IIMCB

Report

2024-2025

International Institute
of Molecular and Cell Biology
in Warsaw

IIMCB

International Institute
of Molecular and Cell Biology in Warsaw

4 Ks. Trojdena Street
02-109 Warsaw, Poland
(48) 225 970 700
secretariat@iimcb.gov.pl

www.iimcb.gov.pl

IIMCBinWarsaw
IIMCB_Poland
International Institute of Molecular and Cell Biology in Warsaw
iimcb_warsaw
iimcb.bsky.social

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RACE

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Two Years in Motion: IIMCB Report 2024–2025

Foreword by Prof. Marta Miączyńska, Director

You are holding a report that captures two full years of IIMCB's work. In 2024-2025, we celebrated IIMCB's 25th anniversary, an opportunity not only to look back at how far we have come since our beginnings in 1999, but also to appreciate the people who have shaped this journey.

Today, our scientific identity is shaped by 15 research groups working in the broad fields of RNA and cell biology, with experimental work spanning levels of complexity from atoms and macromolecules to cells, tissues, and whole organisms. Our program in RNA biology encompasses, among others, studies on RNA metabolism, structure and interactions, as well as the biology of RNA viruses, and it has strong links to RNA-based therapies of infectious diseases and cancer. The cell biology pillar involves investigating intracellular mechanisms and cellular responses relevant to congenital rare diseases, neurodegeneration and cancer. This broad portfolio of research by our laboratories is strongly supported by professional core facilities that form an integrated infrastructure platform IN-MOL-CELL and offer state-of-the-art scientific services and methodological expertise.

Throughout 2024 and 2025, IIMCB researchers published extensively in leading international journals (see section on Best Papers Awards), confirming the high impact and global relevance of our work. Our results not only advance fundamental knowledge but also create foundations for translational applications in biomedicine and biotechnology. The growing number of competitive grants and high-quality publications demonstrates that our science stands up to the most demanding international standards.

Acceleration through RACE

Importantly, January 2024 marked the official inauguration of the Horizon Europe Teaming for Excellence RACE project, a milestone that strengthened our ambitions for the future and allowed for the dynamic growth of IIMCB.

RACE is a project designed to further boost the quality of our science by providing a framework to attract and retain outstanding researchers through comprehensive research and organizational support. A defining strength of RACE is the ecosystem it connects us to. We work closely with two partner institutions: the MRC Human Genetics Unit of the University of Edinburgh and the Flanders Institute for Biotechnology (VIB) in Belgium. These partnerships matter for learning, benchmarking, and building long-term capability, so that excellence becomes a durable feature of IIMCB.

Thanks to RACE, in 2024-2025, we established two new laboratories and expanded our core facilities, also through major infrastructural investments into the IN-MOL-CELL platform funded by the Polish National Recovery Plan. Our dedicated Technology Transfer Office, established in 2024, helps move promising research results toward real-world application, supports researchers in protecting intellectual property, and builds pathways for collaboration with industry and other partners.

At the same time, we reinforced the Institute's long-term mission of education. Thanks to the right to confer PhD degrees, we were able to reach a historic milestone in 2025 – the first PhD defense held at IIMCB. Now the entire doctoral journey can take place within our Institute from education and research to the final award of the degree. It is an important step toward building a fully integrated academic environment and taking responsibility for every stage of scientific development of young researchers.

Over the past two years, nearly 230 people have contributed their talent, energy, and commitment to our shared progress. Scientists, core facility specialists, and administrative professionals work side by side, not in parallel but together.

Marta Miączyńska, PhD, Professor

Community, Proven in Practice

Our administration is not a background function. It quietly shapes the conditions that allow science to thrive by ensuring compliance, safeguarding financial stability, enabling partnerships, and keeping the Institute visible and credible. Especially in times of rapid growth and change, such as those described in this report, this collective effort becomes most visible.

Our community further solidified its national and international standing through prestigious scientific awards, invitations to high-level advisory bodies, and positions that place IIMCB at the heart of European science and policy conversations. Notably, through EU-LIFE, we participated in strategic dialogues in Brussels regarding the future of European research and innovation — driven by the conviction that scientific excellence must have a decisive voice.

The sense of acceleration and confidence that we are experiencing today at IIMCB is not a coincidence. It stems from the community that thrives because people believe in it and in one another. For that, I am deeply grateful to everyone who helps make IIMCB what it is. I am convinced the dynamism of the recent developments will stay with us in the years ahead.

To place these two years in a wider perspective, I also invite you to explore our 25th anniversary brochure, available via a QR code. It offers a complementary narrative of where we come from, what shaped our culture, and what we have achieved together so far. The future will undoubtedly bring new exciting chapters to this story.

25 YEARS OF IIMCB BROCHURE

About IIMCB

The International Institute of Molecular and Cell Biology in Warsaw (IIMCB) stands at the forefront of life sciences research, dedicated to uncovering the mechanisms that govern organisms at the cellular and molecular levels. With a commitment to both basic and applied research, IIMCB seeks to deepen our understanding of the biological foundations of life.

Mission

We support ambitious scientists of any nationality driven by a passion to pursue frontier research that aims to make a difference in society.

We follow the principles of scientific freedom, integrity, and responsibility.

We help researchers develop their careers through training and mentoring at all levels and encourage collaboration among them.

We provide efficient administrative support that enables scientists to focus on their research.

Research Areas and Laboratories

Focusing primarily on RNA and cell biology, the Institute aims to understand the fundamentals of human disease, which form the basis for the development of innovative therapeutic and diagnostic methods. IIMCB's research focuses on infectious, neurological, oncological, and rare diseases. It spans multiple levels of biological organization, integrating molecular, cellular, and organismal approaches to address complex biomedical questions. By combining fundamental discovery with translational potential, the Institute bridges basic science and innovation, fostering research that can ultimately impact clinical practice.

Bioinformatics and Protein Engineering
Cell Biology
Cellular Genomics
Cellular Proteostasis
Iron Homeostasis
Molecular and Cellular Neurobiology
Neurodegeneration
Protein Metabolism
Protein Structure
Prokaryotic Gene Regulation
RNA Biology
RNA-Protein Interactions
RNA Viruses
Structural Biology
Zebrafish Developmental Genomics

25 Years of IIMCB Science in Numbers

1519
publications & preprints

61
average citations per article

2/3
papers in JCR category Q1

Q1
Q2
Q3
Q4

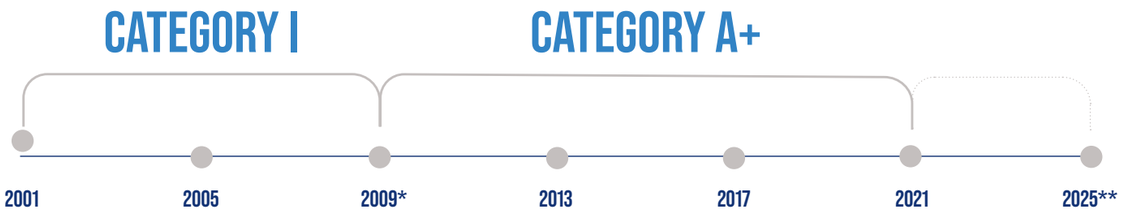
127
Hirsh Index by WoS

391
grants

Poland's Top Research Institute

The Institute has consistently received the highest scientific category in evaluations conducted by the Ministry of Science and Higher Education of Poland.

Ministry of Science and Higher Education recognises the work of IIMCB in its evaluation



*In 2009, the evaluation system was changed.
** Evaluation in progress.

Unique Legal Status

IIMCB was established in 1995 by an international agreement between the Government of the Republic of Poland and UNESCO, and was further confirmed by the Act of the Polish Parliament of June 26, 1997.

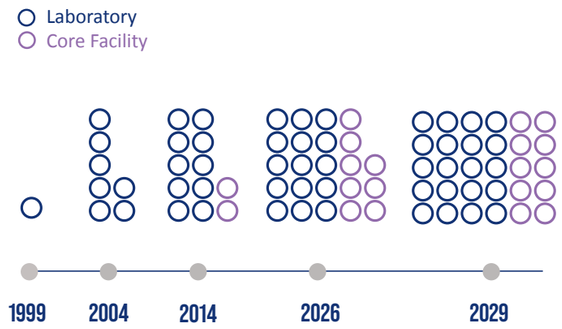
The Institute was granted special status. This recognition ensures the Institute's independence and international character and brings it into line with the standards of the world's leading research institutions.

Signing of the agreement establishing IIMCB between the Government of Poland and UNESCO on May 26, 1995, in Paris.

Dynamic Growth

IIMCB is in a phase of dynamic scientific and institutional growth. The Institute continues to expand its research capacity and infrastructure while maintaining a strong focus on RNA and cell biology. Research groups operate within and across these two areas, reflecting both disciplinary depth and scientific collaboration. The ongoing development of core facilities ensures that researchers have access to the tools and technologies needed to address increasingly complex biological questions.

A dedicated Technology Transfer Office supports efforts to connect research with practical applications. This integrated approach positions IIMCB as a center where high-quality science is supported by a forward-looking research environment.



Strategic Projects Driving IIMCB's Growth

Since 2023, the Institute has been leading the EU-funded RACE project (RNA and Cell Biology – from Fundamental Research to Therapies), aimed at transforming IIMCB into a world-class center of excellence in RNA and cell biology. Another initiative, RACE-PRIME, focuses on developing new approaches to treat diseases that currently lack effective therapies. Additionally, funding from the National Recovery Plan supports the purchase of cutting-edge research infrastructure. These three strategic grants, fueled by both national and international funding, are the pillars of the Institute's growth.

Institutional & scientific development	**RACE** €15,000,000
Scientific development	**RACE-PRIME** €8,000,000
Infrastructure development	**IN-MOL-CELL Infrastructure** €17,000,000

Shaping European Science Policy through EU-LIFE

IIMCB, as a member of the EU-LIFE alliance, collaborates with 16 leading independent research institutes to achieve and maintain excellence in the life sciences. This collaboration promotes cutting-edge and responsible science and contributes to discussions on European science policy. EU-LIFE brings together internationally renowned research centers recognized for scientific excellence, knowledge transfer, and talent development. In 2024-25, director Marta Miączyńska served as Vice-Chair, and in 2026-27, she serves as Chair of EU-LIFE.

EU-LIFE

PhD education:

Training the Next Generation of Scientists

IIMCB provides doctoral training within the framework of the Warsaw PhD School in Natural and Biomedical Sciences (Warsaw-4-PhD). PhD candidates complete the full doctoral cycle at the Institute, from structured training to dissertation defense.

The Warsaw-4-PhD School was established by nine research institutions in Warsaw and offers doctoral education in four disciplines: biology, chemistry, physics, and medical sciences. Candidates apply to specific research projects carried out within one of the participating institutions.

Recruitment is organized as an open international competition held three times a year, with studies beginning in the winter or summer semester.

Doctoral candidates at IIMCB are recruited from among graduates holding a Master's degree or equivalent, with a strong interest in biological research and sufficient proficiency in English to work effectively in an international environment.

Each doctoral student follows an individual research plan under the supervision of a dedicated supervisor. Progress is assessed through a mid-term evaluation conducted halfway through the program.

21 PhD degrees were awarded in total in 2024 and 2025, including 5 with distinction.

Supporting PhD Researchers at IIMCB

- Free education at the doctoral school.
- Support from the Grants Office in applying for additional funding.
- Academic supervision and mentoring – close cooperation with a supervisor and support from a research team.
- Representation through the PhD Council – ensuring PhD students' voices are heard through regular dialogue with IIMCB management and the International Advisory Board.
- An international working environment with English as the main language of communication.
- Comprehensive support for foreign students – assistance with obtaining a visa, legalizing residence, and completing all other formalities.
- Opportunities for international development through participation in conferences and workshops, foreign internships, with financial support for travel.
- Administrative assistance from the PhD Office.
- Health and social benefits – co-financing of private medical care, sports cards, training, cultural events, and other benefits available to IIMCB employees.

IIMCB Puts into Practice its Authority to Confer Doctoral Degrees.

In 2025, IIMCB started to award PhD degrees with its affiliation, enabling the completion of the entire doctoral pathway within a single institution.

SCAN FOR MORE

April 3, 2025: Anne Spang, Chair of the International Advisory Board, ceremonially presented Michał Brouze with his doctoral diploma.

Organizational Structure

International Advisory Board

Chair of the Board

Anne Spang, University of Basel

Secretary of the Board

Juan Valcárcel Juárez, Center for Genomic Regulation

Members

Shelley Berger, University of Pennsylvania

Jo Bury, Flanders Institute for Biotechnology

Aaron Ciechanover, Technion – Israel Institute of Technology

Susan Gasser, Foundation of the Swiss Institute for Experimental Cancer Research

Reinhard Jahn, Max Planck Institute for Multidisciplinary Sciences

Jolanta Jura, Jagiellonian University

Caroline Kisker, University of Würzburg

Brenda Schulman, Max Planck Institute of Biochemistry

Lilianna Solnica-Krezel, Washington University in St. Louis

Eric Westhof, University of Strasbourg

Joanna Wysocka, Stanford University

Permanent Advisor

Angelo Azzi, Tufts University

Director
(Marta Miączyńska)

Directors Office

- PhD Office
- Communications Office
- Scientific Coordination Unit
- Technology Transfer Office
- Centre of Innovative Bioscience Education

Deputy Director for Development
(Urszula Białek-Wyrzykowska)

Deputy Director for Science
(Jacek Jaworski [2024], Marcin Nowotny [2025-])

- Laboratory of Structural Biology
- Laboratory of RNA Viruses
- Laboratory of Bioinformatics and Protein Engineering
- Laboratory of RNA Biology - ERA Chairs Group
- Laboratory of Molecular and Cellular Neurobiology
- Laboratory of Cellular Genomics
- Laboratory of Neurodegeneration
- Laboratory of Prokaryotic Gene Regulation
- Laboratory of Cell Biology
- Laboratory of RNA-Protein Interactions - Dioscuri Centre
- Laboratory of Iron Homeostasis
- Laboratory of Protein Structure
- Laboratory of Protein Metabolism
- Laboratory of Zebrafish Developmental Genomics
- Laboratory of Cellular Proteostasis
- Laboratory of Biomolecular Interactions and Transport AMU/IIMCB
- Grants Office

Director's Representative for Organizational Transformation

- Human Resources Unit
- Auresine Project
- Self-contained position for OHS
- Self-contained position for controlling
- Technology Development Unit
- Institute's Archives

Deputy Director for Finance / Chief Accountant
(Hanna Iwaniukowicz - until May 2025)

- Financial and Accounting Unit

Deputy Director for Operations
(Anna Zolnik)

- IT Unit
- Operations Unit
- Public Procurement Unit

Director's Representative for Core Facilities
(Andrzej Dziembowski)

- Bioinformatics Facility
- Biophysics and Bioanalytics Facility
- Cellular Models and Organoids Facility
- Genome Engineering Facility
- Genomics Facility
- Mass Spectrometry Facility
- Microscopy Facility
- Preclinical Drug Development Facility
- Rodent Facility
- Zebrafish Core Facility

2024–2025 at a Glance

Expanding Horizons

2 NEW LABS

New laboratories established:

- Laboratory of Cellular Proteostasis – **Dr. Lidia Wróbel**
- Laboratory of RNA Viruses – **Dr. Stefan Bresson**

CORE FACILITIES UPGRADED

New and expanded infrastructure:

- Bioinformatics Facility – **Dr. Anna Hojka-Osińska, Dr. Jacek Szymański**
- Mass Spectrometry Facility – **Dr. Vanessa Linke**
- Genome Engineering Facility **Dr. Michał Brouze**

IN-MOL-CELL LAUNCHED

IN-MOL-CELL launched as an integrated research infrastructure, ultimately comprising 10 core facilities, including technologies unique in Poland (e.g. the country's first mass photometer).

Steering Progress in Life Sciences

RECOGNITIONS:

National recognitions:

- Prime Minister's Award – **Prof. Marcin Nowotny**
- Minister of Science Award & PAS Prize – team of **Prof. Wojciech Pokrzywa**
- Herbert Reisner Prize – **Dr. Ewa Liszewska** and **Prof. Jacek Jaworski**
- Minister of Science and Higher Education Award for lifetime achievements – **Prof. Jacek Kuźnicki**
- PAS distinction – team led by **Prof. Gracjan Michlewski**
- Jakub Karol Parnas Award – team led by **Prof. Andrzej Dziembowski**

International standing:

- **Prof. Janusz Bujnicki** and **Dr. Vladimir Korzh** listed among the top-cited scientists in report by Stanford University and Elsevier.

146 SCIENTIFIC PUBLICATIONS

MODOMICS

Major resources for the field: MODOMICS expanded, including release of 48,000 RNA sequences with modified residues; IIMCB contribution to the global Human RNome Project.

TALENT & RECOGNITION:

Dr. Lidia Wróbel – EMBO Installation Grant; L'Oréal-UNESCO For Women in Science Fellowship.

Empowered by Funding

68 GRANTS

running in 2024–2025 with total awarded funding of 346,441,596 PLN.

1 M PLN DONATION

1 M PLN private donation to Parkinson's disease research (Laboratory of Neurodegeneration, **Prof. Jacek Kuźnicki).**

347 M PLN AWARDED IN GRANTS

Example: Medical Research Agency-funded study by the Laboratory of Cellular Genomics led by **Dr. Aleksandra Kołodziejczyk** recruiting 400 participants (liver state and gut microbiota; diagnostic development).

Strengthening Collaboration & Visibility

98 SEMINARS

In total: 50 external and 48 internal

TECHNOLOGY TRANSLATION CAPACITY:

Technology Transfer Office led by **Dr. Kornelia Mikuła** established; RACE Incubator launched; strategic partnership with LIFE bioCEEd to identify translational projects initiated.

HORIZON EUROPE TEAMING FOR EXCELLENCE:

RACE

The official inauguration of Horizon Europe Teaming for Excellence: RACE, with strategic partners supporting institutional development.

Skills for innovation: participation in VIB Innovation & Business Summer School (Ghent) and delivery of the Technology Transfer & Commercialization Course (1st edition at IIMCB).

European research policy engagement via EU-LIFE (Director Marta Miączyńska meeting with Ekaterina Zaharieva, European Commissioner for Startups, Research and Innovation).

600+

high-quality media coverage over two years.

The Architecture of Excellence:
Three Strategic Projects

Three complementary strategic projects – RACE, RACE-PRIME, and IN-MOL-CELL Infrastructure – form a structured development framework for IIMCB. Together, they strengthen institutional capacity, advance cutting-edge research in RNA and cell biology, and expand state-of-the-art infrastructure, positioning the Institute for sustained scientific and translational impact.

From Past to Future – RACE Sets the Course

In 2023, the IIMCB launched the “RNA and Cell Biology – from Fundamental Research to Therapies” project (acronym RACE). The project aims to transform the Institute into a world-class Centre of Excellence in RNA and Cell Biology, combining scientific excellence with a strong emphasis on commercialization activities to translate research outcomes into market-ready therapies.

By 2029, the Institute plans to reach a critical mass of 20 scientific groups with complementary expertise in RNA and cell biology; train the next generation of entrepreneurial researchers; develop sustainable core facilities tailored to industry needs; establish a professional technology transfer incubator; and digitalize administrative processes. All activities are implemented with the support of the project partners: the Medical Research Council Human Genetics Unit (MRC-HGU) at the University of Edinburgh, UK, and the Flanders Institute for Biotechnology (VIB), Belgium.

RACE is funded by a grant of nearly €15,000,000 from the Horizon Europe Teaming for Excellence programme (GA No. 101059801) and was ranked first in the 2022 call. The implementation period covers September 1, 2023 - August 30, 2029.

Project: RACE Partners: IIMCB VIB THE UNIVERSITY of EDINBURGH Funding: Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Research Executive Agency. Neither the European Union nor the granting authority can be held responsible for them.

From Research to Therapies – RACE-PRIME Delivers Impact

In 2024, the IIMCB launched the “RNA and Cell Biology Platform for Research and Innovation in Medicine” (RACE-PRIME). Complementary to the Horizon Europe Teaming project RACE, RACE-PRIME strengthens our capacity to translate cutting-edge basic research into innovative therapeutic strategies for human diseases where current treatments remain inadequate or unavailable.

The project focuses on two research areas: advanced models of rare diseases aimed at enabling the development of personalized therapies, coordinated by Prof. Marta Miączyńska; and antiviral and antimicrobial therapeutic strategies, coordinated by Prof. Gracjan Michlewski.

RACE-PRIME is funded with €8,000,000 under the International Research Agendas programme of the Foundation for Polish Science (FNP), financed by the European Funds for Smart Economy 2021-2027 (FENG).

European Funds for Smart Economy | Republic of Poland | Co-funded by the European Union | FNP Foundation for Polish Science

From Modern to State-of-the-Art: IN-MOL-CELL Infrastructure Advances the Core

In 2024, the IIMCB launched the “Research Infrastructure for Molecules and Cells” project under Poland’s National Recovery and Resilience Plan. The project strengthens the Institute’s technological capacity through major investment in advanced instrumentation and specialized personnel, supporting both basic and translational research.

Since the end of 2025, six core facilities are fully functional: Biophysics and Bioanalytics Facility; Genome Engineering Facility; Microscopy Facility; Preclinical Drug Development Facility; Rodent Facility; Zebrafish Facility, and four under development: Bioinformatics, Genomics, Mass Spectrometry Facility, and Cell Models and Organoids.

The infrastructure enables end-to-end workflows – from genome editing and *in vivo* disease modelling to multi-omics analyses and preclinical drug development – implemented through a coordinated, multi-platform model aligned with leading European standards.

The Research Infrastructure for Molecules and Cells project is funded by a grant of approximately €17,000,000 under Poland’s National Recovery and Resilience Plan. The implementation period covers 2024–2026 (Agreement No. KPOD.01.18-IW.03-0006/23) within Investment A2.4.1 “Investments in expanding research potential,” Scheme A: Research Infrastructure – initiatives from the Polish Roadmap for Research Infrastructures.

NATIONAL RECOVERY PLAN | Republic of Poland | Funded by the European Union NextGenerationEU

IN-MOL-CELL Infrastructure funded by the European Union – NextGenerationEU under National Recovery and Resilience Plan. IN-MOL-CELL Infrastructure was also funded by the European Union under Horizon Europe (Project 101059801 - RACE) and by RACE-PRIME project carried out within the IRAP programme of the Foundation for Polish Science co-financed by the European Union under the European Funds for Smart Economy 2021-2027 (FENG).

Best Papers Awards

The Best Papers Awards celebrate distinguished publications by researchers at IIMCB.

The Institute annually honors research excellence with its Best Papers Awards, focusing on the significance and content of research, rather than relying on bibliometric indicators. All authors from the IIMCB can submit their scientific experimental work. Laboratory Leaders review the nominated papers, refraining from voting for their own lab's work. The selection concludes in a meeting where the most impactful submissions are chosen, underscoring IIMCB's dedication to scientific excellence.

Authors marked in bold are affiliated with IIMCB.

