 to 90 average research papers published by IMP scientists per year in international peer-reviewed journals

93 patents filed based on discoveries made at the IMP since its founding in 1985

13 IMP research groups, including one joint IMP/IMBA research group, in fields ranging from neurobiology to cancer research

40 countries represented among the IMP’s roughly 200 researchers

700 meals prepared each day by the in-house staff at the IMP cafeteria

280 seats in the lecture hall at the IMP, the largest venue on the Vienna BioCenter campus

2 years to build the IMP’s current home, from March 2015 to March 2017

The IMP's Scientific Advisory Board

Each year, the IMP invites external scientific leaders to review its work and keep the institute's scientists on their toes.

From the early days of the institute onwards, the IMP's Scientific Advisory Board (SAB) has functioned less like a formal checkpoint and more like a recurring deep review by people who help to define modern molecular biology.

From first-generation pioneers to the present SAB, the distinctive feature is a balance between continuity in the evaluation process and innovation in the guidance that results from it: an annual, institute-wide conversation that repeatedly

pressure-tests what IMP research groups have chosen to work on, what they have opted not to work on, and whether the questions asked remain ambitious enough to matter.

Sparring partners, mentors, ambassadors of the institute: members of the SAB are distinguished leaders in their fields and play a vital role in keeping the IMP on its course of excellence.



Top (left to right): **Taekjip Ha**, Harvard Medical School, Boston (US); **Eva Nogales**, University of California, Berkeley (US); **Adrian Bird**, University of Edinburgh (UK)

Bottom (left to right): **Norbert Kraut**, Boehringer Ingelheim RCV, Vienna (AT); **Ruth Lehmann**, Whitehead Institute for Biomedical Research, Cambridge (US); **Scott Lowe**, Memorial Sloan Kettering Cancer Center, New York (US); **Dirk Schübeler**, Chair, Friedrich Miescher Institute for Biomedical Research, Basel (CH)

Sponsors and partners

Discovery does not happen in isolation. Every breakthrough at the IMP is made possible by organizations that believe that fundamental research matters – and that choose to invest in curiosity, talent, and long-term scientific vision.

Scientists at the IMP pursue basic research with the conviction that understanding life at the molecular level can lay the foundations for biomedical innovation. This ambition requires not only outstanding minds in a vibrant intellectual environment but also sustained trust and financial commitment from partners who share the IMP's belief in the power of discovery-driven science.

The IMP is deeply grateful to sponsors and funding organizations for enabling this work. Their support provides the freedom to explore bold ideas, to develop innovative technologies, to train the next generation of researchers, and to create an environment where excellence can thrive.

In particular, the IMP thanks its main sponsor, Boehringer Ingelheim, whose long-standing commitment has been instrumental in shaping the institute's scientific achievements. Together with many other funding partners, they make it possible for IMP scientists to ask fundamental questions – and to pursue answers that can change how we understand biology in health and disease.