Best Papers Awards 2024

1st prize

TENT5-mediated polyadenylation of mRNAs encoding secreted proteins is essential for gametogenesis in mice

Nature Communications

Laboratory of RNA Biology
- ERA Chairs Group

Michał Brouze
Agnieszka Czarnocka-Cieciura
Olga Gewartowska
Monika Kusio-Kobiałka
Kamil Jachacy, Marcin Szpila
Bartosz Tarkowski
Jakub Gruchota
Paweł Krawczyk
Seweryn Mroczek
Ewa Borsuk
Andrzej Dziembowski ✉

READ ARTICLE

Abstract

Cytoplasmic polyadenylation plays a vital role in gametogenesis; however, the participating enzymes and substrates in mammals remain unclear. Using knockout and knock-in mouse models, we describe the essential role of four TENT5 poly(A) polymerases in mouse fertility and gametogenesis. TENT5B and TENT5C play crucial yet redundant roles in oogenesis, with the double knockout of both genes leading to oocyte degeneration. Additionally, TENT5B-GFP knock-in females display a gain-of-function infertility effect, with multiple chromosomal aberrations in ovulated oocytes. TENT5C and TENT5D both regulate different stages of spermatogenesis, as shown by the sterility in males following the knockout of either gene. Finally, Tent5a knockout substantially lowers fertility, although the underlying mechanism is not directly related to gametogenesis. Through direct RNA sequencing, we discovered that TENT5s polyadenylate mRNAs encoding endoplasmic reticulum-targeted proteins essential for gametogenesis. Sequence motif analysis and reporter mRNA assays reveal that the presence of an endoplasmic reticulum-leader sequence represents the primary determinant of TENT5-mediated regulation.

2nd prize

Pheromone-based animal communication influences the production of somatic extracellular vesicles in *C. elegans*

Nature Communications

Laboratory of Protein Metabolism

Agata Szczepańska*
Katarzyna Olek*
Klaudia Kołodziejska
Jingfang Yu
Abdulrahman Tudu Ibrahim
Laura Adamkiewicz
Frank C. Schroeder
Wojciech Pokrzywa ✉
Michał Turek ✉

(*contributed equally)

READ ARTICLE

Abstract

Extracellular vesicles (EVs) are integral to numerous biological processes, yet it is unclear how environmental factors or interactions among individuals within a population affect EV-regulated systems. In *Caenorhabditis elegans*, the evolutionarily conserved large EVs, known as exophers, are part of a maternal somatic tissue resource management system. Consequently, the offspring of individuals exhibiting active exopher biogenesis (exophergenesis) develop faster. Our research focuses on unraveling the complex inter-tissue and social dynamics that govern exophergenesis. We found that ascr#10, the primary male pheromone, enhances exopher production in hermaphrodites, mediated by the G-protein-coupled receptor STR-173 in ASK sensory neurons. In contrast, pheromone produced by other hermaphrodites, ascr#3, diminishes exophergenesis within the population. This process is regulated via the neuropeptides FLP-8 and FLP-21, which originate from the URX and AQR/PQR/URX neurons, respectively. Our results reveal a regulatory network that controls the production of somatic EV by the nervous system in response to social signals.

3rd prize
(ex aequo)

Structure-functional characterization of Lactococcus AbiA phage defense system

Nucleic Acids Research

Laboratory of Protein Structure

Marta Gapińska*
Weronika Zajko*
Krzysztof Skowronek
Małgorzata Figiel
Paweł Krawczyk
Artyom A Egorov
Andrzej Dziembowski
Marcus J O Johansson ✉
Marcin Nowotny ✉

(*contributed equally)

Abstract

Bacterial reverse transcriptases (RTs) are a large and diverse enzyme family. AbiA, AbiK and Abi-P2 are abortive infection system (Abi)RTs that mediate defense against bacteriophages. What sets Abi RTs apart from other RT enzymes is their ability to synthesize long DNA products of random sequences in a template- and primer-independent manner. Structures of AbiK and Abi-P2 representatives have recently been determined, but there are no structural data available for AbiA. Here, we report the crystal structure of Lactococcus AbiA polymerase in complex with a single-stranded polymerization product. AbiA comprises three domains: an RT-like domain, a helical domain that is typical for Abi polymerases, and a higher eukaryotes and prokaryotes nucleotide-binding (HEPN) domain that is common for many antiviral proteins. AbiA forms a dimer that distinguishes it from AbiK and Abi-P2, which form trimers/hexamers. We show the DNA polymerase activity of AbiA in an *in vitro* assay and demonstrate that it requires the presence of the HEPN domain which is enzymatically inactive. We validate our biochemical and structural results *in vivo* through bacteriophage infection assays. Finally, our *in vivo* results suggest that AbiA-mediated phage defense may not rely on AbiA-mediated cell death.

READ ARTICLE

3rd prize
(ex aequo)

scRNA-seq reveals the diversity of the developing cardiac cell lineage and molecular players in heart rhythm regulation

iScience

Laboratory of Zebrafish Developmental Genomics

Karim Abu Nahia
Agata Sulej
Maciej Migdał
Natalia Ochocka
Richard Ho
Bożena Kamińska
Marcin Zagorski
Cecilia Lanny Winata ✉

Summary

We utilized scRNA-seq to delineate the diversity of cell types in the zebrafish heart. Transcriptome profiling of over 50,000 cells at 48 and 72 hpf defined at least 18 discrete cell lineages of the developing heart. Utilizing well-established gene signatures, we identified a population of cells likely to be the primary pacemaker and characterized the transcriptome profile defining this critical cell type. Two previously uncharacterized genes, atp1b3b and colec10, were found to be enriched in the sinoatrial cardiomyocytes. CRISPR/Cas9-mediated knockout of these two genes significantly reduced heart rate, implicating their role in cardiac development and conduction. Additionally, we describe other cardiac cell lineages, including the endothelial and neural cells, providing their expression profiles as a resource. Our results established a detailed atlas of the developing heart, providing valuable insights into cellular and molecular mechanisms, and pinpointed potential new players in heart rhythm regulation.

READ ARTICLE

Best Papers Awards 2025

1st prize

Laboratory of RNA Biology
- ERA Chairs Group

Paweł S. Krawczyk
Michał Mazur
Wiktoria Orzeł
Olga Gewartowska
Sebastian Jeleń
Wiktor Antczak
Karolina Kasztelan
Aleksandra Brouze
Katarzyna Matylla-Kulińska
Natalia Gumińska
Bartosz Tarkowski
Ewelina P. Owczarek
Kamila Affek
Paweł Turowski
Agnieszka Tudek
Małgorzata Sroka
Tomasz Śpiewla
Monika Kusio-Kobiałka
Aleksandra Wesołowska
Dominika Nowis
Jakub Golab
Joanna Kowalska
Jacek Jemielity
Andrzej Dziembowski ✉
Seweryn Mroczek ✉

READ ARTICLE

Re-adenylation by TENT5A enhances efficacy of SARS-CoV-2 mRNA vaccines

Nature

Abstract

Despite the widespread use of mRNA vaccines against COVID-19, little is known about the metabolism of therapeutic RNAs. Here we use nanopore sequencing to analyse individual therapeutic mRNA molecules, focusing on their poly(A) tails. We show that the Moderna mRNA-1273 vaccine has a poly(A) tail of around 100 nucleotides, followed by an mΨCmΨAG sequence. In cell lines, mRNA-1273 undergoes rapid degradation initiated by mΨCmΨAG removal, followed by CCR4–NOT-mediated deadenylation. However, in medically relevant preclinical models, particularly in macrophages, mRNA-1273 poly(A) tails are extended to up to 200 nucleotides by the TENT5A poly(A) polymerase, which is induced by the vaccine. Re-adenylation, which stabilizes target mRNAs, is consistently observed in synthetic mRNAs that encode proteins targeted to the endoplasmic reticulum, such as ovalbumin or antigens from Zika virus8 or the malaria parasite. The extent of re-adenylation varies: the BioNTech–Pfizer BNT162b2 vaccine shows less potent re-adenylation than mRNA-1273, which correlates with a smaller proportion of membrane-associated BNT162b2. This highlights the crucial role of spatial accessibility to ER-resident TENT5A in determining re-adenylation efficiency. *In vivo*, TENT5A is expressed in immune cells that take up mRNA vaccine, and TENT5A deficiency reduces specific immunoglobulin production for mRNA vaccines after immunization in mice. Overall, our findings reveal a principle for enhancing the efficacy of therapeutic mRNAs, paving the way for improvement.

2nd prize

Laboratory of Iron Homeostasis

Gabriela Zurawska
Zuzanna Sas
Aneta Jończy
Raghunandan Mahadeva
Patryk Slusarczyk
Marta Chwałek
Daniel Seehofer
Georg Damm
Rafał Mazgaj
Marcin Skórzyński
Maria Kulecka
Izabela Rumieńczyk
Morgane Moulin
Kamil Jastrzębski
Kevin Waldron
Michal Mikula
Anders Etzerodt
Remigiusz Serwa
Marta Miączyńska
Tomasz P Rygiel ✉
Katarzyna Mleczko-Sanecka ✉

READ ARTICLE

Liver sinusoidal endothelial cells constitute a major route for hemoglobin clearance

EMBO Reports

Abstract

Mild rupture of aged erythrocytes occurs in the spleen, resulting in hemoglobin (Hb) release, whereas pathological hemolysis characterizes several diseases. Hb detoxification is attributed to macrophages, but other routes of Hb clearance remain elusive. Here, we uncover that Hb uptake is chiefly executed by liver sinusoidal endothelial cells (LSECs) via macropinocytosis. Consistently, LSECs display proteomic signatures indicative of heme catabolism, ferritin iron storage, antioxidant defense, and macropinocytic capacity, alongside high iron content and expression of the iron exporter ferroportin. Erythrocyte/Hb transfusion assays demonstrate that splenic macrophages excel in erythrophagocytosis, while LSECs and Kupffer cells scavenge the spleen-borne hemolysis products Hb and erythrocyte membranes, respectively. High Hb doses result in transient hepatic iron retention, LSEC-specific induction of heme-catabolizing Hmox1, along with the iron-sensing Bmp6-hepcidin axis culminating in hypoferremia. Transcriptional induction of Bmp6 in LSECs is phenocopied by erythrocyte lysis upon phenylhydrazine and elicits a distinct transcriptional signature compared to iron. Collectively, we identify LSECs as key Hb scavengers, a function that establishes the spleen-to-liver axis for iron recycling and contributes to heme detoxification during hemolysis.

3rd prize
(ex aequo)

Structural snapshots of the mechanism of ATP-dependent DNA damage recognition by UvrA

Nature Communications

Laboratory of Protein Structure

Shivlee Nirwal
Mariusz Czarnocki-Cieciura
Weronika Zajko
Krzysztof Skowronek
Roman H. Szczepanowski
Marcin Nowotny ✉

Abstract

Nucleotide excision repair is a DNA repair pathway which detects and fixes various DNA lesions that distort the structure of DNA. In bacteria, the pathway starts with the UvrA protein which has two adenosine triphosphatase modules and forms dimers. The DNA is handed over from UvrA to UvrB, which is a weak helicase that verifies the presence of damage. Despite intense studies, the role of the ATPase activity of UvrA in damage recognition is unclear. Here, we present a series of cryo-electron microscopy structures of UvrA in complex with three different DNAs and in the presence and absence of nucleotides. We also present a structure of UvrA:UvrB:DNA complex. These structures reveal a major rearrangement of the UvrA dimer upon ATP binding. We propose that these conformational changes are used to mechanically probe the integrity of DNA for damage localization. Collectively, our results present snapshots of UvrA's ATP-dependent DNA damage detection.

READ ARTICLE

3rd prize
(ex aequo)

Activity and structure of human (d)CTP deaminase CDADC1

PNAS

Laboratory of Structural Biology

Anton Slyvka ✉
Ishan Rathore
Renbin Yang
Olga Gewartowska
Tapan Kanai
George T. Lountos
Krzysztof Skowronek
Mariusz Czarnocki-Cieciura
Alexander Wlodawer ✉
Matthias Bochtler ✉

Abstract

Vertebrates have evolved an understudied protein termed CDADC1 (NYD-SP15) that contains an inactive N-terminal and active C-terminal DCTD-like domain. Here, we show that human CDADC1 is a (d)CTP-specific deaminase, with a roughly 2-fold *in vitro* preference for dCTP over CTP. We determined high-resolution cryo-EM structures of CDADC1 in the absence of substrate and in complex with dCTP and 5-methyl-dCTP. The structures show that CDADC1 forms trimers and dimers of trimers in solution. The (d)CTP substrate is selected by a narrow pocket for the cytosine base and multiple lysine and arginine contacts to the triphosphate. Substrate binding promotes the association of trimers into hexamers and the transition of the hexamers from a loose to a tighter arrangement. Genetic experiments in mice show that loss of Cdadc1 is surprisingly well tolerated, even in the absence of the dCMP deaminase Dctd that is considered as the main source of dUMP, the precursor of dTTP.

READ ARTICLE

IN-MOL-CELL
Core Technologies at IIMCB

IN-MOL-CELL:
INfrastructure for MOLecules and CELLs

IN-MOL-CELL is the place where world-class expertise, and cutting-edge technologies converge in one integrated infrastructure.

Our mission is to enable breakthrough research and discovery for academia and business by providing end-to-end solutions – from experimental design to data acquisition and analysis. For certain equipment, walk-in access is possible after training.

Explore our Core Facilities:

- Bioinformatics Facility
- Biophysics and Bioanalytics Facility
- Cell Models and Organoid (early stage of development)
- Genome Engineering Facility
- Genomics Facility (early stage of development)
- Mass Spectrometry Facility
- Microscopy Facility
- Preclinical Drug Development Facility
- Rodent Facility
- Zebrafish Core Facility

1 Infrastructure

10 Core Facilities

30+ Experts

VIB THE UNIVERSITY of EDINBURGH

Partnership

At a Glance

Expertise: We are a team of more than 30 scientists. Deep expertise, real passion for science and one clear commitment – to make your research succeed.

Technologies: We offer a comprehensive portfolio of cutting-edge technologies delivering a broad range of research solutions – all under one roof.

Synergy: Our integrated infrastructure enables us to deliver multi-platform research projects, tackling the most complex scientific questions.

Impact: For 15+ years, we have partnered with 100+ clients – from academia to Poland's top R&D companies – delivering critical research solutions across preclinical modeling, biosimilarity studies, structural screening and beyond.

Service philosophy: Your research is our research. We take the time to understand your needs, consult to propose the most effective solutions and bring the same passion and care to your project as we do to our own.

Contact Us

inmolcell@iimcb.gov.pl

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Behind every scientific breakthrough stands the right technology and the right people. At IN-MOL-CELL, we are committed to building core facilities where both can thrive. Through continuous investment, we identify and integrate the most advanced technologies to support pioneering research. We firmly believe that science belongs to everyone, which is why IN-MOL-CELL is open and accessible to all researchers, welcoming users from universities, research institutes, and industry alike.

Olga Gewartowska, PhD
Head of the Technology Development Unit

Bioinformatics
Facility

Accelerating Discovery Through Computational Biology.

By working hand in hand with the Genomics and Mass Spectrometry Facilities, we offer a fully integrated data-to-insight service. This unique collaboration ensures exceptional data quality and cutting-edge bioinformatic interpretations.

Services

Next-Generation Sequencing:

- Transcriptomics: Bulk and single-cell RNA-seq analysis, differential expression, pathway enrichment
- Genomics: Whole-genome sequencing, variant calling, annotation

Proteomics:

- Differential abundance analysis from labeled (TMT, SILAC) and label-free MS data

Custom Solutions:

- Tailored pipelines for publication-quality statistical analysis, data visualization, and reproducible reporting

Capabilities

High-Performance Computing Infrastructure
(Deployment planned for 2026)

- Compute Nodes: 10 servers
- Processing Power: 4000 threads
- GPU Accelerators: 8 x NVIDIA RTX 5000 PRO BLACKWELL SE
- Memory: 2TB RAM
- Storage Capacity: 2.3 PB HDD + 280 TB SSD

Testimonial

The Bioinformatics Facility provided solid expertise and high-quality scRNA-seq analysis that offered valuable new insights into our zebrafish neurodegenerative disease model. The data were presented in a well-organized and self-explanatory way, which allowed us to interpret them quickly and effectively. Our collaboration throughout the project was clear, efficient, and supportive.

Prof. Jacek Kuźnicki,
Head of the Laboratory
of Neurodegeneration at IIMCB

Key Outcomes

- We support researchers by transforming complex biological data into clear, actionable insights.
- We provide comprehensive bioinformatic expertise for omics-based projects, delivering high-quality analyses for RNA-seq, single-cell RNA-seq, and proteomics datasets.
- In collaboration with the Genome Engineering and Genomics Facilities, we delivered routine plasmid sequencing and genotyping services for approximately 700 samples.
- We performed Oxford Nanopore-based whole-genome assembly for bacterial and *C. elegans* samples, offering high-resolution data for advanced research applications.

Contact Us

Jacek Szymański, PhD
Coordinator of the Bioinformatics Facility

bf-team@iimcb.gov.pl
jszymanski@iimcb.gov.pl

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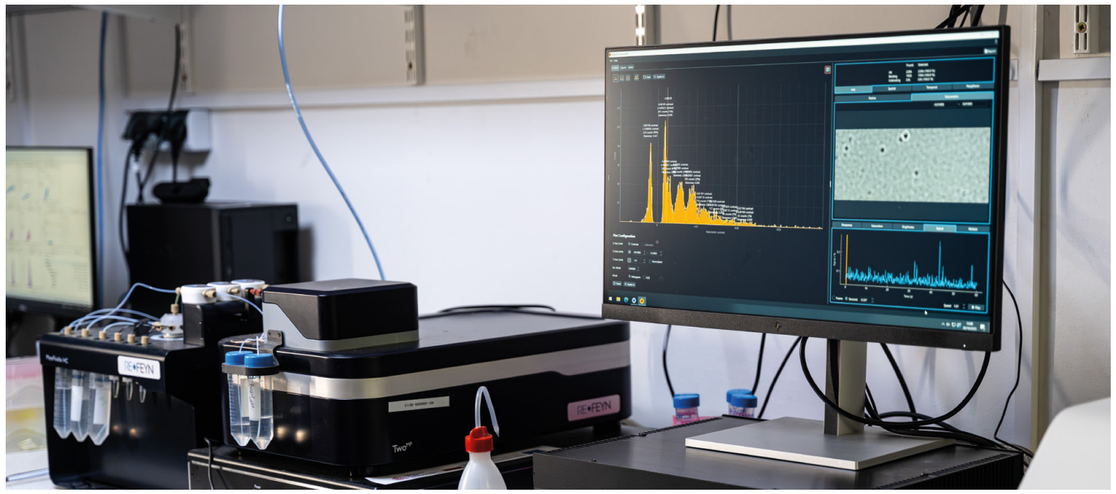
Biophysics and Bioanalytics
Facility

Whatever you want to know about your favorite macromolecule.

Using an extensive portfolio of molecular biophysics methods, we establish the key features of macromolecules and macromolecular complexes, including secondary and quaternary structure, thermal and chemical stability, and intermolecular interactions.



Services

- Size distribution (quaternary structure)
- Secondary structure and macromolecular stability
- Intermolecular interactions

We have broad experience in combining these methods in research and development projects, including biosimilarity studies for academic and commercial clients.

Capabilities

- Analytical Ultracentrifugation
- Dynamic Light Scattering with zeta potential
- Circular Dichroism and Fourier Transform Infrared Spectroscopy
- Differential Scanning Calorimetry
- Isothermal Titration Calorimetry
- Surface Plasmon Resonance
- Microscale Thermophoresis with spectral shift
- Ultra-Performance Liquid Chromatography
- Bioinert High-Performance Liquid Chromatography

Testimonial

Access to this specialized infrastructure, together with the expertise of the IIMCB team, significantly supported the execution of Adamed's Discovery research activities. Based on our experience, I can recommend Biophysics and Bioanalytics Facility team as a reliable and valuable partner for scientific collaboration.

Sebastian Pawlak, PhD,
Head of the Biotechnology
and Recombinant Proteins Group,
Research Department at Adamed Discovery

Key Outcomes

- 29 publications, including 15 with external clients
- Services for many scientific institutions in Poland (e.g. Institute of Bioorganic Chemistry PAS, Mossakowski Medical Research Institute PAS, Małopolska Centre of Biotechnology at the Jagiellonian University, University of Łódź, Centre of New Technologies of the University of Warsaw, University of Gdańsk, Wrocław University of Science and Technology, Hirszfeld Institute of Immunology and Experimental Therapy PAS, Warsaw University of Technology, Nencki Institute of Experimental Biology PAS)
- Participation in R&D projects of several partners (e.g. Selvita Services, Adamed, OncoArendi/Molecure, Captor Therapeutics)
- Biosimilarity studies in several projects of Polpharma on biological drugs

Contact Us

Krzysztof Skowronek, PhD, DSc Habil
Head of the Biophysics
and Bioanalytics Facility

kskowronek@iimcb.gov.pl

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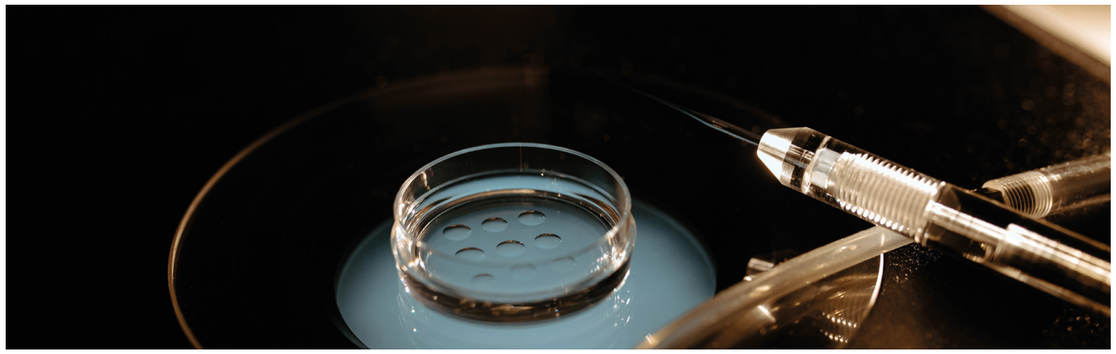
Genome Engineering
Facility

Transgenic mouse models for academic research and rare disease studies.

Combining our molecular biology and embryology expertise, we utilize CRISPR/Cas9 technology to offer genetically modified and transgenic mouse models suitable for a range of applications, from basic research to rare disease studies. Our portfolio, available to both research groups at the IIMCB and external clients, including for-profit and non-profit organizations, also includes a range of other services such as cloning, genotyping, mouse line cryopreservation and rederivation.



Services

- Generation of genetically modified mouse and *C. elegans* models using CRISPR/Cas9 methodology
- Embryological services: *in vitro* fertilization (classical and IntraCytoplasmic Sperm Injection – ICSI), sperm and embryo cryopreservation, mouse line rederivation
- Preparation of plasmids
- Genotyping, including establishing new genotyping protocols
- Mouse breeding and initial phenotyping
- Microinjections into oocytes and zygotes
- Consulting on custom projects

Capabilities

- State-of-the-art setup for microinjections and ICSI
- IVF-grade laminar flow for sterile embryo and animal handling
- Combined expertise in genetic engineering, molecular biology, and embryo manipulation
- Modern IVC breeding infrastructure
- Modern automated platforms for molecular biology applications

Testimonial

We are a patient-driven charitable project and our mission is to improve the lives of all people affected by Myofibrillar Myopathy Type 13 (MFM13) with Rimmed Vacuoles. Our collaboration with the International Institute of Molecular and Cell Biology has been essential for advancing MFM13 research. The development of the MFM13 mouse model will help us gain a better understanding of the molecular mechanisms of the disease and explore potential treatment options.

Sylwia Szwec,
Research Program Manager
at Cure MFM13

Key Outcomes

The Genome Engineering Facility has strong track record of collaborations, providing mouse models and other services to IIMCB research community and external collaborators, both business and non-profit patient foundations. These projects range from studying basic gene function, through the generation of constructs utilized for protein expression, to creating rare disease models utilized for deciphering the molecular basis and searching for potential therapies.

Selected collaborations:

- Knock-out mutation of the Cdadc1 gene enabled the group of Prof. Matthias Bochtler (IIMCB) to determine the enzyme's role in mammals (Slyvka et al., Proc. Natl. Acad. Sci. U.S.A., 2025).
- Several mouse models were used by the group of Prof. Andrzej Dziembowski (IIMCB) and collaborators to reveal the previously unknown impact of TENT5 enzymes on mRNA vaccine metabolism (Krawczyk et al., Nature, 2025).
- Recreation of a patient-derived Trap1 mutation in a mouse model allowed teams from the University of Warsaw and the Medical University of Warsaw to demonstrate a link between mitochondrial dysfunction and autism spectrum disorder (Rydzanicz et al., EMBO Mol Med., 2024).

Contact Us

Michał Brouze, PhD
Head of the Genome Engineering Facility

mbrouze@iimcb.gov.pl
geu-manager@iimcb.gov.pl
+48 668 587 983

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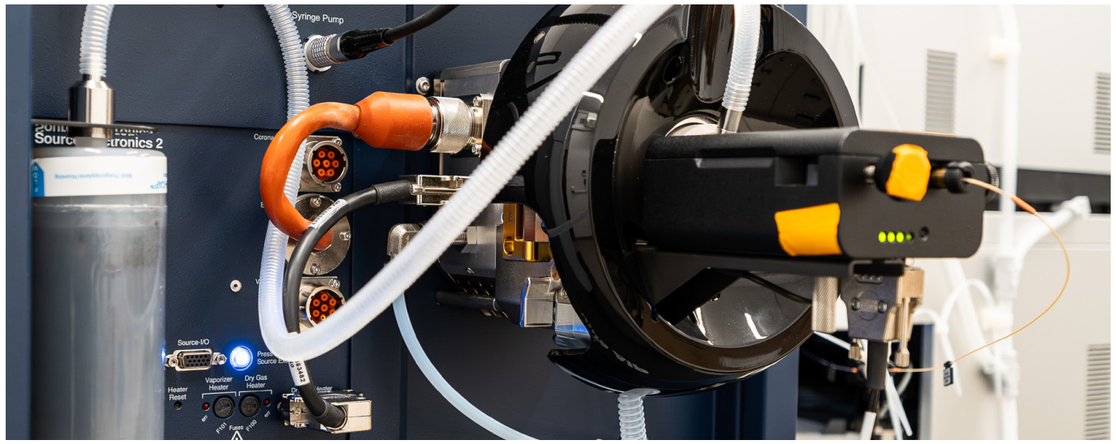
Mass Spectrometry
Facility

From concept to data – mass spectrometry that empowers discovery.

We use cutting-edge instrumentation and a holistic approach to provide high-quality multi-omics data to our clients that advances their research. Our experts are there every step of the way, from conception of the idea to final data interpretation.



Services

- Bottom-up proteomics
- Interactomics
- Consultations and data analysis
- Custom method development

Capabilities

- Bruker timsUltra AIP mass spectrometer coupled to an UltiMate 3000RS nano-LC
- Thermo Excedion Pro BioPharma mass spectrometer with ETD and FAIMS coupled to a Vanquish Neo nano-LC
- Vanquish Horizon UHPLC

Testimonial

Having had the opportunity to see this facility develop from an initial concept to where it is today, I'm truly impressed by the cutting-edge setup the mass spectrometry facility at the IIMCB has achieved, which reflects best practices in modern proteomics. The team is exceptionally well equipped to deliver high-quality, impactful research from the outset. I look forward to seeing what they accomplish next and the value they will bring as a trusted partner to their clients.

Simon Devos, PhD,
Head of the Proteomics Core at VIB

Key Outcomes

Our Mass Spectrometry Facility enables researchers to explore biology in unprecedented detail. Leveraging versatile and advanced technologies such as ion mobility separation and alternative fragmentation, we help you:

- **Resolve complex molecular landscapes:** High-resolution instrumentation enables precise analysis of proteins, metabolites, and lipids across diverse biological systems.
- **Detect subtle molecular changes:** Sensitive instrumentation allows high-throughput studies from limited sample material that inform functional understanding.
- **Expand research horizons:** Flexible workflows support multi-omic studies and structural biology approaches, empowering innovative experiments beyond standard proteomics.
- **Accelerate discovery:** Generate actionable insights that drive biomedical research forward, supported by expert guidance from experimental design to data interpretation.

We translate complex samples into meaningful data, providing researchers with the clarity and confidence to pursue breakthrough science.

Contact Us

Vanessa Linke, PhD
Head of the Mass Spectrometry Facility

msf@iimcb.gov.pl
vlinke@iimcb.gov.pl

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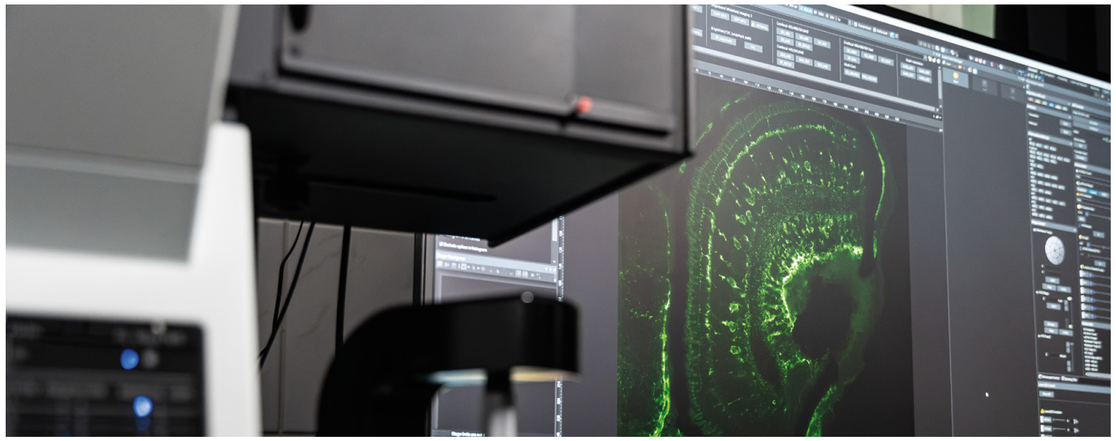
Microscopy
Facility

From organisms to cellular ultrastructure. Accelerate your discoveries with our cytometry and imaging solutions.

Our facility combines light microscopy, electron microscopy, and flow cytometry to support advanced biological research. We offer both walk-in and full-service options, depending on the experiment type, instrumentation, and customer needs.



Services

- Access to advanced fluorescence microscopes
- Cell sorting by flow cytometry
- Cellular ultrastructure analysis using transmission and scanning electron microscopy

Capabilities

- Confocal (LSM990), spinning-disk (spinSR10), super-resolution (Elyra 7), and lightsheet (Lightsheet Z.1 and Blaze) microscopes
- Fluorescence-activated cell sorter with spectral and imaging capabilities (FACSDiscover S8)
- Hydra Bio plasma focused ion beam scanning electron microscope

Testimonial

We thank the Microscopy Facility members for helpful discussions and support in planning the experiments for the study: E3 ubiquitin ligase RNF2 protects polymerase iota from destabilization.

Justyna McIntyre, PhD, DSc Habil,
Institute of Biochemistry
and Biophysics PAS

Key Outcomes

Long-standing expertise:

- Consultation on experimental design and hands-on training for multiple facility users
- Advanced experimental pipelines
- Data analysis and interpretation

Collaborative research with scientists from renowned institutions, including:

- University of Warsaw
- Mossakowski Medical Research Institute PAS
- Institute of Biochemistry and Biophysics PAS

Contribution to peer-reviewed publications:

- Domagala et al., Cancer Res, 2025
- Tempes et al., Cell Mol Life Sci, 2024
- Baranykova et al., Sci Rep, 2024
- Fedorowicz et al., BBA Mol Cell Res, 2024

Contact Us

Tomasz Węgierski, PhD
Head of the Microscopy Facility
twegierski@iimcb.gov.pl

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Preclinical Drug Development
Facility

Revealing molecular beauty with cutting-edge cryo-EM.

We provide a comprehensive and integrated suite of services, spanning every stage from gene cloning to high-resolution protein structure determination, complemented by expert consultations and data analysis support. This unique combination ensures seamless project execution, from concept to structural insight, and maximizes the scientific and practical value of every collaboration.

Services

- Protein production in three different expression systems
- High-quality recombinant protein purification
- Crystallization of proteins and their complexes with ligands
- X-ray data analysis from data collection to structure determination
- Cryo-electron microscopy from sample preparation to 3D structure
- Collaboration with scientific teams to advance discovery

Capabilities

- Glacios 2 cryo-TEM for visualization and high-resolution data collection
- Incubators enabling protein expression in E. coli, mammalian and insect cells
- Advanced chromatographic systems for automated protein purification
- Crystallization robots dispensing solutions in nanoliter volumes

Testimonial

We have already benefited from the services offered by the PDU, particularly in the area of protein purification and crystallization. The professional support and technical capabilities of the facility have contributed meaningfully to our research.

Izabela Sabała, PhD, DSc Habil,
Head of the Laboratory of Protein Engineering at Mossakowski Medical Research Institute PAS

Key Outcomes

Our facility supports researchers across the life sciences, with a particular focus on structural biology.

- Supporting research in drug discovery
- Engaging in collaborative molecular and biomedical projects with IIMCB teams and partners both nationally and internationally
- Providing purified recombinant proteins to our internal and external clients
- Screening cryo-EM grids, collecting data sets, solving structures
- Consulting results and helping to navigate project in the right direction

Publications:

- Kaus-Drobek et al. Sci Rep. (2025)
- López Espinar et al. ACS Appl Bio Mater (2025)
- Czestkowski et al. J. Med. Chem. (2024)
- Borek et al. Mol. Cancer Ther. (2023)

Contact Us

Elżbieta Nowak PhD, DSc Habil
Head of the Preclinical Drug Development Facility

pdu@iimcb.gov.pl
enowak@iimcb.gov.pl

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Rodent
Facility

From breeding to phenotyping: comprehensive support for your research excellence.

We are committed to ensuring the highest standards of humane care for the welfare of animals that are used in research, with the understanding that this commitment is critical to the success of our scientific projects.

Services

- Husbandry & breeding
- Comprehensive metabolic and behavioral analysis using specialized research platform
- Advanced DVC® systems enable continuous, non-invasive animal monitoring insights
- Biochemical and electrolyte analysis in body fluids
- Consulting on scientific projects involving mouse models

Capabilities

- Promethion Core Metabolic and Behavioral Cages from Sable Systems enable efficient line phenotyping and treatment impact analysis
- Digital Ventilated Cage (DVC®) systems – 24/7 tracking technologies enable continuous monitoring and analysis of rodent activity
- ISOcage P – Bioexclusion System enables research with germ-free animals

Testimonial

Working with the Rodent Facility at IIMCB has been instrumental in supporting our research. The facility provides excellent conditions for breeding and maintaining genetically modified mouse models, ensuring high standards of animal welfare and experimental reliability. We particularly value the professional support and expert advice offered by the staff, as well as the regular updates on colony status, which greatly facilitate planning and execution of experiments. It is also impressive to see the facility continuously developing and expanding its equipment and capabilities.

Patrycja Daszczuk, PhD,
Laboratory of Cell Biology
at IIMCB

Key Outcomes

- **Breeding & Animal Husbandry:** The Facility maintains mice under specific-pathogen-free conditions, with full husbandry support and protocol development, providing a clean and controlled baseline for reproducible *in vivo* research.
- **Surgical & *In Vivo* Experimental Support:** The Facility delivers precise anaesthesia and maintains stable physiological conditions during surgery, enabling delicate long-duration procedures and multi-modal imaging studies critical to mechanistic discoveries.
- **Metabolic & Biochemical Phenotyping:** The Facility's integrated suite of metabolic, behavioural, and biochemical phenotyping platforms – including the Promethion Core, Cobas c111, and AVL 9180 – allows comprehensive *in vivo* characterisation of disease models, supporting data-rich grant projects and high-impact publications.
- **Precision Dietary Interventions & Cohort Management:** The Facility implements controlled dietary regimens – such as iron-deficient versus iron-balanced diets – and maintains age-matched cohorts, supporting discoveries advancing the understanding of iron metabolism disorders, mRNA biology & stability, and gut-liver axis biology.

Contact Us

Łukasz Majewski, PhD
Head of the Rodent Facility
rf-team@iimcb.gov.pl

READ MORE

Zebrafish
Facility

Where tiny fish help answer big questions in biology.

We offer long-standing expertise in zebrafish breeding and care. With many years of experience, we provide reliable and high-quality zebrafish lines, ensuring optimal health, welfare, and reproducibility for research.

Services

- Breeding and maintaining healthy *Danio rerio* (zebrafish) for research purposes
- Providing embryos and adult fish for biomedical experiments
- Microinjection of zebrafish embryos
- Screening zebrafish embryos for fluorescence signals to identify transgenic lines
- Cryopreservation of zebrafish sperm to maintain genetic diversity and support long-term line preservation
- Tissue sampling and genotyping
- Fish handling and welfare trainings for new and experienced users

Capabilities

- Advanced microinjection stations for embryo manipulation and genetic studies
- Fluorescence microscopy for screening zebrafish embryos and larvae for transgene expression
- Controlled aquatic systems ensuring optimal zebrafish health and breeding
- Dedicated behavioral testing room, equipped for studies on zebrafish embryos, larvae, and adult fish
- Expertise in the setup, operation and optimization of aquatic systems

Testimonial

ZCF is truly the backbone of our zebrafish research at IIMCB. Their professionalism, care, and deep understanding of zebrafish biology make it possible for us to pursue our science with confidence and precision.

Cecilia Winata PhD, DSc Habil,
Head of the Laboratory of Zebrafish Developmental Genomics at IIMCB

Key Outcomes

Zebrafish Core Facility (ZCF) plays a key role in supporting a wide range of research in life sciences, fostering collaboration and sharing expertise within and beyond the IIMCB.

- Supporting research in developmental biology, genetics, and neurobiology using *Danio rerio* as a model organism
- Collaborating with IIMCB research groups and international partners on molecular and biomedical projects
- Providing zebrafish embryos and established lines to external research institutions, including University of Warmia and Mazury in Olsztyn; University of Warsaw; Warsaw University of Life Sciences – SGGW; Nencki Institute of Experimental Biology, PAS; and The International Institute of Molecular Mechanisms and Machines, PAS.
- Offering consultations and hands-on support for setting up new zebrafish laboratories, sharing our experience in breeding, care, and facility management
- Exchanging zebrafish lines with other research centers to promote scientific collaboration and diversity of genetic models

Contact Us

Magdalena Góra, MSc
Coordinator of the Zebrafish Facility
zcf-team@iimcb.gov.pl

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Research Laboratories

Laboratory of
Structural Biology

READ MORE

We study epigenetics, specifically nucleic acid and histone modifications that control cell fate change and maintenance. Our methods range from various flavors of high-throughput sequencing to classical biochemistry and structural biology. We also rely increasingly on “big data”. Our work has implications in oncology, particularly for hematologic malignancies that have a strong epigenetic component.

Research Summary

Our work is focused on 2’-deoxynucleotide modifications and metabolism. We are interested in the properties and integrity of the 2’-deoxynucleotide pool, and its potential consequences for epigenetics, particularly in a developmental biology or cancer biology context. More recently, we have initiated projects on amino acid metabolism, also in a cancer context.

The biological theme of our projects is hematological malignancies. We have projects on mixed lineage leukemia (MLL), acute myeloid leukemia of complex karyotype (CK-AML), and on asparaginase treatment for acute lymphoblastic leukemia (ALL).

Methodologically, the group uses biochemistry and structural biology, but also relies increasingly on high-throughput sequencing approaches and on animal models to test the relevance of our biochemical concepts in a more physiological setting.

Scientific Impact

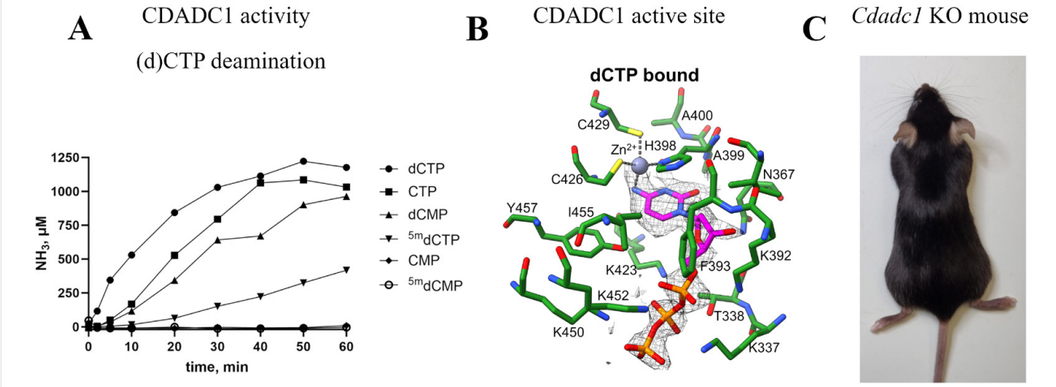
- We have contributed to the understanding of DNA modification pathways.
- We have identified enzymes that balance or sanitize the 2’-deoxynucleotide pool.
- We have contributed molecular insights to the biology of MLL and CK-AML.

Collaborations

Our collaborators come from both academia (e.g. Prof. G. Xu, Prof. J. Weng, Dr. T. Jurkowski, Dr. T. Hore, Dr. C. Winata, Dr. A. Wlodawer) and industry (Dr. P. Weigele). The group also has a growing set of clinical collaborators (Dr. K. Gawle-Krawczyk, Prof. A. Kraemer, Prof. F. Stoelzel, Dr. T. Bochtler, Prof. A. Stenzinger, Prof. O. Neumann, Dr. D. Kazdal).

Future Goals

We would love to see a clinical impact of our work. Therefore, we are currently initiating many new clinical collaborations.



Vertebrate CDADC1 activity, structure and function. (A) CDADC1 is a (d)CTP deaminase. (B) A cryo-EM structure explains the triphosphate specificity. (C) Cdadc1 KO mice are viable and fertile. They show no obvious signs of altered immunity, despite the link between dCTPase activity and immunity in prokaryotes. Source: Activity and structure of human (d)CTP deaminase CDADC1, Slyvka et al. (2025)

After many years of doing purely basic research, it would be nice to also have a practical impact.

Matthias Bochtler, PhD, Professor

Group Leader

Matthias Bochtler is a structural biologist and professor of biological sciences. He graduated from Munich University and completed a postdoctoral fellowship at the Max Planck Institute of Biochemistry (MPIB) in Martinsried. Matthias Bochtler moved to Poland initially to take up a shared position at the Max Planck Institute and the IIMCB. He is a laureate of the Minister of Education and Science Award for significant achievements in scientific activities (2023), Włodzimierz Krzyżosiak Distinction awarded by the Polish Academy of Sciences (2023), the Pieńkowski Award (2005) and EMBO/HHMI Young Researcher Award (2004).

Group Members

Senior Researcher:
Honorata Czapińska, PhD, DSc Habil
PhD Students:
Nashat Akhtar, MSc
Terry Karimi, MSc
Research Specialist:
Natalia Leśniowska, MSc
Lab Technician:
Julia Kędzierska, MSc
Volunteer:
Dominik Rafalski, PhD
Laboratory Support Specialist:
Katarzyna Grzelak, PhD

Laboratory of
RNA Viruses

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We study how RNA viruses exploit host cellular pathways to replicate and evade antiviral defenses. Our research focuses on the molecular mechanisms by which viruses co-opt the host translation machinery. By dissecting virus-host interactions, we aim to identify critical host factors that regulate viral replication and shape cellular responses to infection.

Research Summary

Research in our laboratory is focused on two main areas of interest:

IRES-dependent translation and host factors in RNA virus infection

RNA viruses employ specialized mechanisms to ensure efficient translation of their genomes by host ribosomes. A common strategy involves the use of internal ribosome entry sites (IRESs), which recruit ribosomes directly to viral RNA and bypass canonical cap-dependent translation initiation.

IRES elements rely on cellular RNA-binding proteins known as IRES trans-acting factors (ITAFs) for full activity. These host factors promote correct IRES folding and function and are required for viral, but not host, translation. As such, ITAFs represent attractive targets for antiviral intervention. Our research focuses on identifying and characterizing host proteins involved in IRES-dependent translation in the Hepatitis A virus, a model picornavirus and important human pathogen.

Posttranscriptional mechanisms of viral gene regulation

We also aim to understand how RNA viruses like Hepatitis A virus (HAV) regulate their gene expression. All viruses express a mix of both nonstructural and structural proteins (NSPs and SPs, respectively). NSPs control viral replication and are generally catalytic, while SPs assemble to form virus particles. For this reason, viruses generally express SPs in far greater quantities than NSPs.

HAV encodes both structural and nonstructural genes within a single, very large open reading frame. The resulting polyprotein is subsequently cleaved into individual viral proteins by a virus-encoded protease. This peculiar mechanism suggests that all viral proteins are produced in equal amounts, and that any regulation of viral gene expression must occur at the posttranscriptional level (e.g. protein degradation, posttranslational modifications, and/or ribosome frameshifting). However, the mechanisms involved remain entirely unknown. To explore this question, we are using high-throughput techniques like ribosome profiling and SILAC proteomics to characterize HAV gene expression.

Collaborations

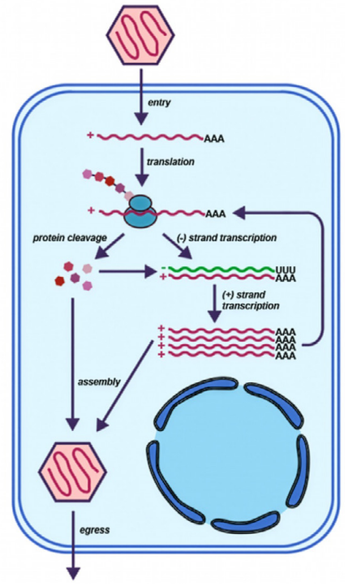
We have ongoing collaborations with Dr. Georg Kustatscher (University of Edinburgh) and Prof. Kathryn Lilley (University of Cambridge).

Scientific Impact and Future Goals

Our overarching goal is to understand how RNA viruses such as HAV express and regulate their genes. By identifying host proteins involved in viral gene expression, we hope to identify key steps in the viral life cycle which are amenable to therapeutic intervention. In the future, we aim to extend these studies to RNA viruses from the Flaviviridae family. We are particularly interested in Usutu virus, a mosquito-borne, zoonotic virus now endemic across most of Europe.

As one of the youngest laboratories at IIMCB, established in 2025, we are focused on building a strong, intellectually curious team and bringing our projects to the stage where they start generating new discoveries. Our ambition is to identify a gene regulatory mechanism that may initially seem virus-specific, but in fact reflects a broader biological principle. If this work also suggests a new antiviral strategy, that would be an added bonus.