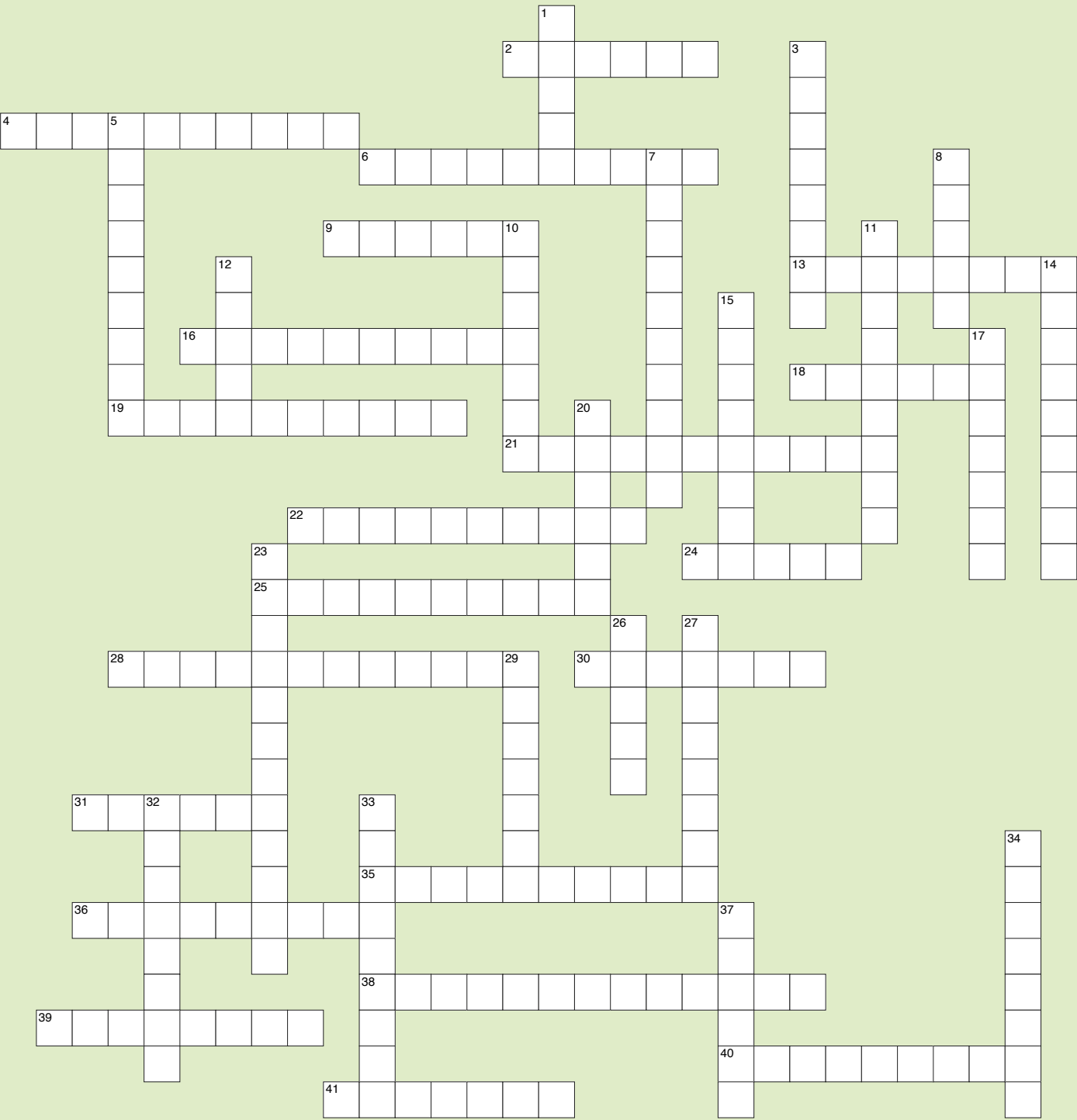
Sponsors and partners in 2025

Alex's Lemonade Foundation
 ÖAW – Austrian Academy of Sciences
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 ERC – European Research Council
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 Swiss National Science Foundation
 The European Lymphoma Institute
 Thermo Fisher Scientific
 WWTF – Vienna Science and Technology Fund



How well do you know the IMP?

Test your knowledge of the institute's science, history, and community, or flip back through the IMP Research Report and Facilities & Community to track down the answers.