Stefan Bresson, PhD



The life cycle and gene expression strategy of the Hepatitis A virus. Illustration by Stefan Bresson.

Group Leader

Stefan Bresson is a molecular biologist specializing in RNA research. He earned his BSc in Molecular and Cell Biology from the University of Texas at Austin in 2009 and his PhD in Biological Chemistry from the University of Texas Southwestern Medical Center in 2015. Stefan Bresson's research experience also includes a postdoctoral position at the University of Edinburgh, where he worked from 2015 to 2024. He is a laureate of SONATA BIS 14, National Science Center grant (2025) and VirHoX Hop-on, Horizon Europe grant (2025).

Group Members

Postdoctoral researchers:
Maja Cieplak-Rotowska, PhD
Agata Zubrycka, PhD
PhD students:
Khashpatika Ganesh, MSc
Swagatika Moharana, MSc
Laboratory Support Specialist:
Marta Jankowska, MSc
MSc student:
Martyna Roszko

Interview:

Why Poland? Building a Eureka Moment at IIMCB

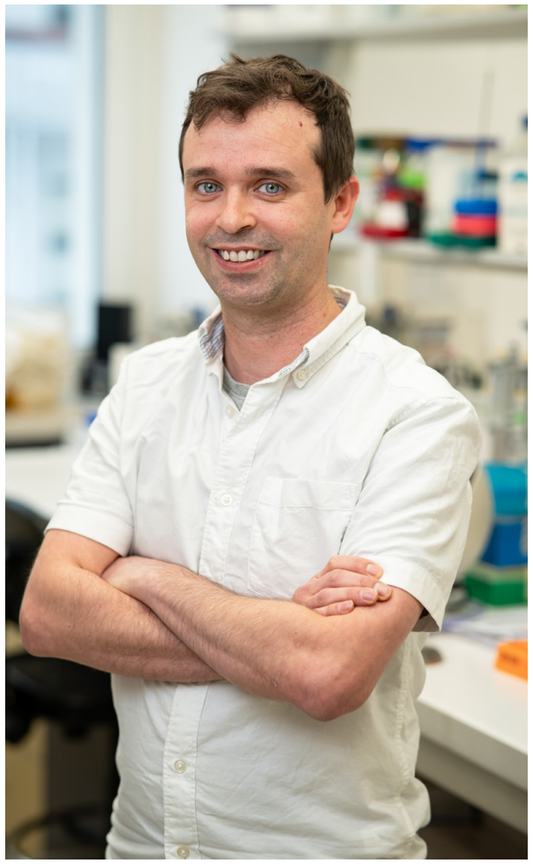
Why would a scientist with experience from renowned American and British research institutions choose Poland as the place to launch an independent laboratory? For **Dr. Stefan Bresson**, IIMCB offered both a strong research environment and the conditions needed to pursue ambitious mechanistic science. His Laboratory of RNA Viruses explores how viral RNAs manipulate cellular machinery, opening a window onto both antiviral strategies and fundamental principles of gene regulation.

You trained and worked in some of the best-equipped research environments, including UT Southwestern and the University of Edinburgh. Given the clear differences in scale and infrastructure, what made IIMCB an attractive place to continue your career? Is this a case of revising an old mental map of where high-level science happens?

Poland's scientific reputation is improving rapidly, but it will take some time for popular perceptions to catch up. When I told friends and colleagues that I was moving to Poland to start my lab, the response was always one of bemusement – "But why Poland?". For me, IIMCB offers a research environment comparable to top institutions in the US and Western Europe, while providing strong support to new PIs. Funding is also more readily attainable in Poland than it would be in US or UK, so IIMCB was an attractive place to establish my independent research career.

Looking back on your research career, what scientific questions have stayed with you throughout this journey?

I've always been fascinated by RNA and its central role it plays in cellular gene expression. RNA viruses are a powerful model system for understanding RNA biology, because they push gene expression to its limits and often reveal mechanisms that we wouldn't otherwise notice.



Give yourself time to understand your project instead of rushing toward quick results. Focus on learning how to think, not just how to produce data.

Dr. Stefan Bresson

When establishing the Laboratory of RNA Viruses at IIMCB, what were the first scientific or strategic priorities you set for the group?

Initially, the most important priority was to build a strong foundation: establishing reproducible protocols, careful record keeping, and a collegial lab culture. The next step – and this is where we are right now – is building a team of talented scientists with complementary skills and expertise.

RNA viruses depend heavily on host cell machinery. Which aspects of this relationship are currently most central to your research, and why do they matter beyond virology?

We study some of the unusual mechanisms by which viruses express their genes, including internal ribosome entry sites (IRESs) and single open reading frames that encode numerous viral proteins.

IRESs are RNA structures that some viruses use to recruit ribosomes and translation factors directly to the viral genome. Because of their complex structures, IRESs often rely on cellular RNA-binding proteins to stabilize them and promote folding into their active conformations. Identifying these host factors may reveal potential antiviral targets. Moreover, understanding how viral IRESs work can inform the design of synthetic RNAs for applications such as mRNA vaccines and other therapeutic platforms.

A second major focus of the lab is understanding how viruses coordinate the production, processing, and regulation of multiple proteins from a single open reading frame. We use techniques like ribosome profiling and high-throughput proteomics to characterize translational and posttranslational mechanisms of gene expression control. By understanding the genetic 'tricks' that these viruses use, we can gain insight into gene expression in normal cells.

If you were to imagine a defining scientific discovery for your laboratory, what would that "Eureka moment" look like?

For me, the ideal moment would be discovering a gene regulatory mechanism that initially appears to be virus-specific but turns out to reflect some broader biological principle. If such a discovery also suggested a new antiviral strategy, that would be an added bonus.

Based on your own experience, what advice would you give to researchers at the beginning of their scientific careers?

My advice would be to give yourself time to understand your project instead of rushing toward quick results. Focus on learning how to think, not just how to produce data. Hard work and motivation count for a lot, but setting aside time to think deeply about your project is the key to long-term success.

As your laboratory develops, what are you most looking forward to in the coming years?

I'm looking forward to building a strong, intellectually curious team and seeing our projects reach the stage where they start producing new discoveries. I am excited to see the lab contribute to strengthening the Institute's international visibility through collaborations and high-quality mechanistic work.

Laboratory of
Bioinformatics and Protein Engineering

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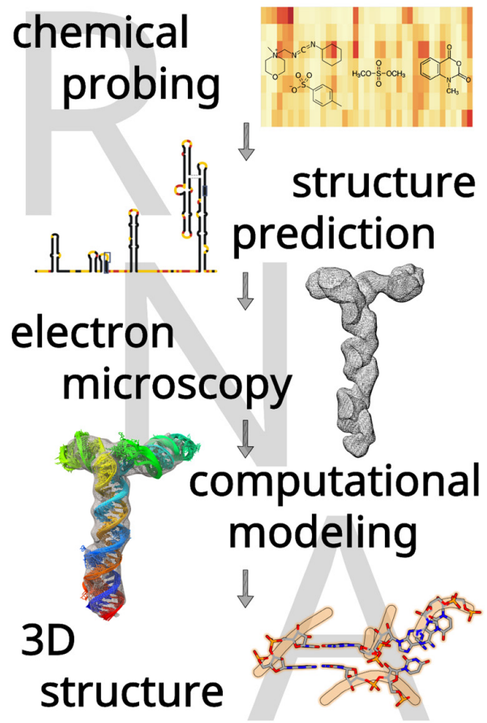
We explore the universe of RNA, not just as a messenger of genetic blueprints but as a dynamic entity that shapes life at the molecular level. Our work treats RNA as a puzzle, where each piece is a clue to its myriad roles from catalysts to regulators within the cell. With advanced computational models and experimental techniques, we decode the complex structures and interactions of RNA, especially with proteins and small molecules.

Research Summary

Our work is focused on the development and applications of new methods for RNA structure determination and modeling RNA interactions, combining computational predictions with experimental analyses. This approach is vital for delving into the role of RNA in biological processes, contributing significantly to the fields of molecular biology, bioinformatics, and structural biology. Our contributions include software tools like ModeRNA and SimRNA, which have become essential for researchers globally. We investigate the three-dimensional structures of RNA from viruses, bacteria, and humans, focusing on potential targets for small molecules. Our research is enriched by interdisciplinary collaborations with various research groups and with commercial partners in Poland and worldwide.

Scientific Impact

- Tools for RNA modeling & small molecule interactions.
- 20 years of the MODOMICS database.
- Participation in the Human RNome Project Consortium.



Determination of RNA 3D structure and dynamics, using a combination of computational and experimental methods. Example for the 5′-proximal region in SARS-CoV-2 RNA. Illustration by Dr. Tales Rocha de Moura.

Key Collaborations

- Cryo-EM & RNA structure: S. Glatt (Poland/Austria), Z. Su (China).
- RNA CD and FTIR: V. Arluison, F. Wien (France).
- RNA modifications: Human RNome Project Consortium.
- RNA structure comparisons: E.F. Baulin (Poland).

Future Goals

We aim to deepen our understanding of RNA structure and function, particularly by studying molecules with therapeutic potential. Our advances in computational methods, integrated with experimental studies, are geared towards contributing to both fundamental research and future practical applications, with the ultimate goal of impacting scientific knowledge and human health.

Group Leader

Janusz M. Bujnicki is an interdisciplinary structural biologist, professor of biological sciences. He graduated with an MSc and received a PhD from the University of Warsaw. Alumnus of the Leadership Academy for Poland. Visiting professor at the Adam Mickiewicz University (2006-2020). Executive Editor at Nucleic Acids Research (2013-). Elected member of European Molecular Biology Organization, Academia Europaea, and Polish Academy of Sciences. Founding member and president (2011- 2013) of the Polish Bioinformatics Society. Member of European Commission's Group of Chief Scientific Advisors (2015-2020). Member (2019-2024) and the first chair of the University Council at the University of Warsaw. Founding member of the Association of ERC Grantees. Laureate of numerous national and international awards.

Group Members

Senior Researchers: Elżbieta Purta, PhD; Filip Stefaniak, PhD, DSc Habil; Tales Rocha de Moura, PhD
Postdoctoral Researchers: Sunandan Mukherjee, PhD; Gregory Nikolaev, PhD; Rui João Loureiro, PhD; Kuntal Mondal, PhD
Programmers: Masoud Amiri Farsani, PhD; Seyed Naeim Moafinejad, MSc
Research Assistants: Agata Bernat, MSc; Dominik Sordyl, MSc; Anastasiya Shavina, MSc
Research Technician: Iwona Ptasiewicz
Laboratory Support Specialist: Katarzyna Grzelak, MSc
Volunteers: Satyabrata Maiti, PhD; Xareni Ryes Soto, MSc; Zuzanna Lubas, BSc

Our aim is to determine RNA structures and interactions and to design new molecules with functions relevant to medicine and biotechnology. In 2024-2025 we combined cryo-EM with computational modeling to determine 3D structures of diverse RNAs. We developed new computational tools for nucleic acid 3D structure comparison and motif identification. On the 20th anniversary of MODOMICS we substantially expanded the database by adding thousands of human transcript sequences with mapped RNA modifications and we continue this effort in collaboration with the Human RNome Project Consortium.

Janusz M. Bujnicki,
PhD, Professor

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Laboratory of
RNA Biology – ERA Chairs Group

We are molecular biologists who are trying to understand how the stability of mRNA is regulated. We have recently discovered a previously overlooked mechanism that increases the stability of both naturally produced and therapeutic mRNA (like mRNA vaccines), operating only in specific cell types and tissues. In the future, we plan to understand this new mechanism better and exploit it to design more effective mRNA-based therapeutics.

Research Summary

Although mRNA degradation has been studied for years, and the major decay pathways conserved between eukaryotes are already established, we know very little about how these are integrated *in vivo*. The stability of mRNA is mainly controlled by the dynamics of 3' terminal poly(A) tails initially synthesized in the nucleus. At the same time, the analysis of poly(A) tails is challenging as for any other homopolymeric tract. In the lab, we implemented direct RNA sequencing on nanopores to study the metabolism of poly(A) tails. This methodology enables us to look more comprehensively at the dynamics of poly(A) tails *in vivo*. We discovered that a metazoan-specific family of cytoplasmic poly(A) polymerases (TENT5), by extending mRNA tails, plays crucial roles in mammalian physiology. TENT5B, C, and D participate in gametogenesis, while TENT5A regulates collagen expression in osteoblasts. In immune cells, TENT5A and C enhance the expression of innate immunity effector proteins. Notably, we have recently described the unexpected role of TENT5A in the regulation of the stability of anti-COVID-19 mRNA vaccine.

Scientific Impact

- Description of TENT5 cytoplasmic poly(A) polymerases as important regulators of physiological processes.
- Discovery that TENT5A re-adenylates and stabilizes anti-SARS-CoV-2 mRNA vaccine, enhancing antigen production and vaccine efficacy.

Future Goals

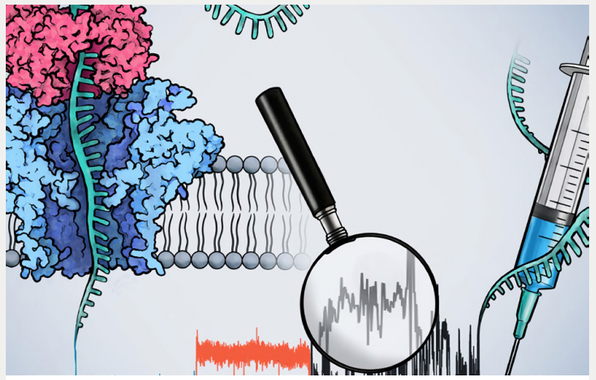
Within the framework of the recently funded ERC Advanced Grant "ViveRNA", we plan to comprehensively study the stability of both endogenous and therapeutic mRNA *in vivo*. We will enhance the accuracy of the methods used to determine the properties of mRNAs, especially computational protocols for the analysis of poly(A) tails. These, combined with carefully designed transgenic mouse models, primary cell cultures, and synthetic biology approaches, should, in the future, enable the design of next-generation mRNA therapeutics. In parallel, together with collaborators from the Virtual Research Institute (WIB – Wirtualny Instytut Badawczy), we are actively working on improving mRNA-based therapies using chemical approaches and applying them for cancer immunotherapy.

Collaborations

Prof. Marcin Nowotny and Prof. Marta Miączyńska (IIMCB), Prof. Jacek Jemielity, and Dr. Joanna Kowalska from the University of Warsaw, as well as Prof. Dominika Nowis and Prof. Jakub Gołąb from the Warsaw Medical University. At the same time, we have several other ongoing collaborations. These mainly focus on mRNA stability and include Prof. Magdalena Dziembowska (University of Warsaw, Poland), Prof. Bertrand Séraphin (IGBMC, France), Dr. Agnieszka Tudek (Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, Poland), Prof. Torben Jensen (Aarhus University, Denmark), Prof. Grzegorz Kudła (Human Genetics Unit at the University of Edinburgh, UK).

We are very intrigued by the fact that although the machinery involved in mRNA metabolism is the same everywhere, there is high variability in mRNA stability and poly(A) tail dynamics in all tissues. This is reflected, for instance, by high differences in the average lengths of poly(A) tails depending on the cell type. Understanding this variation is particularly important in the context of future applications for mRNA-based therapeutics. This research direction was reflected in our landmark 2025 Nature paper, "Re-adenylation by TENT5A enhances efficacy of SARS-CoV-2 mRNA vaccines", which explained mechanisms of mRNA-based therapeutics.

Andrzej Dziembowski,
PhD, Professor



We aim to use nanopore sequencing to identify factors that affect mRNA stability. This will allow the design of better therapeutic mRNAs to help fight diseases. Illustration by Natalia Gumińska.

Group Leader

Andrzej Dziembowski is a molecular biologist and professor of biological sciences. He graduated from the University of Warsaw. After postdoctoral studies at the CNRS Molecular Genetics Centre in Gif-sur-Yvette, France, and several years of a PI position at the Polish Academy of Sciences, he assumed the ERA Chairs group leader position at IIMCB in 2019. His work has been recognized with numerous awards and prestigious grants, including the ERC Advanced Grant (2023), the Prime Minister Award (2022) and the Prize of the Foundation for Polish Science (2018). He is a member of the European Molecular Biology Organization, Polish Academy of Sciences, Academia Europaea and RNA Society. He has been elected to the RNA Society's Board of Directors for the 2025-2026 term.

Group Members

Senior Researchers: Seweryn Mroczek, DSc Habil; Bartosz Tarkowski, PhD
Postdoctoral Researchers: Aleksandra Brouze, PhD; Natalia Gumińska, PhD; Michał Małszycki, PhD; Tomasz Kuliński, PhD; Agnieszka Czarnocka-Cieciura, PhD; Michał Mazur, PhD; Paula Castañeda Londoño, PhD
Research Assistant: Karolina Kasztelan, MSc;
PhD Students: Wiktoria Orzeł, MSc; Wiktor Antczak, MSc; Magdalena Jawor, MSc; Tola Tame, MSc; Usman Hameed, MSc
Research Technicians: Ewelina Patrycja Owczarek, MSc; Kamila Affek, MSc; Julia Szeptycka, MSc; Agnieszka Machowska, MSc
Laboratory Technician: Alina Zielińska, BSc
Laboratory Support Specialist: Paula Kwapisz, MSc
Volunteers: Alicja Bień-Gryber, BSc; Alicja Stachurska, Julia Łucyn, Anna Modrzejowska, Wojciech Mordań

Laboratory of
Molecular and Cellular Neurobiology

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A major focus of our research is neuronal morphology, as neuronal shape is a key determinant of function. To better understand the molecular mechanisms underlying neuronal development, we focus on elucidating the function of the mTOR kinase. However, neuronal architecture changes not only during development but also during aging and disease processes in the adult brain, for example in depression. For the past five years, we have therefore investigated molecular mechanisms underlying dendritic stabilization and its disruption in the mature nervous system.

Research Summary

Since the establishment of our laboratory, we have focused on the role of the mTOR kinase in neurons, particularly in nervous system development, as dysregulation of mTOR activity leads to neurodevelopmental disorders such as tuberous sclerosis complex (TSC). mTOR is a central regulator of cellular metabolism, integrating information on energy status, amino acid availability, and extracellular signals, including trophic factors. In recent years, our work has addressed mTOR-dependent processes such as translation, transcription, autophagy, and intracellular trafficking, many of which are essential for neuronal development and function. More recently, we have concentrated on the role of mTOR in the cell nucleus, a non-canonical and poorly characterized localization. We have shown that in neurons mTOR accumulates in the nucleus in response to increased neuronal activity (Macias et al., 2013). Regarding studies on the stability of mature neuronal morphology, our work has identified mTOR as a key protein in this process. However, we have also discovered a number of novel proteins involved, such as ITPKA, whose molecular functions we are now seeking to better understand in this context.

Scientific Impact

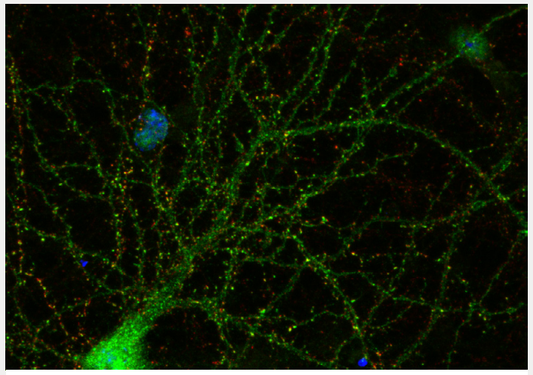
- Demonstrating that inhibition of mTOR activity via activation of autophagy regulates lysosome transport along microtubules (Tempes et al., 2024).
- Identifying dilazep and penbutolol through screening approaches as candidate antidepressant compounds (patent application pending).

Future Goals

- Comprehensive characterization of nuclear mTOR in brain development, physiology, and pathology.
- Further analysis of molecular mechanisms controlling dendritic stability and destabilization in the adult nervous system.

Collaborations

Our key collaborators include Prof. Kathrin Thedieck, Prof. Sergiusz Jóźwiak, Prof. Katarzyna Kotulska, Prof. David Kwiatkowski, Prof. Eleonora Aronica, Prof. Leszek Kaczmarek and Prof. Ewelina Knapska. We are working to understand how molecular biology translates into clinical features of tuberous sclerosis or depression and how this knowledge can be used to help patients.



Rat hippocampal neurons cultured *in vitro*. Immunofluorescence labeling shows GluA1 (green), Bassoon (red), and cell nuclei (blue). Illustration by Karolina Protokowicz.

Group Leader

Jacek Jaworski is a neurobiologist and professor of biological sciences. He graduated from the University of Warsaw and later received a PhD from the Nencki Institute of Experimental Biology PAS. After his postdoctoral studies at the Massachusetts Institute of Technology, USA, Jacek Jaworski established his own laboratory at IIMCB in 2005 that focuses on the molecular basis of the development and stability of neuronal networks. He is a member of the European Molecular Biology Organization and the President of the Polish Society for Neuroscience (2025-2027).

Group Members

Senior Researchers:
Ewa Liszewska, PhD
Małgorzata Urbańska, PhD
Postdoctoral Researcher:
Roberto Pagano, PhD
PhD Students:
Olga Doszyń, MSc
Shiwani Kumari, MSc
Katarzyna Orzoł, MSc
Research Specialists:
Katarzyna Machnicka, MSc
Katarzyna Durczyńska, MSc
Karolina Protokowicz, MSc
Lab Technician:
Alina Zielińska, BSc
Laboratory Support Specialist:
Angelika Jocek, MSc
Volunteers:
Julia Łukasiewicz
Gabriela Chmurzyńska
Wiktoria Kowalska

Our research focuses on the molecular basis of the development and stability of neuronal networks. In particular, we focus on the molecular functions of the mTOR protein, which will enable better diagnosis and potential therapy of mTORopathies, diseases caused by mTOR hyperactivity.

Jacek Jaworski, PhD, Professor

Laboratory of
Cellular Genomics

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We are a research group working on functional, metabolic, and immune aspects of gastrointestinal health. We use experimental and computational methods to describe mechanisms underlying chronic gut and liver diseases. Our goal is to understand the role of microbiota in driving disease-associated changes in the state of cells and their interactions.

Research Summary

We investigate the bidirectional crosstalk between the liver and the intestine, with a particular emphasis on the role of the resident microbiota. Our research focuses on the gut-liver axis as a central regulatory interface linking host metabolism, immunity, and microbial communities in chronic liver diseases, especially metabolic dysfunction-associated steatotic liver disease (MASLD). By integrating metagenomics, metabolomics, proteomics, and single-cell transcriptomics across human cohorts and experimental models, we aim to identify microbiota-derived biomarkers and molecular pathways that drive disease onset and progression. To uncover the underlying mechanisms, we combine these approaches with high-throughput functional screening in cell lines and primary cells, enabling systematic assessment of microbial metabolites and their effects on host biology. Advanced bioinformatics plays a key role in generating predictive models and hypotheses, which are subsequently validated experimentally.

In parallel, we investigate acute liver failure caused by *Amanita phalloides* poisoning, where we have shown that the microbiota exacerbates liver damage, likely through immune activation associated with increased gut permeability. Ongoing studies integrate transcriptomics, immune profiling, and patient-derived samples to dissect toxin-induced RNA degradation and identify susceptible cell populations. At the same time, we are exploring strategies to neutralize α-amanitin, including biological and computational approaches.

In addition, embracing a “data parasitism” approach, we systematically reuse and integrate underutilized public datasets to extract new biological insights and strengthen our findings.

Scientific Impact

We work on genomic, metabolic, and immune aspects of gastrointestinal health. We use experimental and computational methods to describe mechanisms for underlying chronic gut and liver diseases, focusing on cellular phenotypes, associated niches, and host-microbiota crosstalk.

Future Goals

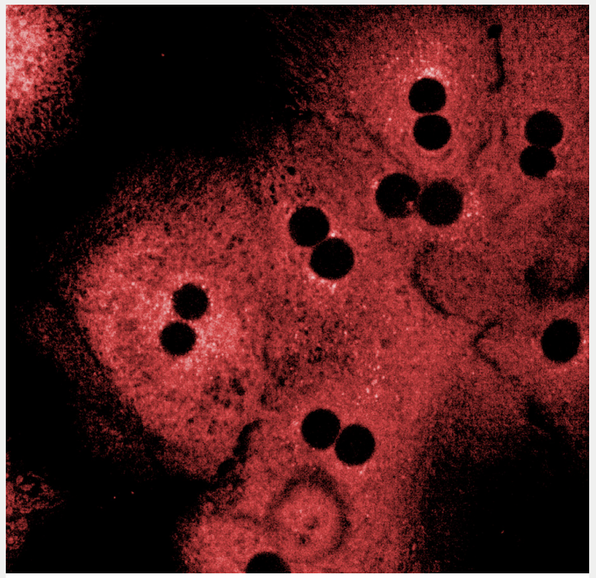
Our goal is to understand the host-microbiota interactions and to utilize that knowledge in the treatment and prevention of gastrointestinal diseases. In the coming years, our research will prioritize discovery of microbiome-derived diagnostic markers for MASLD, mechanistic dissection of microbiota-host interactions in this disease using high-throughput functional screening platforms and multiomics. We envisage that our results will lay a stepping-stone for new prebiotics, probiotics and postbiotics, which will allow better clinical outcomes.

Collaborations

Prof. Samuel Nobs, Institute for Research in Biomedicine (IRB), Switzerland
Prof. Michal Grąt, Łukasz Masior, PhD, Medical University of Warsaw, Poland
Dr. Eng. Tomasz Kamiński, University of Warsaw, Poland

In our lab, we study the complexity of the interactions between food, microbiota and host cells of the gastrointestinal system in health and disease. There are many components to this system, different chemicals in food, different microbes and different cell types, which all interact with each other in various ways. We want to describe this system and understand its underlying laws.

Aleksandra Kołodziejczyk, PhD



Primary murine hepatocytes stained with MitoTracker Deep Red dye. Illustration by Zofia Link.

Group Leader

Aleksandra Kołodziejczyk is an interdisciplinary biologist. She initially completed an international first-level degree in biotechnology, run by a consortium of European Universities at the University of Perugia. She then completed her MSc degree in molecular biosciences, majoring in molecular and cellular biology at the University of Heidelberg, Germany. In 2012, to pursue her PhD, she joined the group of Dr. Sarah Teichmann at the EMBL EBI and the Wellcome Trust Sanger Institute and worked in the emerging field of single-cell transcriptomics. Awarded by the EMBO Long Term Fellowship and the Marie Skłodowska-Curie Action Individual Fellowship, she attained funding to undertake postdoctoral training at the Weizmann Institute of Science. She established her own research group at the IIMCB in 2023, which employs cutting-edge “omic” technologies to study host-microbiota interactions and gastrointestinal health.

Group Members

Postdoctoral Researchers: Justyna Binkowska, PhD; Aneta Grymanowska, PhD; Karen Gimenez Orenga, PhD; Martyna Krupińska, PhD; Krzysztof Szczepaniak, PhD
PhD Students: Konstancja Gałat, MSc; Natalia Rzepka, MSc; Julia Sobieska, MEng; Joanna Słota, MEng; Aleksandra Uryga, MSc; Anna Węgrzycka, MSc
Research Coordinators: Marta Mysza, MSc; Martyna Wysokińska, MSc
Lab Technician: Katarzyna Kaca, MEng
Laboratory Support Specialist: Karolina Komorowska, MSc
MSc Students: Karolina Krupa, BSc; Wojciech Moryl, BEng; Maria Szczerbińska, BSc

Laboratory of
Neurodegeneration

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We study the molecular and cellular roles of ions (Ca^{2+}, K^{+}, Fe^{2+}) and associated molecules in development, neuronal degeneration in Parkinson's disease (PD), Huntington disease, epileptic encephalopathy, hearing loss and retinal pathology. We use cultured iPSCs-derived human cells, zebrafish, and mice models of these pathologies.

Research Summary

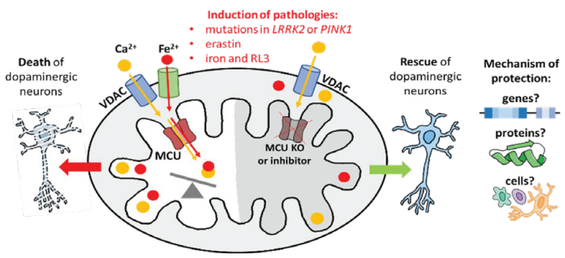
Parkinson disease (PD) is an incurable neurodegenerative disorder. Its pathological hallmarks include the aggregation of α-synuclein and loss of dopaminergic neurons.
In various PD animal models and in cells from PD patients, perturbations of calcium and iron homeostasis occur.
Our major focus is on Ca^{2+} dependent mechanisms on ferroptosis involved in the development of PD.
Its three types can be distinguished: most prevalent sporadic with a late onset, familial that is caused by mutations of genes such as PINK1 or LRRK2, and environmentally-induced by drugs such as MPTP.
Our published data show that degeneration of dopaminergic neurons in zebrafish PD models as a result of a *pink1* mutation or MPTP toxicity are rescued by inactivation of the mitochondrial calcium uniporter (MCU).
Others showed that MCU inhibition rescues neurons with mutation in LRRK2. If different factors that cause PD have a common denominator that is related to MCU activity, then what is it? Our hypothesis is that specific genes are turned on or off, likely involved in ferroptosis, when MCU inactivation exhibits protection of dopaminergic neurons.
The aim of the main project is to identify ferroptosis associated genes that are turned on or off in *pink1* and *lrrk2* PD zebrafish models and in hiPSCs-derived cells when MCU inactivation rescues dopaminergic neurons, and to understand the mechanism of protection.

Scientific Impact

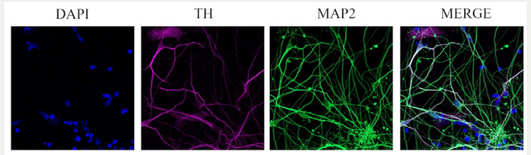
- We showed that the loss of dopaminergic neurons in PD zebrafish models can be delayed by inhibiting Mitochondrial Calcium Uniporter (MCU).
- We showed that the loss of Ca^{2+} sensor Stim2 in zebrafish induces the glaucoma-like phenotype.

Future Goals

- We aim to identify the genes regulated by MCU and induced during ferroptosis – the most common type of cell death in dopaminergic neurons in the course of PD.
- We expect to identify genes that are turned on or off when ions cannot enter mitochondria via MCU and cells in which proteins encoded by these genes operate.
- We analyze mechanisms responsible for loss of retinal ganglion cells in stim2 zebrafish knockout.
- We search for regulatory regions of the human SLC26A4 (Pendrin) which polymorphism has been associated with the CEVA (Caucasian Enlarged Vestibular Aqueduct), which is a common inner ear abnormality causing sensorineural hearing loss.



Graphical abstract. Ilustration by Jacek Kuźnicki.



Staining of iPSC-dopaminergic neurons at day 60.
Illustration by Weronika Skarżyńska and Aleksandra Moskal.

Group Leader

Jacek Kuźnicki is a neurobiologist and professor of biological sciences. He graduated from the University of Warsaw and later received his PhD from the Nencki Institute of Experimental Biology PAS. He was a postdoctoral fellow at the National Institutes of Health in Bethesda, MD, USA. He was a Director of the IIMCB in 1999-2018, the President of the National Science Centre Council in 2020-2022, and has been an ordinary member of the Polish Academy of Sciences since 2020. He is a laureate of many awards, for example, the Officer's and Knight's Crosses of Polonia Restituta (1998, 2008), the Prime Minister's Award for Scientific Achievements (2003), the Crystal Brussels Sprout Award for outstanding achievements in 7FP EU (2013), Award of the Polish Society for Supporting People with Inflammatory Bowel Disease "J-elita" (2025), and Award of the Minister of Science and Higher Education for lifetime achievements (2025).

Group Members

Senior Researcher:
Vladimir Korzh, PhD, DSc Habil
Postdoctoral Researchers:
Weronika Skarżyńska, PhD
Narges Sotoudeh, PhD
Krystyna Żyżyńska-Galeńska, PhD
Research Assistant:
Aleksandra Moskal, MSc
PhD Students:
Razieh Amini, MSc
Sofiia Baranykova, MSc
Mrudula Dileep, MSc
Lab Technician:
Monika Matuszczyk (part-time)
Laboratory Support Specialist:
Dominika Dubicka, MSc
Volunteers:
Magdalena Czeredys, PhD, DSc Habil
(from Mossakowski Medical Research Institute PAS)
Iga Wasilewska, PhD (from Mossakowski Medical Research Institute PAS)

In various animal models of Parkinson's (PD) and in cells from PD patients, perturbations of calcium and iron homeostasis occur. Studying these processes may identify mechanism responsible for PD pathology. We use iPSC differentiated dopaminergic neurons and zebrafish with LRRK2 mutations.

Jacek Kuźnicki, PhD, Professor

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Laboratory of
Prokaryotic Gene Regulation

Our lab investigates the molecular choreography of post-transcriptional gene regulation in bacteria, focusing on the critical moments when these networks are challenged by stress or viral attack. Our research spans from the molecular level – using single-molecule microscopy to visualize real-time assembly of protein-RNA complexes – to the cellular level, where bacteriophages help identify novel antibacterial strategies. This integrated approach is applied to commensal and pathogenic *E. coli* as well as high-priority pathogens like antibiotic-resistant *Acinetobacter baumannii*.

Research Summary

Our research program deciphers the rules of bacterial gene expression across multiple scales. At the molecular level, we use biochemical methods and advanced single-molecule TIRF microscopy to dissect how small regulatory RNAs and the RNA chaperone Hfq function. By capturing real-time interactions between proteins, ribosomes, and RNAs, we seek to understand the fundamental principles governing bacterial gene expression. We then bridge this deep mechanistic insight to the systems level by studying the effects of bacteriophage infection. Here, we deploy transcriptomic and proteomic studies to reveal novel vulnerabilities that can be potentially targeted for antibacterial design. Our work is supported by a SONATA-BIS and OPUS grants from the National Science Centre, Poland, EMBO Installation Grant, and we are part of European Innovation Council-funded consortium.

Scientific Impact

- Mechanistic insights: our work provides a mechanistic understanding of how sRNAs select targets and orchestrate gene silencing. By dissecting the dynamics of targeting and degradation, we move beyond static models to reveal fundamental principles of regulatory control in bacteria.
- Cutting-edge technology: we are using a state-of-the-art microscope to monitor single molecules in action. RNA targeting, translation, and degradation can be visualized simultaneously in real time.
- Potential applications: our work on phage-encoded factors targeting antibiotic-resistant bacteria may unlock new antimicrobial strategies against ESKAPE pathogens. Understanding sRNA design rules will enable the development of programmable bacterial regulators for synthetic biology, metabolic engineering, and targeted therapeutic interventions.

Future Goals

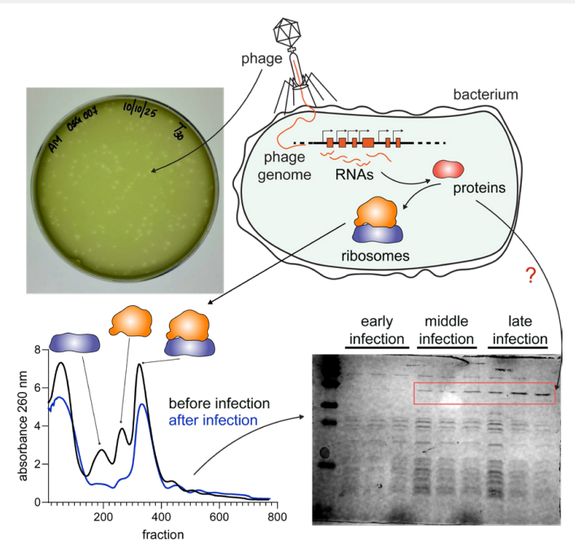
Looking ahead, our research will bridge fundamental discovery with therapeutic innovation. We aim to expand our single-molecule analysis to capture the entire regulatory journey of an mRNA, from its initial targeting by sRNA-Hfq complexes to its ultimate fate at the ribosome. We will leverage this deep mechanistic insight to dissect the phage-host arms race in more clinically relevant contexts, such as within ESKAPE pathogens.

Collaborations

We collaborate with Prof. Sander Granneman (University of Edinburgh) to integrate single-molecule visualization with *in vivo* protein-RNA mapping, and with Prof. Ben Luisi (University of Cambridge) to connect regulatory dynamics to the mechanics of RNA degradation. Dr. Tom Gräfenhan (Core Unit Systems Medicine, Würzburg) helps us with transcriptomics in phage infection studies.

Our lab studies bacterial gene regulation, with two main focuses: (I) how RNA-binding proteins and small RNAs control translation and couple it to RNA degradation, and (II) how bacteriophages reprogram host RNA metabolism and translation. We combine single-molecule TIRF microscopy, which directly visualizes RNA-protein complex assembly in real time, with high-throughput transcriptomics and proteomics to identify interaction partners and regulatory targets in cells. In 2024-2025 we established experimental systems in drug-resistant Acinetobacter baumannii and E. coli together with their phages, and identified phage-encoded factors that modulate bacterial translation and RNA regulation. These mechanistic studies are being pursued across four active, competitively funded research grants.

Ewelina Małecka, PhD



Bacteriophage infection and host translational response. (Top left) Representative agar plate showing plaques formed by bacteriophage infection of a Acinetobacter baumannii lawn, indicating successful lysis of host cells. (Top right) Schematic of the phage infection process: the phage injects its genome into the bacterium, leading to transcription of phage RNAs and their translation by host ribosomes to produce viral proteins. (Bottom left) Polysome profiling before and after infection, illustrating a redistribution of ribosomal fractions upon phage takeover. (Bottom right) SDS-PAGE analysis of samples collected at early, middle, and late stages of infection from polysome fractions. A distinct band pattern (Highlighted box) emerges over time, suggesting the binding of additional proteins to the polysomes upon phage infection. Illustration by Aiswarya Mohan (top left), Ewelina Małecka (top right and bottom left), Ewa Izebska (bottom right).

Group Leader

Ewelina Małecka is a biochemist who graduated with an MSc and then received a PhD from the Adam Mickiewicz University, Poznań. After completing her postdoctoral studies in 2022 at Johns Hopkins University, USA, she established her own laboratory at the IIMCB that focused on studying RNA-protein interactions, RNA metabolism in bacteria, and bacteria-phage interactions. She is a member of the RNA Society.

Group Members

Research Specialist: Maciej Dylewski, PhD
PhD Students: Ewa Izdebska, MSc; Aiswarya Mohan, MSc
Junior Research Scientist: Daria Demina, MSc
Technician: Katarzyna Kaca, MSc
Laboratory Support Specialist: Karolina Komorowska, MSc
MSc student: Zuzanna Grzegorczyk, BSc
Intern: Sebastian Machera, BSc

Laboratory of
Cell Biology

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We explore how two key intracellular processes – endocytosis and receptor signaling – are functionally interconnected in healthy cells and under pathological conditions, such as in cancer or in certain rare diseases.

Research Summary

We have been studying the roles of endosomal sorting complexes required for transport (ESCRT) in cell physiology and oncogenesis. Our research has revealed that the dysfunction of endosomes caused by the loss of proper ESCRT function induces three types of cellular responses, namely sterile inflammatory signaling, lysosome biogenesis and metabolic reprogramming towards enhanced use of extracellular nutrients. Together, these findings demonstrate a broad role of ESCRT complexes in coordinating membrane trafficking, signaling, and metabolism. In addition, the synthetic lethality we identified between the two paralogous ATPases of the ESCRT machinery, VPS4A and VPS4B, has uncovered a novel pair of druggable targets for personalized oncology. We also investigate how mutations in ESCRT components found in rare neurological disorders alter cellular functions and may underlie disease pathogenesis.

In a separate line of research, we focus on macropinocytosis, the least characterized route of endocytic cargo internalization. Yet, this pathway plays a crucial role in nutrient acquisition by cancer cells. We discovered that the AXL receptor tyrosine kinase – a receptor frequently overexpressed in late-stage, therapy-resistant cancers – is a potent inducer of macropinocytosis. Upon activation by its ligand GAS6, AXL drives extensive actin cytoskeleton remodeling that promotes the formation of dynamic membrane ruffles. These ruffles extend and fold back onto the plasma membrane, eventually closing to generate macropinosomes – large, irregular vesicles containing extracellular fluid and associated cargo such as nutrients, growth factors, and membrane receptors. The newly formed macropinosomes subsequently mature through sequential fusion and fission events with endosomal compartments, enabling the sorting, degradation, or recycling of internalized material. Building on our identification of AXL-interacting proteins, we are currently characterizing effectors and regulators that mediate macropinocytosis.

Scientific Impact

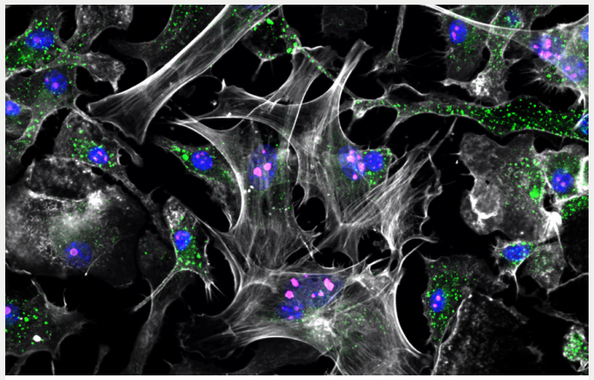
Our studies provide proof of concept that intracellular trafficking and the molecules regulating it can represent a viable therapeutic target in personalized oncology. For example, the synthetic lethality between VPS4A and VPS4B ATPases provides a rationale for developing VPS4 inhibitors for the precision treatment of VPS4B-deficient cancers. Our ongoing studies of AXL-dependent macropinocytosis aim to uncover ways of blocking this process in metastatic and drug-resistant cancers with AXL overexpression.

Future Goals

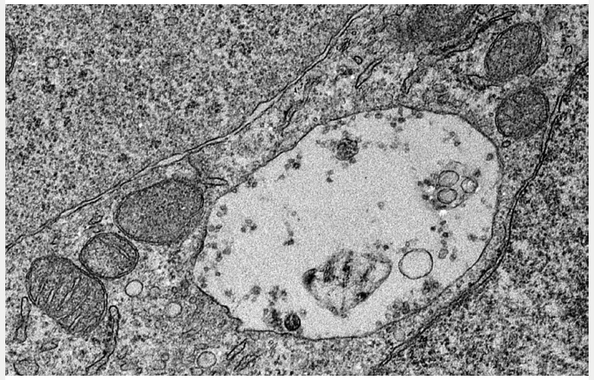
We wish to understand how altered expression or mutations of ESCRT components, observed in cancer or some rare diseases, modify cell physiology. In parallel, we aim to elucidate the mechanisms and effector proteins by which the activated AXL receptor drives macropinocytosis to fuel growth of cancer cells.

Collaborations

We collaborate with partners from the IIMCB and external institutions within the HERO consortium project, which aims to develop the next generation of mRNA-based cancer immunotherapies.



Murine bone marrow–derived macrophages cultured *in vitro*. Nuclei are stained blue, endosomes green, nucleoli magenta and actin grey. Image by Patrycja Daszczuk.



Transmission electron microscopy image of membrane organelles (multivesicular endosome containing internal vesicles; mitochondria) in a HEK293 cell. Image by Ewelina Szymańska, Matylda Macias, Aleksandra Szybińska.

Group Leader

Marta Miączyńska is a molecular cell biologist, professor of biological sciences, and Director of IIMCB. She graduated from the Jagiellonian University and received her PhD from the University of Vienna. She was a postdoctoral fellow at the European Molecular Biology Laboratory in Heidelberg and the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden. Since 2026, she has served as Chair of the EMBO Council and of EU-LIFE.

Group Members

Senior Researcher: Ewelina Szymańska, PhD
Postdoctoral Researchers: Patrycja Daszczuk, PhD; Ranjana Maurya, PhD
Research Assistant: Agnieszka Świstek, MSc
PhD Students: Marta Chwałek, MSc; Malwina Grębowicz-Maciukiewicz, MSc; Bartosz Jary, MSc; Zuzanna Miciak, MSc
Lab Technician: Monika Matuszczyk (part-time)
Laboratory Support Specialist: Renata Wyszyńska, MSc
MSc Student: Anna Witowska, BSc

In 2024-2025, we continued to study the principles of cellular logistics, namely how cells take up and transport various substances within their interior, and which signals initiate these processes. Our aim was to understand how these trafficking rules are altered in disease, for example in cancer cells with increased metabolic demands or in cells carrying mutations that cause rare genetic disorders. We believe that elucidating these underlying mechanisms can ultimately guide the development of new therapeutic strategies.

Marta Miączyńska, PhD, Professor

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Laboratory of
RNA-Protein Interactions – Dioscuri Centre

We explore how RNA-binding proteins control gene activity and help fight off RNA viruses. Combining techniques from structural biology to live cell experiments, we have discovered RNA-binding proteins (RBPs) and small molecules that influence production of a key protein responsible for Parkinson's disease. We also identified a new RBP that plays a key role in the immune system's response to viral infections. Our research not only answers core questions in molecular biology but also opens new paths for treating both infectious and non-infectious diseases.

Research Summary

RNA is a fundamental molecule essential for life, carrying genetic instructions from DNA to build proteins and performing crucial regulatory and catalytic roles. One leading hypothesis suggests that life originated in an RNA world prior to the appearance of DNA. However, RNA depends on RBPs, which ensure it is properly processed, transported, and translated, supporting genetic information flow and maintaining cell function. RNA-protein interactions also underpin immune defenses; certain RBPs detect virus-derived RNAs, triggering immune responses. Disruption of these interactions contributes to disease, including viral immune evasion and neurodegenerative disorders such as Parkinson's disease (PD).

At the Dioscuri Centre for RNA-Protein Interactions in Human Health and Disease at the International Institute of Molecular and Cell Biology in Warsaw, we study how these interactions influence cellular systems. Our research addresses two main areas: how RBPs enable immune detection of viral and therapeutic RNAs and how targeting RNA-protein interactions may help treat human diseases, especially viral infections and PD.

We investigate how RBPs recognize features of viral RNA and initiate immune responses by triggering molecules such as interferons. Understanding these processes could support antiviral drug or vaccine development. In PD, we focus on regulation of alpha-Synuclein by RBPs and microRNAs. We study how RNA-protein interactions can be modulated to restore healthy regulation, aiming to influence disease progression at the molecular level.

Scientific Impact

- Advancement in understanding of RNA-protein interactions as key regulators of innate immunity, enabling the development of novel antiviral strategies.
- Identification of molecular mechanisms underlying Parkinson's disease, revealing novel therapeutic targets.