ACROSS

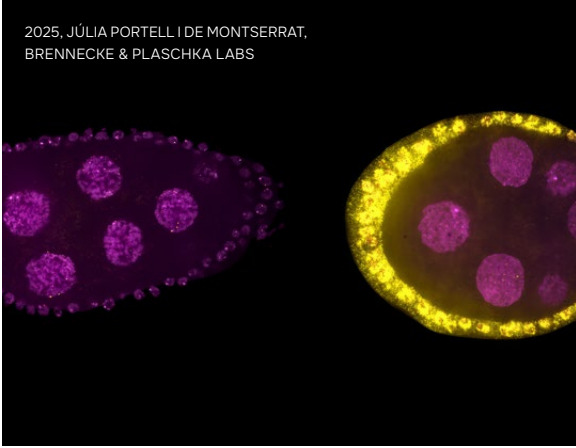
- 2. Tissue whose proteins are studied by the Clausen lab at the IMP to understand how disease-associated mutations lead to dysfunction and premature aging (6)
- 4. The model organism maintained by a Vienna BioCenter Core Facility whose animal stocks support between 400 and 500 publications per year (10)
- 6. IMP scientist whose lab builds new microscopes and develops the mathematical methods that allow individual molecules to be tracked inside living cells with nanometer precision (10)
- 9. An early stage in the development of multicellular organisms that the Pinheiro lab recreates using stem cells, to study how the protective membrane surrounding it builds its distinct structure (6)
- 13. Annual prize for early-career researchers, established in memory of a former IMP PhD student (8)
- 16. The international song contest, whose Vienna staging forced a complete rescheduling of a Vienna BioCenter scientific conference after every hotel room in the city was booked (10)
- 18. The platform launched in March 2025 by the Vienna BioCenter Scientific Training Unit that grew to nearly 1000 members within months, connecting former researchers with current students for career guidance (6)
- 19. The skill that researchers develop through repeated setbacks, and is a facet of almost every scientific career (10)
- 21. The TV soap opera that the IMP's first generation of PhD students and postdocs watched together at five o'clock each day before returning to the labs (two words) (11)
- 22. The structure that packages DNA in the cell nucleus, whose abnormal organization when cohesin is defective can contribute to cancer and birth defects, according to research from the Peters lab at the IMP (10)
- 24. IMP scientist who discovered that mammals, like plants and bacteria, use a sensing mechanism called Effector-Triggered Immunity to detect and respond to the activities of invading pathogens (5)
- 25. The category of disease that can result from mutations in FOXP3, the master protein studied in a lab at the IMP that keeps the immune system from attacking the body's own tissues (10)
- 28. IMP scientist whose lab engineers mouse models to study how regulatory T cells maintain immune balance, preventing the body from attacking its own healthy tissues (three words) (12)
- 30. Biannual award for cancer research, won by IMP scientists in both 1988 (Hartmut Beug) and 2025 (Anna Obenauf) (7)
- 31. IMP scientist whose lab discovered that the protein cohesin organizes the genome by reeling DNA into loops, a mechanism now recognized as fundamental across all kingdoms of life (6)
- 35. The ability of tumor cells to survive treatment by rewiring their signaling pathways and manipulating the immune system, and the central problem that the Obenauf lab at the IMP works to understand and overcome (10)
- 36. The radio and electronics company whose former factory in St. Marx was converted into the IMP's first laboratory building in 1988 (9)
- 38. The fundamental process by which a cell reads its DNA to produce RNA, whose control by enhancers and other regulatory sequences is decoded by the Stark lab at the IMP using a combination of experiments and artificial intelligence (13)
- 39. A particle formed by a group of atoms, held together by chemical bonds—which the Balzarotti lab aims to resolve microscopically, using DNA barcoding techniques that assign each target a unique code, allowing dozens of different species of such a particle to be mapped simultaneously at nanometer resolution (8)
- 40. One of the theatrical formats the Vienna BioCenter Amateur Dramatic Club has staged on campus since 2008, alongside rehearsed readings with visiting playwrights (9)
- 41. IMP scientist whose lab studies how cells mark unwanted proteins for destruction, with implications for developing new antibiotics and understanding muscle disease (7)