Collaborations

- Together with Prof. Juri Rappsilber (Berlin Technical University), we use mass spectrometry for whole proteome studies as well as structural analyses. Prof. Rappsilber is a German partner of the Dioscuri Centre for RNA-Protein Interactions in Human Health and Disease.
- Together with Prof. Andrzej Dziembowski (IIMCB) and Prof. Gunther Hartmann (Bonn Medical University), we are investigating the immunogenicity of therapeutic RNAs.
- Together with Dr. Elżbieta Nowak, and Prof. Marcin Nowotny (IIMCB), we are elucidating the structures of RNA-binding proteins (RBPs).
- Together with Dr. Katarzyna Mleczko-Sanecka (IIMCB), Dr. Wojciech Pokrzywa (IIMCB), and Prof. Tilo Kunath (University of Edinburgh), we are elucidating the effects of RBP-targeted compounds in cells and whole organisms.
- Together with Prof. Michele Vendruscolo (University of Cambridge), we are using AI to screen small molecules that inhibit RNA binding proteins.

In 2024-2025 we were focused on RNA-protein interactions in innate antiviral defense and on safer RNA-based therapy. We showed that the 5' terminal nucleotide drives the formation of immunogenic dsRNA by-products in IVT RNAs, influencing therapeutic RNA design. We helped define the mechanisms and structures of the major antiviral protein TRIM25. We mapped key cellular effects of HuR inhibition and advanced small-molecule approaches to disrupt HuR-RNA complexes. In December 2025, we received the Polish Academy of Sciences, Division II, Distinction for an exceptional research achievement entitled "New mechanisms and therapeutic prospects in innate immune response to viruses and RNA based therapy".

Gracjan Michlewski, PhD, Professor

Future Goals

We aim to employ a multidisciplinary approach to explore the links between RNA biology and human diseases. We will be probing the involvement of RBPs in viral signaling pathways, which can lead to the identification of a novel and broad range of antiviral therapies. Furthermore, we will be expanding our understanding of RNA regulatory pathways and seeking compounds to decrease alpha-Synuclein expression in Parkinson's disease.

The laboratory studies RNA-protein interactions in the context of viral infections and neurodegenerative disorders. This image is an AI-generated abstract representation of these topics.

Group Leader

Gracjan Michlewski is a molecular biologist and professor of biological sciences. He graduated from the Adam Mickiewicz University, Poznań and received his PhD from the Institute of Bioorganic Chemistry PAS, Poznań. He worked as a postdoctoral fellow at the MRC Human Genetics Unit in Edinburgh, United Kingdom (2005-2010). In 2011, he founded a laboratory at The Wellcome Trust Centre for Cell Biology, University of Edinburgh, supported by an MRC Career Development Award. From 2018, he held roles as Senior Lecturer and Reader at the Infectious Medicine Department of the University of Edinburgh, and concurrently served as an Associate Professor at the Zhejiang University-University of Edinburgh Institute in Haining, China. In 2021, he established a laboratory at the IIMCB with the Dioscuri Centre for RNA-Protein Interactions in Human Health and Disease. He is a member of the RNA Society. Additionally, he co-organized the successful 1st Polish RNA Biology Meeting in September 2023 in Warsaw as well as 2nd Polish RNA Biology Meeting in September 2025 in Poznań.

Group Members

Postdoctoral Researchers: Emilia Baranowska, PhD; Justyna Sobich, PhD; Ivan Trus, PhD; Magdalena Wołczyk, PhD
PhD Students: Agnieszka Bolembach, MSc; Mouad Fakhri, MSc; Michał Lechowski, MSc; Zara Naz, MSc; Jacek Szymański, MSc
PhD Student/Technician: Nathalie Idlin, MSc
Technician: Julia Kędzierska, MSc (part-time)
Laboratory Support Specialists: Lena Majchrowicz, PhD; Eliza Ratkowska, Eng

Laboratory of
Iron Homeostasis

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Iron is essential for numerous biological processes, including oxygen transport, DNA synthesis, and cellular respiration. However, tight regulation of iron balance is crucial, as both iron deficiency and iron overload can lead to severe health issues. At the Laboratory of Iron Homeostasis, we aim to elucidate iron regulatory mechanisms across tissues and cell types, with a particular focus on iron recycling from erythrocytes and the systemic sensing of body iron burden. Through this work, we advance the understanding of mammalian physiology and the pathogenesis of diseases associated with iron dyshomeostasis.

Research Summary

One major aspect of our research focuses on iron recycling, a process primarily orchestrated by splenic red pulp macrophages (RPMs), which break down aging erythrocytes and release iron back into the bloodstream. Despite representing the dominant source of bioavailable iron, knowledge about RPM biology and the mechanisms governing iron turnover efficiency remains limited.

Our findings revealed a pronounced impairment of this process during aging. Specifically, we demonstrated that age-associated iron accumulation in RPMs leads to their functional decline and eventual demise, a challenge partially alleviated by dietary iron restriction in mice. Another major research line explores distinct functional and metabolic adaptations of RPMs in response to iron deficiency, shedding light on how the organism adjusts to restricted iron availability. In addition, our research identified liver sinusoidal endothelial cells (LSECs) as the primary cell type responsible for the clearance of free hemoglobin from the circulation, thereby contributing to physiological iron recycling and hemoglobin detoxification, particularly under hemolytic conditions. Concurrently, we uncovered previously unrecognized mechanisms by which LSECs sense excessive systemic iron levels, including elevated hemoglobin burden.

Scientific Impact

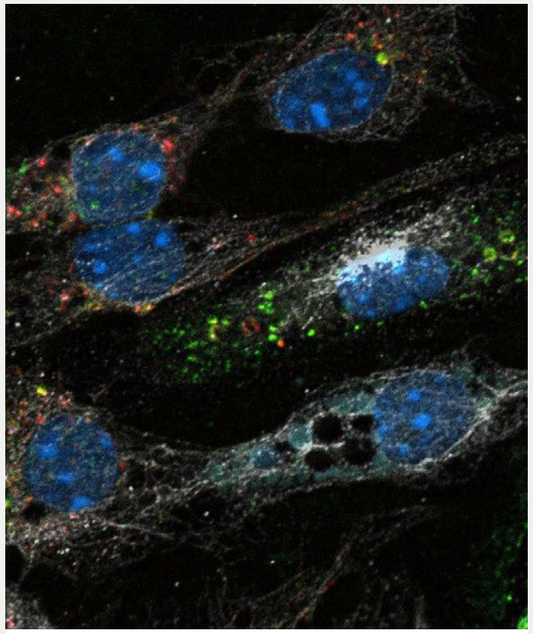
- We identified impaired iron recycling as an early hallmark of aging.
- We deciphered how splenic macrophages adapt their phagocytic capacity and metabolism in response to nutritional iron deficiency.
- We revealed an unexpected role of liver endothelium in the clearance of free hemoglobin under both physiological and hemolytic conditions.
- We discovered a novel signaling pathway involved in iron sensing by liver endothelium.

Future Goals

Our future work will investigate how iron recycling efficiency shapes splenic immune functions and contributes to broader immune homeostasis. We also aim to establish defective iron recycling as a contributing factor in human disease. In parallel, we will further dissect the links between macrophage metabolism and iron recycling from erythrocytes.

Collaborations

We work closely with peers from the iron metabolism field, researchers in immunology, cancer biology, infectious diseases, and liver physiology, and experts in modern omic technologies to understand how different cell types cooperate to maintain iron balance and support immune function. These collaborations enable us to translate mechanistic insights from mouse models and cellular systems into human-relevant contexts, including primary liver cells.



Primary murine LSECs performing uptake of fluorescently-labeled hemoglobin. Illustration by Aneta Jończy.

Group Leader

Katarzyna Mleczko-Sanecka is a biomedical researcher interested in signaling and intercellular communication, with a longstanding focus on principles governing iron metabolism. She graduated from the Jagiellonian University, Kraków. As a fellow of the Louis-Jeantet Foundation, she obtained a joint PhD degree from the European Molecular Biology Laboratory in Heidelberg and Heidelberg University. In 2017, she established her research group at the IIMCB, and in 2023, she received the Gunshin Levy Award from the BioIron Society, recognizing her dedication, commitment, and contributions to the research field of iron homeostasis.

Group Members

Postdoctoral Researcher:
Aneta Jończy, PhD
PhD Students:
Komal Kumari Chouhan, MSc
Raghunandan Mahadeva, MSc
Pratik Kumar Mandal, MSc
Research Specialist:
Marta Niklewicz, MSc
Technician:
Iwona Łopata, MSc
Laboratory Support Specialist:
Patrycja Rojek, PhD

In our research, we are driven by the realization that long-standing assumptions about iron biology and macrophage function often capture only part of the underlying reality. By looking closely at how individual cell types, such as splenic macrophages and liver endothelial cells, adjust their clearance functions, signaling, and metabolism to changing iron availability, we see that iron homeostasis is not a fixed program but a highly plastic, cell-type-specific process. Each time we revisit pre-existing concepts through the lens of metabolic rewiring and tissue context, we uncover new layers of organization that reveal how elegantly systemic iron balance is maintained.

Katarzyna Mleczko-Sanecka, PhD

Laboratory of
Protein Structure

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Our group studies the systems that process genetic information in living cells. This information is encoded in DNA and RNA. Special protein machines in the cell decode this information, ensure its stability, and copy it. To understand how they work, we study these machines at the level of individual atoms. For example, we have determined the molecular mechanisms of machineries that repair chemically damaged DNA.

Research Summary

Our group uses structural biology, mainly cryo-electron microscopy, and protein biochemistry to elucidate the mechanism of action of enzymes involved in the processing of genetic information encoded in DNA and RNA. In particular, we study DNA repair and transposition, reverse transcription, viral replication, RNA processing, and bacterial antiphage systems.

Future Goals

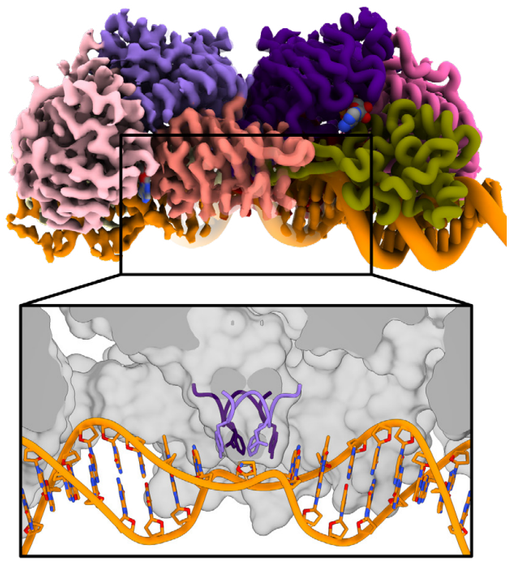
In the near future, we will continue our studies on DNA repair and transposition. We would like to fully elucidate the mechanism of action of the RecFOR complex and provide an understanding of the *in vivo* mechanism of antiphage reverse transcriptases.

Scientific Impact

In our recent work we determined the molecular architecture of a key complex in one of the major DNA repair pathways in bacteria: homologous recombination. This complex, consisting of the RecF, RecR, and RecO proteins, is responsible for the formation of a RecA protein filament of single-stranded DNA. This filament promotes the search for homologous DNA in the repair process.

The UvrA protein is a vital part of the nucleotide excision repair process in bacteria. We have demonstrated that ATP-driven conformational changes in UvrA are used to mechanically probe the flexibility of DNA, an increase in which indicates the presence of damage. This is a new paradigm in DNA repair – localization of the damage through mechanical probing of the integrity of the double helix.

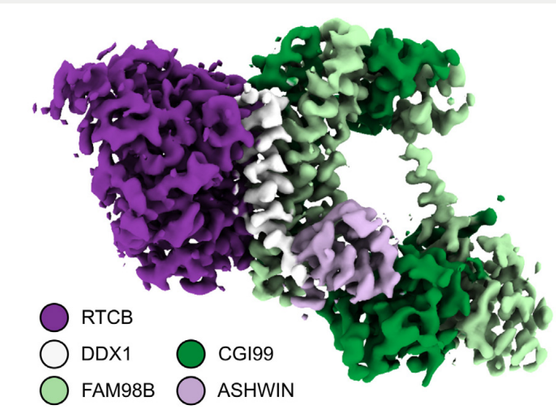
We have also determined the structures and mechanisms of action of unusual reverse transcriptases involved in the antiphage response – AbiK, Abi-P2, AbiA and UG10/DRT7. These enzymes are unique in that they produce long stretches of single-stranded DNA in a template and primer independent manner. They initiate synthesis by covalently attaching the first nucleotide to their tyrosine residue.



Novel ATP-bound conformation of UvrA-DNA complex (cryo-EM map on the left, structure on the right). Lower panel shows the new element (the “wedge”) which probes the integrity of the double helix. Illustration by Mariusz Czarnocki-Cieciura.

Our current research activities focus on processing of information encoded in DNA and RNA. For instance, we study DNA repair in bacteria, the mechanisms of reverse transcriptases and tRNA ligases, and the replication of DNA in herpesviruses. We use cryo-electron microscopy, protein crystallography, and protein biochemistry to elucidate the molecular basis of these processes and mechanisms. We solved a series of cryo-EM structures of UvrA, a DNA damage sensor in bacteria, and demonstrated how it detects DNA modifications. We also determined the molecular architecture of the vertebrate tRNA complex. Additionally, we determined the structure and mechanism of the unique bacterial reverse transcriptase AbiA, which is involved in antiphage defense.

Marcin Nowotny, PhD, Professor



Cryo-EM structure of the five-subunit *D. rerio* tRNA ligase complex. Illustration by Mariusz Czarnocki-Cieciura.

Group Leader

Marcin Nowotny is a structural biologist and professor of biological sciences. He graduated from the University of Warsaw and received his PhD from the Nencki Institute of Experimental Biology, PAS. After postdoctoral studies at the National Institutes of Health (USA), in 2008 he established the laboratory he leads at the IIMCB. He is the laureate of numerous awards, such as the Prime Minister’s award for scientific achievement (2024), Jan Karol Parnas Award (2023), and the Prize of the Foundation for Polish Science (2022). He is a member of the European Molecular Biology Organization and Academia Europaea.

Group Members

Postdoctoral Researchers:
Supreet Bhattacharya, PhD
Mariusz Czarnocki-Cieciura, PhD
Małgorzata Figiel, PhD
Markéta Šoltysová, PhD
Michał Tyras, PhD
Krzysztof Wycisk, PhD
PhD Students:
Girish Apte, MSc
Vysakh Komathattu Viswanath, MSc
Shuvankar Patra, MSc
Research Specialists:
Julia Rybakowska, MSc
Małgorzata Sroka, MSc
Weronika Stelmaszczyk, MSc
Weronika Zajko, MSc
Technician:
Iwona Ptasiewicz (part-time)
Laboratory Support Specialist:
Kamila Gajdek, MEng

Laboratory of
Protein Metabolism

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Our research focuses on proteostasis, the coordinated control of protein synthesis, folding, and degradation. We study how this balance is maintained by the ubiquitin-proteasome system (UPS), molecular chaperones, and extracellular quality-control pathways such as exophers. In this context, we investigate the nucleolus as a stress-responsive proteostasis hub that supports protein quality control under challenging conditions. We also explore the molecular basis of rare diseases associated with proteostasis defects.

Research Summary

Nucleolus as a Stress-Responsive Hub: We investigate the nucleolus as a dynamic regulator of proteostasis. Our work focuses on how proteotoxic stress induces reversible nucleolar remodelling into a compartment that transiently prioritises protein quality control over ribosome biogenesis, enabling efficient recovery of proteome integrity.

Rare Diseases of Proteostasis: We study the molecular basis of rare diseases caused by defects in protein quality control, with particular emphasis on ubiquitin-dependent regulation and cullin-RING E3 ligase substrate receptors. Our aim is to understand how impaired substrate recognition disrupts tissue proteostasis and drives disease phenotypes.

Proteostasis in Adaptive Stress States: We investigate how proteostasis is maintained under prolonged or recurrent stress conditions, with a particular focus on cold-induced adaptive states resembling hibernation. Our work addresses how cells reorganise proteome maintenance pathways when growth and biosynthesis are temporarily suppressed.

Lipid-Proteasome Axis in Stress and Aging: Using *C. elegans* and human cell systems, we analyse how lipid metabolism and inter-tissue signalling modulate proteostasis during chronic stress and aging. We aim to define how metabolic rewiring supports long-term proteome stability and adaptation.

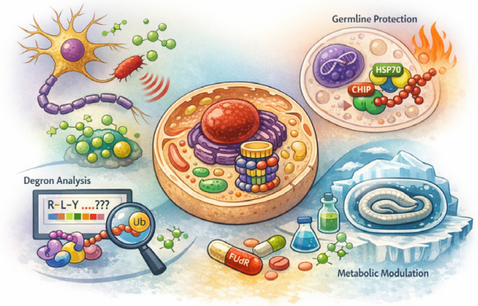
Scientific Impact

Neuroendocrine Control of Proteostasis: We uncovered a neuroendocrine circuit linking environmental and social cues to organismal proteostasis through regulation of exopher biogenesis (Szczepańska et al., Nat Commun 2024). Extending this concept, we demonstrated that pathogen threat proximity modulates extracellular vesicle production prior to infection, revealing a pre-emptive, environment-sensing layer of proteostasis regulation (Kołodziejska et al., Nat Commun 2025).

Mechanisms of Proteostasis in Reproduction and Stress: We demonstrated that HSP70-CHIP interactions are essential for maintaining germline integrity under heat stress by preventing excessive degradation of reproductive proteins (Thapa et al., J Biol Chem 2024), revealing a protective layer of ubiquitin-dependent regulation.

Computational Resources for the Community: We established DEGRONOPEDIA (Szulc et al., Nucleic Acids Res 2024), an open-access platform for degron identification and prediction, now supporting community-wide studies of ubiquitin-mediated regulation.

Metabolic Modulation of Proteostasis: We identified unexpected links between detoxification pathways and UPS activity, demonstrating that small-molecule interventions (e.g. floxuridine) can modulate proteostasis independently of canonical germline signalling (Dubey et al., PLOS Genetics 2024).



Research framework of the Laboratory of Protein Metabolism (2024-2025). The graphic summarises our integrative approach to proteostasis, linking environmental inputs (pathogens, chemical modulators, and cold-induced adaptive states in C. elegans) with cellular responses. Central elements include degron-based substrate recognition and ubiquitin signalling, stress-induced nucleolar remodelling, germline protection via HSP70-CHIP, and metabolic regulation. Together, these axes define how organismal proteostasis is coordinated across tissues under stress, ageing, and disease-relevant conditions. AI-generated image.

Future Goals

Our future work will focus on how proteostasis is reorganised under chronic and adaptive stress, with emphasis on the nucleolus as a spatial regulator of protein quality control and its interplay with the UPS, including the immunoproteasome. We will investigate how metabolic rewiring, including suppression of lipid biosynthesis, restores proteasome function under stress, and how proteostasis is maintained in cold-induced adaptive states resembling hibernation. In parallel, we aim to define how dysfunction of cullin-RING ubiquitin ligases reshapes proteostasis in human disease.

Group Leader

Wojciech Pokrzywa is a molecular biologist with expertise in *C. elegans* animal models. He graduated from the University of Wrocław and received his PhD from the Catholic University of Louvain, Belgium. He was a postdoctoral fellow at the Cologne Excellence Cluster on Cellular Stress Responses in Aging-Associated Diseases (CECAD) at the University of Cologne, Germany. In mid-2017, he established his own research group that focuses on mechanisms of protein metabolism at the IIMCB. He and his team were recognised for outstanding scientific achievement with an award from the Minister of Science and Higher Education (2024), as well as with a distinction from the Second Division of the Polish Academy of Sciences (2024).

Group Members

Postdoctoral Researchers: Andrés Felipe Leal Bohórquez, PhD; Bogdan Cichocki, PhD; Małgorzata Piechota, PhD; Agnieszka Sztyler, PhD; Pankaj Thapa, PhD
PhD Students: Lilla Biriczová, MSc; Karolina Milcz, MSc; Smriti Raina, MSc; Anwesha Sarkar, MSc; Natalia Szulc, MSc
Specialists: Khushboo Jaggi, MSc; Marta Niklewicz, MSc
Technician: Iwona Łopata, MSc
Laboratory Support Specialist: Gabriela Skrzyńska, MSc

In 2024-2025, our work helped define proteostasis as a coordinated system connecting organelles, cells, and tissues, rather than a set of separate pathways. We found that cells not only respond to stress, but can anticipate it, reshape structures such as the nucleolus, and communicate through extracellular pathways. Many of these responses are encoded in degradation signals and can be tuned with small molecules.

Wojciech Pokrzywa, PhD,
DSc Habil

Laboratory of
Zebrafish Developmental Genomics

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Our research utilizes the zebrafish model organism to study how gene expression is regulated in the developing embryo, examining its links to congenital malformations in humans. We specifically focus on heart development and diseases, employing classical genetics alongside bulk and single-cell genomics techniques.

Research Summary

Embryonic development is orchestrated through highly precise regulatory mechanisms that ensure genes are expressed in the right cells, at the right time, and at appropriate levels. Understanding how this spatiotemporal control is achieved remains a central challenge in biology.

Our lab investigates the fundamental principles of gene regulation during vertebrate development, using zebrafish as a powerful *in vivo* model system. We focus on how cis-regulatory elements, chromatin accessibility, and higher-order genome organization interact with transcription factors to control gene expression programs that drive cell fate decisions and organ formation. By combining genomics approaches with experimental embryology, genetics, and biochemistry, we aim to define gene regulatory networks in their native developmental context and understand how disruptions in these mechanisms lead to human congenital disorders.

Our work places particular emphasis on cardiac development. While many genes essential for heart formation have been identified, how their activity is coordinated across developmental time and integrated with epigenetic regulation remains incompletely understood. We focus on cardiomyocytes and cardiac pacemaker cells, investigating how distinct cardiac cell types emerge and acquire specialized functions. Through large-scale transcriptomic and epigenomic analyses, including single-cell approaches, we have generated resources that reveal cellular diversity and regulatory elements in the developing heart.

Ultimately, our research aims to bridge gene regulation, cellular differentiation, and organ function, contributing to a deeper understanding of cardiovascular development and its links to human disease.

Scientific Impact

- Generated comprehensive transcriptomic and epigenomic resources of the developing zebrafish heart, focusing on cardiomyocytes and rare cell types such as pacemaker cells.
- Established a single-cell atlas of the developing zebrafish heart revealing previously uncharacterized cardiac cell types and their molecular profiles.
- Identified novel regulatory elements underlying cardiovascular development and disease.
- Developed and validated a computational tool for the discovery of human congenital heart disease (CHD)-associated non-coding variants affecting gene regulation.

Future Goals

We aim to develop zebrafish models of human genetic diseases, particularly those driven by non-coding regulatory variation, to enable in-depth investigation of disease mechanisms in a physiologically relevant *in vivo* context. By integrating genome editing with transcriptomic and epigenomic profiling, we seek to directly link genetic variants to their effects on gene regulation, cellular identity, and cardiac function.

Building on our expertise in gene regulatory networks, we will further dissect how disruptions in cis-regulatory elements and chromatin organization alter developmental trajectories, with a focus on cardiomyocytes and cardiac pacemaker cells. We also aim to establish an integrated single-cell transcriptomic and epigenomic atlas of the developing heart, offering a unified view of regulatory landscapes across cell types and developmental stages.

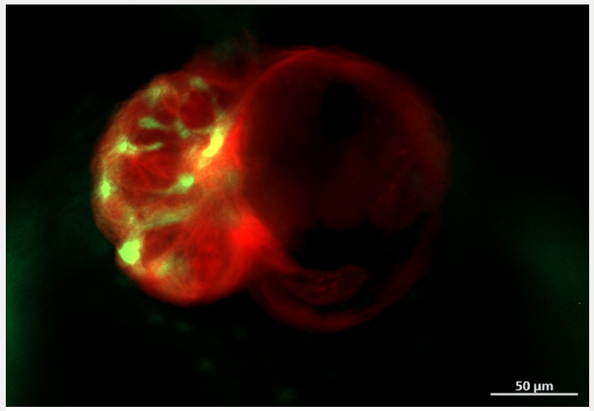
Ultimately, our goal is to bridge human genetic data with experimental biology, contributing to a more comprehensive understanding of the molecular basis of congenital heart diseases and informing future precision medicine approaches.

Collaborations

We actively collaborate with research groups within IIMCB as well as with leading international laboratories in genomics and clinical genetics. We seek cross-disciplinary partnerships that integrate developmental biology with clinical research, methods development, and computational modeling, enabling us to connect fundamental mechanisms with disease relevance.

Our research seeks to uncover the fundamental logic of gene regulation in development, with the ultimate goal of translating these insights to human health. Using zebrafish, a model with human-relevant developmental and genetic programs, we aim to understand how regulatory disruptions lead to congenital diseases and to guide future experimental and clinical studies.

Cecilia Lanny Winata, PhD, DSc Habil



Cellular diversity of the myocardium. The zebrafish heart from the transgenic line Tg(myl7:mRFP) x Tg(–6.8got2b:cfos:EGFP) at 72 hours post-fertilization highlights distinct cardiomyocyte populations using dual fluorescent labeling. All myocardial cells are marked in red, while a specialized subset of trabecular cardiomyocytes is labeled in green. Green fluorescence is driven by a newly identified enhancer element, representing the earliest known molecular marker of trabecular cardiomyocytes and providing a vivid illustration of cellular diversity within the developing heart. Image by Costantino Parisi.

Group Leader

Cecilia Lanny Winata is a developmental biologist with an expertise in genomics and gene regulation. She received her PhD from the National University of Singapore and completed a postdoctoral fellowship at the Genome Institute of Singapore. In 2014, she established her own research group at IIMCB through a project funded by the European Union's FP7 program in partnership with the Max Planck Institute for Heart and Lung Research. Her lab investigates gene regulation during embryonic development using the *D. rerio* as a model organism. Besides advancing the understanding of various aspects of developmental gene regulation, her research has generated invaluable genomics resources that contributed to enhancing the annotation of the zebrafish genome as part of the international DANIO-CODE consortium.

Group Members

Postdoctoral Researcher:
Shikha Vashist, PhD
PhD Students:
Aman Suryan, MSc
Arunabha Sen, MSc
Research Technicians:
Adrianna Pakuła, MSc
Konrad Kulesza, MSc
Lab Technician:
Julia Kędzierska, MSc
Laboratory Support Specialists:
Agnieszka Konkol, MSc
Patrycja Rojek, PhD
Internship Students:
Pola Klinowska
Wojciech Mordan

Laboratory of
Cellular Proteostasis

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Our laboratory investigates how cells maintain the health of their proteome – a process known as proteostasis. We are particularly interested in the spatial and temporal regulation of protein degradation pathways in mammalian cells. We aim to understand how disruptions in these quality control systems contribute to the development of neurodegenerative diseases, such as Alzheimer's, Parkinson's, and Huntington's disease.

Research Summary

The cellular proteome is extraordinarily complex, comprising thousands of proteins that must be correctly folded, localized, and removed when damaged or no longer needed. This balance – proteostasis – is maintained by coordinated systems controlling protein synthesis, quality control, and degradation. Our laboratory focuses on the mechanisms governing protein clearance, particularly the ubiquitin-proteasome system (UPS), and how they are regulated across different cellular compartments.

Our research aims to dissect the molecular pathways that maintain nuclear protein quality control and to understand how these pathways interact with cytosolic degradation systems. We are especially interested in the nucleocytoplasmic transport of UPS components, including the unfoldase VCP/p97. Impaired communication between nuclear and cytosolic proteostasis networks may contribute to the early stages of neurodegeneration, yet the molecular underpinnings of this phenomenon remain poorly understood.

To investigate these mechanisms, we use a combination of cutting-edge molecular biology, high-throughput CRISPR/Cas9-based genetic screening, quantitative mass spectrometry, and advanced fluorescence microscopy. We apply these tools to cellular models of neurodegenerative diseases, including human iPSC-derived neurons and brain organoids. Our ultimate goal is to identify how proteostasis networks fail in disease and to uncover new therapeutic strategies aimed at restoring protein homeostasis in affected cells.

Scientific Impact

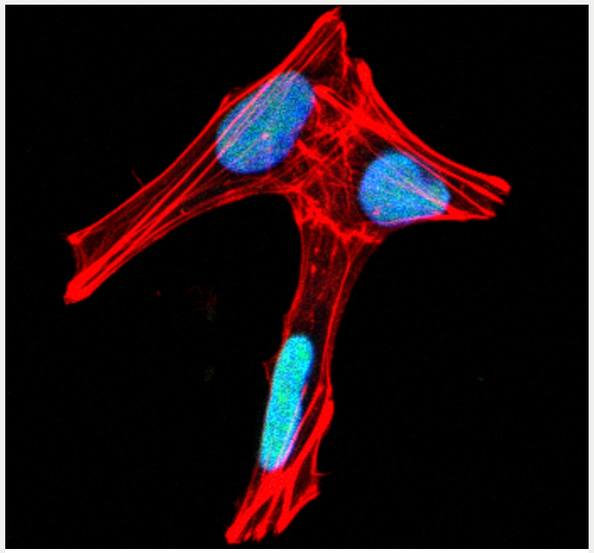
- Identification of mechanisms regulating nuclear proteostasis and their crosstalk with cytosolic degradation pathways.
- New insights into how alterations in protein clearance pathways contribute to neurodegenerative disease pathology.
- Development and application of human neuronal models to study disease-associated proteostasis defects.

Future Goals

We aim to define how the ubiquitin-proteasome system functions within the nucleus and how nuclear proteostasis is integrated with broader cellular protein quality control. Our research will also explore how impairments in these systems lead to the accumulation of toxic protein aggregates – a hallmark of many neurodegenerative diseases. Ultimately, we hope to identify novel molecular targets for therapies that can restore cellular proteostasis in disease-affected tissues.

Collaborations

We actively seek interdisciplinary collaborations to bridge molecular proteostasis research with translational neuroscience. Our partnerships include experts in neurobiology, cellular imaging, proteomics, and regenerative medicine. Collaborative efforts are focused on uncovering therapeutic targets and validating findings in disease-relevant human models.



Induced pluripotent stem cells; proteasome activity reporter in the nucleus (green signal), actin (red signal). Illustration by Lidia Wróbel.

Group Leader

Lidia Wróbel is a cell biologist. Her scientific journey began with an MSc in Biotechnology at the Warsaw University of Life Sciences (SGGW), completed in 2009. As an Erasmus student, she had the opportunity to carry out a research project at Ghent University in Belgium – an experience that sparked her long-standing interest in protein quality control. In 2010, she joined Prof. Agnieszka Chacinska's lab at the International Institute of Molecular and Cell Biology in Warsaw, where she focused on understanding the mechanisms of mitochondrial biogenesis and their crosstalk with cytosolic protein degradation systems. In 2016, thanks to an EMBO Long-Term Fellowship, Lidia Wróbel moved to join Prof. David Rubinsztein's group at the University of Cambridge. There, she focused on the autophagy-lysosomal pathway and its role in neurodegenerative diseases. After her postdoctoral training in 2024, she took an exciting step forward by establishing her own research group at the IIMCB.

Group Members

Postdoctoral Researcher:
Patrycja Mulica, PhD
PhD Students:
Aroosa Mir, MSc
Gabriela Piórkowska, MSc
Junior Research Specialist:
Nikkei Carreras, MSc
Laboratory Support Specialist:
Angelika Jocek, MSc
MSc Student:
Kamila Kurzajak

We aim to elucidate the spatial and temporal regulation of protein clearance by the ubiquitin-proteasome system, uncover new mechanisms of nuclear protein quality control and its coordination with cytosolic pathways, and identify proteostasis defects driving neurodegeneration. Because nuclear protein degradation in mammals remains poorly understood, we use a CRISPR/Cas9 whole-genome screen and endogenous protein trafficking methods to identify new regulators, define substrates, and dissect crosstalk with cytosolic degradation. In parallel, we study VCP, a key protein unfoldase, to determine how disease-linked mutations promote tau accumulation in frontotemporal dementia (FTD).

Lidia Wróbel, PhD

Interview:

Where Curiosity Meets Support

What does scientific independence really mean today? After years of international research experience, **Dr. Lidia Wróbel** returned to Poland to build something new: a laboratory, a team, and a scientific culture. Her Laboratory of Cellular Proteostasis is relatively new at IIMCB, yet is already providing real impact.

In 2024, you established the Laboratory of Cellular Proteostasis at IIMCB after a long international research path. How do you look back on this first phase of building a new research group?

It was definitely a major milestone in my career and a significant challenge. After spending so many years as a lab-based researcher (a so-called “pipetting scientist”), you suddenly become a scientist who has to create an ecosystem in which science can happen. Building a lab from scratch is extremely demanding, but it offers a rare freedom to shape a scientific niche and establish a lab culture from the very beginning. It is deeply rewarding to see that, after one year, the ideas I have are working and the projects are growing beyond what I could achieve on my own.

Do you ever envy the stability of long-established laboratories, or does the agility of a young lab outweigh those concerns?

The freedom to shape the science, the culture, and the research direction from the start is energizing and worth the uncertainty. On the other hand, long-established labs benefit from decades of accumulated know-how, refined methods, and broad expertise within their teams. As a new lab, I must build these strengths deliberately, with a clear vision of where I want the lab to excel over the next few years.

Your career connects basic cell biology with disease-oriented research. How important was this continuity – from fundamental mechanisms to patient relevance – in shaping your scientific identity?

I have always been fascinated by the natural world. I still remember the moment I realized that our bodies are made up of cells and that these cells can be grown in a dish and observed under a microscope. That still fascinates me! Core cellular mechanisms lie at the heart of disease and understanding them can translate into meaningful benefits for human health.

Photo: L’Oréal-UNESCO For Women in Science Program Materials.

For this reason, the journey from the cell to the patient has been a deliberate choice in my career. Working at the interface of basic mechanisms and human disease shapes how research questions are framed in my laboratory and gives my work a clear purpose: ultimately, my goal is to better understand disease and to guide the development of new therapeutic directions.

In support of this scientific trajectory, I was awarded an EMBO Installation Grant, which provides funding and integration into a pan-European research network as I establish an independent laboratory. This grant has been instrumental in advancing the lab’s research into protein quality control and proteostasis. In addition, I am a recipient of the 2025 L’Oréal–UNESCO For Women in Science Fellowship (habilitation category) – an award that recognizes sustained scientific excellence and supports mid-career development for outstanding female researchers.

By offering both recognition and support, as well as valuable networking opportunities, this fellowship empowers me to expand my research efforts and pursue my long-term goals.

> *The freedom to shape the science, the culture, and the research direction from the start is energizing and worth the uncertainty.*
>
> Dr. Lidia Wróbel

Neurodegenerative diseases develop long before symptoms appear. How does this silent phase shape the way your lab approaches research?

We focus on protein quality control and degradation mediated by autophagy and the ubiquitin–proteasome system. Because aging is a major risk factor for neurodegeneration and is closely associated with a progressive collapse of proteostasis, we aim to investigate how disruptions in protein homeostasis contribute to the earliest events that trigger neurodegenerative diseases. Investigating these initial cellular disruptions is critical, since by the time clinical symptoms emerge, neuronal damage is already widespread and largely irreversible.

Despite their major societal impact, neurodegenerative diseases still lack broadly effective disease-modifying therapies, particularly when compared with the therapeutic advances achieved in oncology. Why?

A key limitation is our still incomplete understanding of the underlying molecular mechanisms. As in cancer, successful therapies ultimately depend on deep biological insight. In my laboratory, we study protein quality control and degradation pathways as potential therapeutic targets, with the goal of uncovering novel mechanisms that can be exploited to restore proteostasis imbalance that arises during aging and contributes to the onset of neurodegenerative diseases. Restoring cellular “fitness” is considered a promising strategy, but one that is particularly challenging in the brain. While improving proteostasis could help neurons withstand multiple stresses, any intervention must be extremely precise due to the brain’s complexity and sensitivity.

Looking ahead, what role would you like the Laboratory of Cellular Proteostasis to play within IIMCB and broader scientific community?

My goal is to build a lab known for rigorous science and strong mentorship, contributing fundamental knowledge relevant to future therapies. I would also like it to be a vibrant space where students and postdocs can explore their curiosity, dive into hands-on science, and really fuel their passion for discovery.

Laboratory of

Biomolecular Interactions and Transport AMU/IIMCB

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We search for hidden passages that allow the transport of various small molecules through proteins. To achieve these goals, we develop new computational protocols and tools and apply them to analyzing biotechnologically relevant proteins, enabling us to engineer them to become better biocatalysts. In the long term, we aim to understand the role of transport processes in the function of living cells and to reveal the molecular nature of transport-related pathologies.

Research Summary

The primary research focus of our laboratory is to disclose molecular mechanisms involved in enzymatic catalysis in a broad sense. More specifically, we investigate principal factors involved in the function of enzymes with buried active sites connected to a bulk solvent through molecular tunnels, which is the case for more than 50% of known enzymes. Molecular mechanisms governing the functions of tunnels are poorly understood despite their central importance to enzyme selectivity and efficiency required for the survival of the living cell. Hence, such knowledge has key implications for precision medicine, protein engineering, and drug discovery. To establish the link between the structure of putative tunnels and their transport function, we have to overcome several challenges spanning from the predominantly transient nature of tunnels, thwarting their detection, and the rare character of the actual ligand transport events motivating us to plunge into the development of dedicated software and methods.

Scientific Impact

- Enabling high-throughput analyses of transport processes by developing Transport Tools Python library and divide-and conquer methods for long simulations based on this library.
- Exposing molecular basis of quorum quenching activity shared among N-terminal serine hydrolases.
- Assembling and verifying the first structural model of a full-size ABCG transporter, which sheds light on its initial selectivity.
- Unlocking high-throughput investigation of transport tunnels in enzymes using coarse-grained simulation methods.

Future Goals

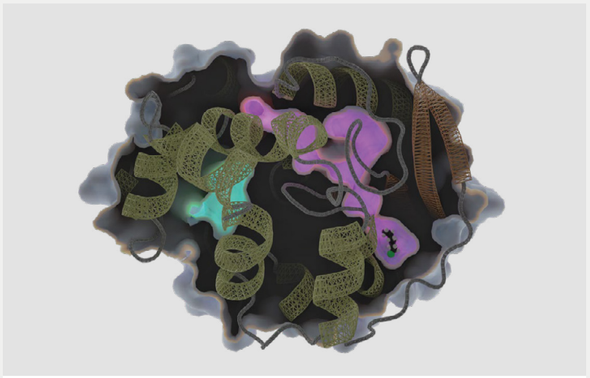
Since the activation of functional tunnels is a recent discovery, we lack even elementary insights into the mechanisms underlying the pathologies linked to the emergence of such tunnels. Therefore, we want to learn where the potential tunnels amenable to activation are located in the majority of relevant proteins and what their characteristic properties are, so that we can adopt a more holistic approach to predicting the effect of mutations on protein function.

Collaborations

- With the group of Prof. Michał Jasiński (Institute of Bioorganic Chemistry, Polish Academy of Sciences), we study the unique selectivity of ABCG transporters.
- With Dr. Michal Grulich (Institute of Microbiology, Czech Academy of Sciences), we investigate molecular details of the quorum quenching enzymes to develop new antimicrobial agents.
- With the groups of Prof. Siewert Jan Marrink (Biomolecular Sciences and Biotechnology Institute, University of Groningen) and Prof. Adolfo B. Poma (Institute of Fundamental Technological Research, Polish Academy of Sciences), we develop coarse-grained simulation methods as tools to analyze molecular tunnels in enzymes.

You can find the tunnels everywhere, hidden in the voids of protein structures, often just waiting for an impulse to open them – be it a conservative mutation or the binding of other molecules from their environment. Then, the real fun begins – we often witness unexpected consequences for a protein function when such tunnels are activated.

Jan Brezovsky, PhD, DSc Habil



Complexity of ligand transport pathways inside a hydrolytic enzyme. Ligand transport pathways (light green and pink volumes) connect the interior of the enzyme (yellow and orange ribbons) with its surface (overall light gray shape) and enable migration of cognate small molecules (shown with black, white, and green spheres inside the pink pathway).

Group Leader

Jan Brezovsky is a biophysicist and bioinformatician, who led a joint group between the IIMCB and the Adam Mickiewicz University (AMU) until 2025. He graduated and received his PhD from the Masaryk University in Brno. He has co-authored over 60 peer-reviewed publications and 4 international patents related to protein engineering and drug discovery. He has also contributed to the development of several widely used software in the field of molecular transport, precision medicine, and rational protein engineering, which are regularly used by 10,000s of users worldwide. He served as an elected member of the executive body of the national Head of Nodes Committee of the European Life-Science Infrastructure for Biological Information consortium (ELIXIR).

Group Members

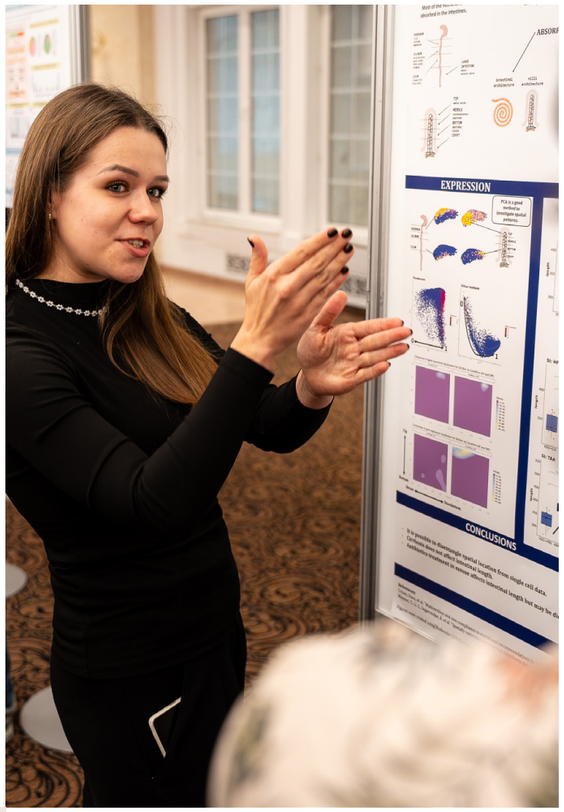
Postdoctoral Researchers:
Aaftaab Sethi, PhD (AMU)
Bartłomiej Surpeta, PhD
PhD Students:
Igor Marchlewski, MSc (AMU)
Aleksandra Bigos, MSc (AMU)
Undergraduate Students:
Ceren Ogutcu, BSc (AMU)
Maciej Hryc, BSc (AMU)

Insights and Opportunities

27 Reasons To Work at IIMCB

Organization

1. The highest scientific category A+ from the Ministry of Science and Higher Education in Poland.
2. Specialization in rapidly growing fields of RNA and cell biology.
3. A unique legal status based on the agreement between the Polish Government and UNESCO, which guarantees independence and the international character of IIMCB.
4. Operating based on the standards of leading scientific institutions worldwide.
5. Supervised by the International Advisory Board consisting of eminent scientists from all over the world, including Professor Aaron Ciechanover, a Nobel Prize laureate.
6. One of the leaders among research institutes in Poland in terms of obtaining EU funds.
7. Publications in renowned scientific journals.
8. Dynamic growth thanks to the RACE project. The Institute is on its way to becoming a center of excellence in RNA and cell biology.



Work Environment

9. Professional and collaborative work environment.
10. English as the official language of communication.
11. Close institutional cooperation with leading scientific centers in Europe within the EU-LIFE alliance and the RACE project.
12. Comprehensive support for foreigners (processing documents related to residency, assistance in finding accommodation, 24/7 emergency number, etc.)
13. Mentoring program for researchers.
14. Efficient and friendly administration.
15. Flat management structure.

Work Culture

16. ”HR Excellence in Research” standard.
17. Organized work system with clearly defined premises, goals, and tasks.
18. A culture of personal development.
19. Flexible working hours.
20. Hybrid work mode for administration with up to 50% remote work.

Benefits

21. 13th-month salary for employees.
22. 36 days of annual leave for scientific staff.
23. Additional paid annual leave up to 36 days for non-scientific staff.
24. Competitive scholarships for PhD students.
25. Co-financing of private healthcare.
26. Co-funding for training and language courses.
27. Access to social benefit packages: subsidies for vacations, sports cards, and cultural activities, nursery and preschool, and holiday benefits.

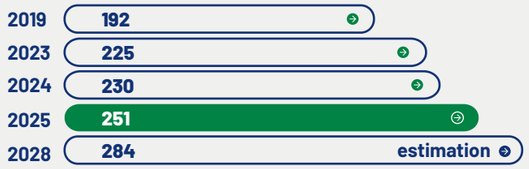
HR Excellence in Research

Since 2013, the IIMCB has been a holder of the HR Excellence in Research Award. It is a prestigious recognition acknowledging that the Institute is an attractive place for researchers to work and develop their careers. It confirms IIMCB’s commitment to implementing fair and transparent recruitment and appraisal procedures for researchers.

HR EXCELLENCE IN RESEARCH

Employment Structure

Staff increase:

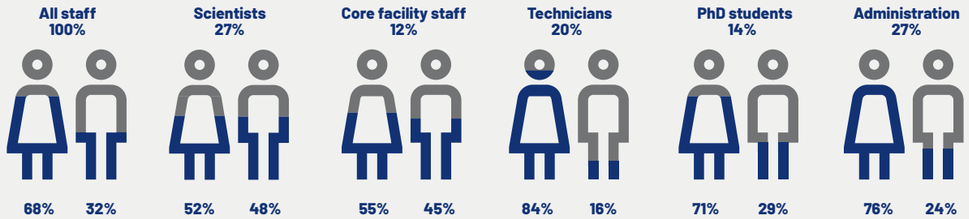


International work environment:

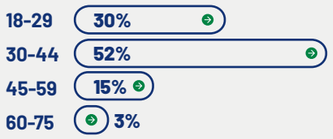
22%
of international staff

Citizenships: American, Armenian, Belarusian, Brazilian, British, Colombian, Czech, French, German, Indian, Iranian, Italian, Kenyan, Moroccan, Pakistani, Portuguese, Russian, Singaporean, Slovakian, Ukrainian

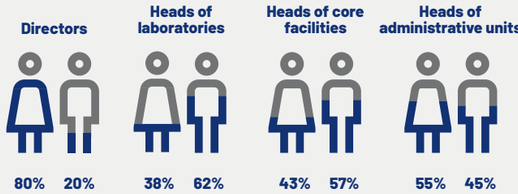
Employment diversity:



Age structure:



Gender division in management:



Administration Overview

Managing directorial processes in fast-changing environment

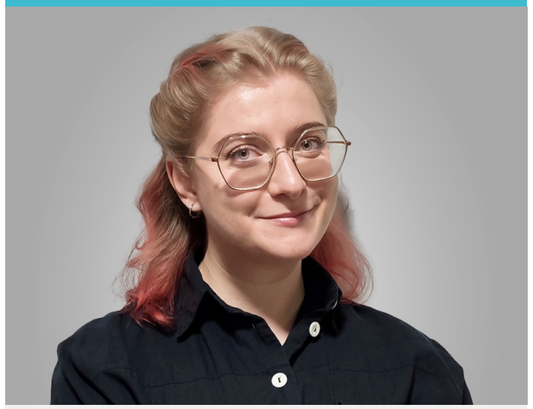
Ewa Jack-Górska,
Head of the Director's Office

In 2024-2025, the Director's Office supported the Institute's efficient functioning and development. It managed directorial processes, ensured proper document circulation, and effective information flow. Moreover, it participated in decision-making and managerial activities.