DOWN

- 1. IMP scientist whose lab designs rational drug combinations that target the specific vulnerabilities of cancer cells, with the goal of preventing tumors from adapting and developing resistance to treatment (5)
- 3. IMP scientist who investigates the mechanical and chemical forces that drive cells to self-organize into the right shapes during the earliest stages of embryonic development (8)
- 5. Computational scientist who completed three collaborative publications during a one-year visiting stay at the IMP in 2025, making machine learning tools accessible to experimental researchers (9)
- 7. A gene that can copy and reinsert itself throughout the genome, posing a constant threat to genome stability that the Klumpe lab at the IMP investigates in fruit fly germline cells (10)
- 8. The approximate number of countries represented among the roughly 255 researchers at the IMP in 2025 as given in this report (5)
- 10. IMP scientist whose lab developed CaTCHseq, a platform that traces in real time how tumors develop resistance to treatment and how cancer cells learn to evade immune attack (7)
- 11. The molecular tag attached to damaged or unwanted proteins to mark them for recycling, whose chain structures and signals are studied by the Haselbach lab at the IMP (9)
- 12. IMP scientist whose lab combined AI-based protein structure prediction with experiments to identify the protein complex behind the first molecular contact between sperm and egg, described as the first kiss of life (5)
- 14. IMP scientist whose cryo-electron microscopy technology platform studies how the proteasome adapts its structure to meet the cell's changing needs (9)
- 15. IMP scientist whose lab investigates how molecular machines package and export messenger RNA from the cell nucleus to the site of protein production (8)
- 17. The AI research institute co-founded at the Vienna BioCenter in September 2024 to make artificial intelligence a partner in generating scientific hypotheses (7)
- 20. Scientist now at IMBA and the IMP, whose cryo-electron tomography partnership with the Brennecke lab at IMBA produced a landmark paper in the journal *Cell* in 2025 (6)
- 23. Visual design element created by algorithmically mirroring and tessellating microscopy images submitted by research groups at IMBA and the IMP (12)
- 26. IMP scientist whose lab developed DeepSTARR, a neural network that predicts how DNA sequences control gene activity, enabling the design of entirely synthetic enhancers (5)
- 27. The reversible “freeze” in embryonic development used by species including killifish, bears, and marsupials to wait for better conditions, whose molecular mechanisms are studied by the Pauli lab at the IMP (8)
- 29. The compartment inside every cell that acts as a gatekeeper between the DNA blueprint and the protein-making machinery, and whose molecular gates the Plaschka lab at the IMP studies by investigating how messenger RNA passes through them (7)
- 32. The number of research groups at the IMP in its 41st year, working across fields from genome organization to cancer research (8)
- 33. Founding scientific director of the IMP, who recruited its first staff members and initiated the partnership with the University of Vienna that gave rise to the Vienna BioCenter (9)
- 34. A disease-causing organism whose DNA, when detected floating in the cell's interior rather than safely stored in the nucleus, triggers a powerful immune alarm studied by the Gaidt lab at the IMP (8)
- 37. The gene-editing technology used by the Zuber lab at the IMP to run large-scale screens that reveal which genes cancer cells depend on to survive (6)



Scan the code to check your answers.



Transposon expression (yellow) is silenced by PIWI in *Drosophila melanogaster* ovaries (left), but activates in the absence of PIWI and its partners (right).

Imprint

Published by

IMP Research Institute of Molecular Pathology
Campus Vienna BioCenter 1, 1030 Vienna, Austria

imp.ac.at

Managing Directors: Jan-Michael Peters (Scientific), Harald Iseemann (Finance and Administration)

Project management and editing

IMBA / IMP Communications & Events
Project lead: Adam Cooper
Contributions: Semhar Araya, Adam Cooper, Manel Llado, Benedikt Mandl, Anna Stanescu, Sylvia Weinzettl

Writing and editorial lead

Curio & Co, Kristie Shepherd

Copyeditor

Oliver Gascoigne

Further contributors

Researchers and staff contributing interviews, insights, and survey responses.

Photography

Lukas Beck and Anna Stöcher, with additional photography by IMP researchers and staff.
Photoshoots supported by GMI Communications.

Production

Creative, design, and layout: The Gentlemen Creatives
Printing: Riedel Druck
Paper: Cover, Magno Satin PEFC standard matt, 200 g/m², double-sided cellophane lamination;
Inside, Olin Smooth Ultimate White, 120 g/m²

Font

The headings and titles in this book are set in Purista, a sans serif typeface designed by Tomáš Brousil and released by Suitcase Type Foundry in Prague in 2012. The text is set in Onest, a typeface designed by Dmitri Voloshin in the early 21st century. It was originally created as a modern national typeface for Moldova and released as an open-source font.

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