The Office coordinated collaboration among the Institute's organizational units, supported regulatory and organizational processes, and drove improvements in administrative and operational functions. It also handled selected central budgets, contributed to selecting a new administrative headquarters, and implemented the related organizational and substantive tasks.

The Director's Office coordinated and co-organized reporting sessions for the Institute, Group Leaders, and Directors, as well as internal seminars, high-level and strategic events, including International Advisory Board meetings. The Office further assisted the Directors with international cooperation, particularly in the EU-LIFE network, and partnerships with external institutions.

Serving as a key interface between scientific teams and administrative units



Paula Kwapisz,
Laboratory Support Specialists Coordinator

Laboratory Support Specialists (LSS) at IIMCB provide comprehensive operational and organizational support across research laboratories, acting as a key interface between scientific teams and the Institute's administrative units. We coordinate ordering processes, laboratory supplies, communication flow, and day-to-day logistics, ensuring that research activities run smoothly and efficiently.

Our responsibilities are diverse and tailored to the specific needs of each lab, reflecting the dynamic nature of the Institute. As IIMCB continues to grow, we have begun to take part in standardization and updated procedures to improve internal processes.

The temporary appointment of an LSS Coordinator further supports this development. Alongside the rapidly expanding core facilities and the evolving Core Facility Support Specialist role, our function is becoming increasingly visible. As described by the Director, we serve as the Institute's "circulatory system" – often behind the scenes, yet essential to every laboratory's success.

Since 2024, a new Technology Transfer Office aims to set the framework for research translation

Dr. Kornelia Mikuła,
Head of Technology Transfer Office (RACE Incubator)

The RACE Incubator empowers pioneering research by protecting intellectual property, enabling knowledge exchange, co-creation with industrial and academic partners, and facilitating translation of scientific discoveries into impactful innovations.

To address early-stage valorization challenges, in 2025, we entered a strategic partnership with LIFE bioCEEd, a biotechnological investment & venture-building company. The goal is to define effective development pathways for translational projects aligned with patients' needs.

The unit also launched an annual Technology Transfer and Commercialization Course, delivering practical knowledge on IP protection and research translation through interactive workshops led by European experts.

In 2024, Head of the Incubator was awarded the prestigious LifeArc Knowledge Transfer Innovation Fellowship. In 2023-2025, members of the Incubator were trained in residence within VIB Innovation & Business Team, gaining hands-on experience at a leading biotechnology institute.

Strategic collaboration with VIB and membership in EU-LIFE, ASTP, and AUTM ensures high standards in IP management, agreement processing, science valorization, and international networking.

Guiding researchers through grants opportunites and complex funding regulations

Dorota Libiszowska,
Head of the Grants Office

In 2024-2025, the Institute implemented 68 externally funded projects with a total budget of over 364 M PLN, confirming its strong position in diverse funding programs. The portfolio included both individual investigator-driven grants and large-scale institutional projects of strategic importance for the Institute's development. The Grants Office (GO) supported these projects at all stages, providing formal, financial, and strategic assistance and guiding researchers through complex funding regulations.

The GO team played a key role in flagship initiatives such as RACE, RACE-PRIME, IN-MOL-CELL Infrastructure, and WIB HERO, acting as project managers responsible for work progress, financial oversight, partner relations, risk mitigation, and monitoring of impact and sustainability.

During this period, the GO also supported 77 grant proposals and introduced an electronic pre-application system alongside regular NCN grant-writing training, strengthening the Institute's long-term grant acquisition capacity.

Creating a transparent, reliable and student-centered doctoral environment

Katarzyna Fiedorowicz,
PhD Office Coordinator

In 2024-2025, the PhD Office focused on strengthening high-quality support for doctoral candidates throughout the entire doctoral journey. A key milestone was the introduction in 2024 of a new procedure for awarding the doctoral degree, which improved transparency and efficiency. The PhD Office provided comprehensive organizational and administrative support to PhD students, supervisors, and doctoral committees at all stages, from enrollment to degree completion.

At the same time, the educational offering was expanded beyond core scientific training to include courses on commercialization, technology transfer, the use of artificial intelligence in research, and the development of soft skills. Through ongoing process improvements and close cooperation with administrative and research staff, the PhD Office helped create a transparent, reliable, and student-centered doctoral environment, reinforcing IIMCB's long-term commitment to excellence in doctoral education.

We are proud of the first PhD degrees awarded with IIMCB affiliation: Michał Brouze, Ewelina Latoszek, Zuzanna Mackiewicz, and Agnieszka Czarnocka-Cieciura.

Strengthening IIMCB's research governance with a focus on open science

Dr. Iwona Pilecka,
Head of the Scientific Coordination Unit

In 2024-2025, the Scientific Coordination Unit (SCU) strengthened IIMCB's research governance with a focus on open science, responsible animal research, and infrastructure support. The SCU implemented new internal rules for open-access publishing and advised researchers on cost eligibility in compliance with funders' open-access (OA) requirements. It streamlined laboratory animal studies by standardizing documentation and improving reporting. In 2025, the English-language theoretical e-learning course for researchers planning to work with laboratory animals was updated, expanded, and visually refreshed. The unit also contributed to the IN-MOL-CELL review for the Polish Roadmap for Research Infrastructures and to the successful SPUB grant application.

Importantly, SCU specialists actively participated in IIMCB's preparations for the evaluation of its scientific activity. They curated and optimized the Institute's research outputs in the Polish Scientific Bibliography and developed evidence-based societal and economic impact case descriptions.

Where reporting ends, the audience begins: a strategic shift to people-centered communication

Jan Piechna,
Head of the Communications Office

Over the past two years, communication at IIMCB has come into focus not as a set of outputs, but as a process of gradual change. We moved away from a reporting-driven model toward one focused on research visibility, value for audiences, and long-term institutional objectives.

Working with the Institute's directors, researchers, and administrative teams, we clarified what communication should support and what it should leave aside. Media relations were rebuilt with an emphasis on quality and relevance, leading to over 500 earned media publications generated directly by the Communications Office. Social media evolved from basic information-sharing into consistent positioning of research and people. Supported by the expanding use of audio-visual formats, this shift secured substantial growth in reach and engagement. We repositioned recruitment communication around the needs of potential candidates.

We are now halfway through implementing our target communication model. This progress reflects the engagement of the entire team and the openness of IIMCB staff to new ways of working. The focus now is on consolidating progress and deliberately driving further development.

Structuring career paths and advancing the internationalization of the Institute

Katarzyna Fiedorowicz,
Head of the Human Resources Unit

One of the most significant achievements has been the preparation of two fundamental strategic documents: the Human Resources Strategy and the Equality, Diversity, and Inclusion (EDI) Plan for the coming years. In parallel, we have successfully initiated and implemented the digitization of HR processes, aiming to streamline administrative procedures.

In collaboration with the working group, we successfully developed and implemented structured career paths for the core facilities. Further important milestones were the implementation of a new onboarding process, designed to ensure a smooth, structured, and welcoming introduction for new employees, and, in cooperation with the Communications Office, the development of new "Careers" and "Education" sections on the Institute's website to enhance IIMCB's visibility and attractiveness as an employer.

Furthermore, the HR Unit has successfully acquired and launched two strategic projects aimed at the internationalization of the Institute. These include projects under the "Welcome to Poland" program, as well as participation in the partner project "NAWA Network – EURAXESS."

Accelerating digital transformation and hardening immunity against cyberattacks

Łukasz Munio,
Head of the IT Unit

In 2024-2025, we focused on strengthening the Institute's digital security and reliability. The team delivered a comprehensive cybersecurity training program for all employees, raising awareness and promoting safe working practices in the digital environment. The team deployed advanced EDR solutions on users' computers, significantly enhancing protection against malware, ransomware, and other advanced cyberattacks.

Simultaneously, the unit replaced the core network infrastructure and modernized the Wi-Fi environment, improving performance, stability, and coverage across all floors. IT staff also carried out a full migration of the virtualization platform together with its backup systems, ensuring higher resilience, scalability, and continuity of critical services. In addition, the team designed and configured the entire IT infrastructure for the Institute's new office space, enabling a smooth start of operations in the relocated areas.

The IT Unit continued to provide ongoing end-user support. We accelerated digital transformation by replacing paper forms with Microsoft Power Platform low-code solutions. These applications streamline administrative processes, reduce manual effort, and enhance governance and approval efficiency across the organization.

Ensuring efficient and compliant public procurement processes across organisational activities

Jakub Wielgus,
Head of the Public Procurement Unit

In 2024-2025, the Public Procurement Unit supported the Institute's activities by ensuring the timely and compliant delivery of goods, services, and construction works essential for research and daily operations. The unit combined procurement expertise with close cooperation with researchers and administrative teams, providing practical guidance, preparing documentation, and supporting responses to audits and grant-related requirements. This helped streamline internal processes and reduce the administrative burden on project teams.

Over the two-year period, more than 120 procurement procedures were completed, including national and EU-level tenders covering laboratory equipment, IT infrastructure, staff services, and institutional events. A major undertaking was the implementation of procurements under the IN-MOL-CELL project financed by the National Recovery Plan, involving over 30 procedures and contracts with a total value exceeding 58 M PLN (net). Through consistent support, the unit contributed to financial discipline and the development of the Institute's research infrastructure.

Driving strategic operations, infrastructure and investments

Anna Zolnik,
Deputy Director for Operations

In 2024-2025, the Operations Unit focused on ensuring operational continuity while supporting organizational development related to infrastructure planning and workspace transformation.

A key milestone was the workspace optimization plan developed in close collaboration with laboratories, designed to accommodate new research groups under the EU-funded Teaming for Excellence project RACE and to enable the allocation of space for research infrastructure procured under the IN-MOL-CELL project, co-funded under Poland's National Recovery Plan (KPO).

During this period, we completed the full relocation of administrative functions by moving the remaining teams out of the main building and consolidating the entire administration in a newly leased location, with minimal disruption to core services. In parallel, we supported the development of the new building project through requirements gathering, space planning, and the operational assumptions needed for future workplace design. Through efficient coordination across multiple units, we continued to refine resource allocation and internal processes to provide reliable, day-to-day operational support for researchers.

High accounting standards to meet new regulations and expanding operations

Magdalena Grządkowska,
Acting Chief Accountant

In 2024-2025, the Financial and Accounting Unit provided comprehensive financial and accounting services for individual grants and large institutional projects. In cooperation with the Grants Office and project leaders, the Unit supported the execution of awarded budgets, ensuring effective coordination, oversight, and reporting.

Particular focus was placed on the administration of strategic initiatives, including RACE, RACE-PRIME, IN-MOL-CELL, and WIB HERO. A major organizational challenge was securing multi-million funding under the National Recovery Plan. Its implementation required the introduction of new formal regulations, precise coordination of contractual delivery schedules with project agreement provisions, and continuous financial liquidity management.

From 2025 onward, internal procedures were further developed, document circulation streamlined, and management control mechanisms strengthened to prepare the Institute for expanding operations and new regulatory obligations. High accounting standards were maintained while effectively supporting the Institute's scientific activities.

From Laboratory to Classroom:

Advancing Bioscience Education and Public Engagement

The Centre for Innovative Bioscience Education (BioCEN) has served as a bridge between research and education for over two decades. It was founded together by IIMCB, the Nencki Institute of Experimental Biology PAS, the Institute of Biochemistry and Biophysics PAS, and the Warsaw Science Festival in 2002. Since 2015, IIMCB has been its strategic sponsor. BioCEN's mission is practical: to translate bioscience into direct laboratory experience.

An unspoken truth is bound to perish. BioCEN provides a channel through which cutting-edge discoveries can reach and inspire a broader audience. In recent years, we have focused on modernizing our laboratory and expanding our reach nationwide. We are now facing our most ambitious challenges yet – but our team believes that discovery is only the beginning.

Mikołaj Cup,
Head of BioCEN

3,500 Students in the Lab

Throughout 2025, BioCEN conducted continuous laboratory workshops for students from primary through secondary school, at both basic and advanced levels. The program covered molecular biology, microbiology, cell biology, and histology, with elements of medical biology. Participants were introduced to experimental design, hypothesis formulation, and hands-on laboratory techniques. Approximately 3,500 students attended on-site workshops.

Experimental Kits Beyond the Institute

BioCEN distributed proprietary educational kits enabling students to conduct chromatography, electrophoresis, DNA isolation, and plant pigment experiments in school settings. In 2025, more than 30 kits were ordered, reaching several hundred students.

Pol'and'Rock Festival 2025

BioCEN exhibited in the "Akademia Sztuk PRZEpięknych" (Academy of EXTRAordinary Fine Arts) sector of the Pol'and'Rock Festival. The booth presented microscopic specimens and preserved *in vitro* cultures of non-pathogenic fungi and hosted workshops on proper oral hygiene. Open daily from 8:00 a.m. to 8:00 p.m., it attracted several thousand visitors. Educators provided information on STEM study paths and doctoral career opportunities.

From Blood Donation Campaigns to Science Picnics

BioCEN participated in "Motoserce 2025" (Motoheart 2025) in Warsaw (May 31, 2025) and Ciechanów (July 19, 2025), supporting blood donation initiatives and demonstrating quantitative analysis of vitamin C in food products. Participants received instructions enabling replication of the experiment at home. At the "Eksploracje" (Explorations) science picnic in Rzeszów (May 22, 2025), visitors conducted microscopic observations of fungal specimens.

450 Students in the "Summer Laboratory of Mysteries"

In 2025, within Warsaw's "Lato w Mieście i Młodzi Kompetentni" (Summer in the City and Young and Competent) program, BioCEN delivered 20 laboratory workshops applying scientific techniques to forensic-style problem solving. Approximately 450 primary school students participated.

1,050 Students in Smaller Municipalities

Under the Ministry of National Education's "Odkrywcy" (Discoverers) program, BioCEN implemented "BioCEN on Tour: Experimental Biology in Small Towns." In 2025, educators visited 15 rural and urban-rural municipalities outside the Mazowieckie Voivodeship, delivering three workshops in each location. Students performed DNA electrophoresis, prepared microscopic slides, and conducted enzymatic reactions using research-grade equipment. A total of 1,050 students participated.

Engaging Educators and Young Scientists

BioCEN served as patron of the 3rd Young Scientists Forum (September 12, 2025), organized by the Center of Postgraduate Medical Education, contributing to a panel discussion on contemporary education. Secondary school students attended as participants.

On December 6, 2025, BioCEN co-organized the 24th Symposium for Biology Teachers with the Nencki Institute; more than 100 teachers participated on-site or remotely. On the same day, a free EMBLconnect course for teachers, organized with EMBL and the Nencki Institute, introduced the MoBIE educational platform. Approximately 50 teachers took part.

Biology and Chemistry Students Visit IIMCB

On June 13, 2024, IIMCB welcomed 22 students from chemistry-focused classes at the Vocational and Continuing Education Center No. 1 in Racibórz, accompanied by two teachers. The interactive program included an overview of the Institute's activities, a knowledge quiz, a popular science lecture delivered by Mikołaj Cup from BioCEN, and a guided tour led by Dr. Krzysztof Skowronek and Dr. Roman Szczepanowski from the Biophysics and Bioanalytics Facility, providing participants with direct insight into the Institute's research environment.

National Children's Fund Scholars at IIMCB

In 2024 and 2025 IIMCB welcomed 30 scholarship recipients from the National Children's Fund for an intensive introduction to the Institute's research environment and career pathways. The program combined a popular science lecture delivered by BioCEN with direct exposure to laboratory work, where selected students engaged in hands-on experimental sessions within active research groups. The visit aimed to familiarize participants with experimental research practice and encourage further scientific development.

DEGRADATOR

Societal Impact at the Intersection of Science and Entertainment

How can molecular biology reach a general audience? Researchers at IIMCB tackle this with DEGRADATOR – an educational game that turns protein degradation research into accessible, engaging science education.

DEGRADATOR was developed by PhD student **Natalia Szulc and Dr. Wojciech Pokrzywa** from the Laboratory of Protein Metabolism at IIMCB. Launched in 2024, the game introduces players to one of the crucial processes that maintain cellular function: the removal of abnormal or damaged proteins. In living cells, specialized molecular mechanisms continuously identify and eliminate proteins that are misfolded, damaged, or no longer needed, helping to maintain cellular balance and health.

Inside the Ubiquitin-Proteasome System

In DEGRADATOR, players take on the role of an E3 ubiquitin ligase – a key enzyme within the ubiquitin-proteasome system (UPS) responsible for recognizing damaged or unwanted proteins and tagging them with ubiquitin, a small protein that acts as a molecular “destroy me” signal. This ubiquitin chain flags proteins for elimination by the proteasome. Through successive levels, players learn how the UPS functions and how its molecular components cooperate in protein degradation. The gameplay is complemented by short quizzes that reinforce key concepts introduced during the game.

The game also introduces players to therapeutic strategies based on PROteolysis TArgeting Chimeras (PROTACs), which hijack the cell’s natural degradation pathways to selectively remove disease-related proteins. By presenting these mechanisms through gameplay, DEGRADATOR helps explain biological processes that are increasingly discussed in the context of biomedical research and innovative therapies.

The game was created to introduce the key molecular mechanisms of protein degradation in an attractive and entertaining way. In an era where misinformation is widespread, especially concerning advanced medical treatments, it is important to make scientific knowledge accessible and understandable.

Natalia Szulc,
PhD student

Rich Educational Resources

The educational experience is supported by a set of learning materials developed by IIMCB scientists, including the Great Encyclopedia of Protein Degradation, quizzes and an educational comic exploring how viruses such as HIV hijack the host cell’s UPS for their own benefit.

A particular highlight are detailed lesson plans developed in collaboration with the Centre for Innovative Bioscience Education (BioCEN). Designed for primary and secondary school teachers, the plans guide educators on how to incorporate DEGRADATOR into a single lesson unit, outline the molecular topics the game covers and help connect the gameplay to school curricula. All resources are freely available online in Polish and English.

The project also expanded into global learning environments. DEGRADATOR and its educational materials were incorporated into LabXchange, an online learning platform developed by Harvard University.

Together, the game and its supporting resources form a learning package designed for users aged 12+, suitable for classrooms and informal settings. DEGRADATOR shows that rigorous science and engaging design can work together – making even complex cellular mechanisms fun to explore.

Science Outreach and Public Engagement

IIMCB supported the promotion of DEGRADATOR through an active media relations campaign. The project attracted significant attention, generating 14 media publications and two radio interviews with Natalia Szulc. It also gained visibility on social media, with coverage across LinkedIn, Facebook, and X, and was featured in four newsletters – helping the game reach audiences well beyond the scientific community.

The game was promoted during several public engagement events:

- March 2024 – Ochota Campus Discoverers’ Day; Official Debut
  Educational stand introducing visitors to the mechanisms of protein degradation and the biological concepts presented in the game.
- September 2024 – 28th Science Festival in Warsaw
  Workshops for school students explaining how misfolded or excess proteins are marked with ubiquitin and directed to degradation.
- October 2024 – 14th Mazovia Development Forum
  Interactive exhibition stand where visitors could play the game and discuss protein degradation mechanisms with the creators.

Recognition

DEGRADATOR was awarded 3rd place in the Fully Developed Games category at the 12th International Educational Games Competition, held as part of the 18th European Conference on Games Based Learning 2024 at Aarhus University in Denmark. The game was also the subject of a peer-reviewed publication in the Journal of Chemical Education, validating both its scientific accuracy and educational effectiveness.

These recognitions highlight how research institutions can contribute meaningfully to science communication by connecting expertise with accessible formats.

FREE ACCESS TO THE GAME AND SUPPORTING MATERIALS

DEGRADATOR funded by the European Union – NextGenerationEU under National Recovery and Resilience Plan. DEGRADATOR was also funded by the European Union under Horizon Europe (Project 101059801 - RACE) and by RACE-PRIME project carried out within the IRAP programme of the Foundation for Polish Science co-financed by the European Union under the European Funds for Smart Economy 2021-2027 (FENG).

European Funds for Smart Economy | Republic of Poland | Co-Funded by the European Union | FNP Foundation for Polish Science

Finance and Funding

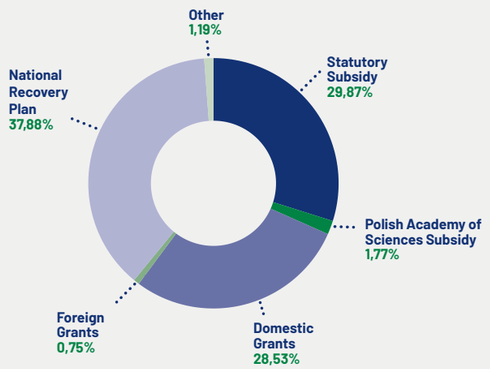
2024-2025

Sources of Funding

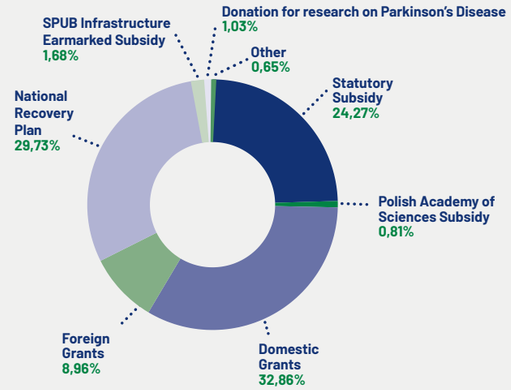
	2024		2025	
	PLN	EUR	PLN	EUR
Statutory Subsidy	22,552,300.00	5,281,569.09	23,578,000.00	5,578,203.79
Polish Academy of Sciences Subsidy	1,339,427.00	313,683.14	787,000.00	186,492.89
Domestic Grants	21,541,709.59	5,044,896.86	31,915,688.35	7,562,959.32
Foreign Grants	569,768.28	133,435.19	8,707,609.04	2,063,414.46
National Recovery Plan	28,600,000.00	6,697,892.27	28,874,497.95	6,842,298.09
SPUB Infrastructure Earmarked Subsidy	–	–	1,635,100.00	387,464.45
Donation for research on Parkinson's Disease	–	–	1,000,000.00	236,966.82
Other	899,649.84	210,690.83	632,944.17	149,986.77
Total	**75,502,854.71**	**17,682,167.38**	**97,130,839.51**	**23,016,786.61**

1 EUR = 4.27 PLN as at December 29, 2024, 1 EUR = 4.22 PLN as at December 29, 2025

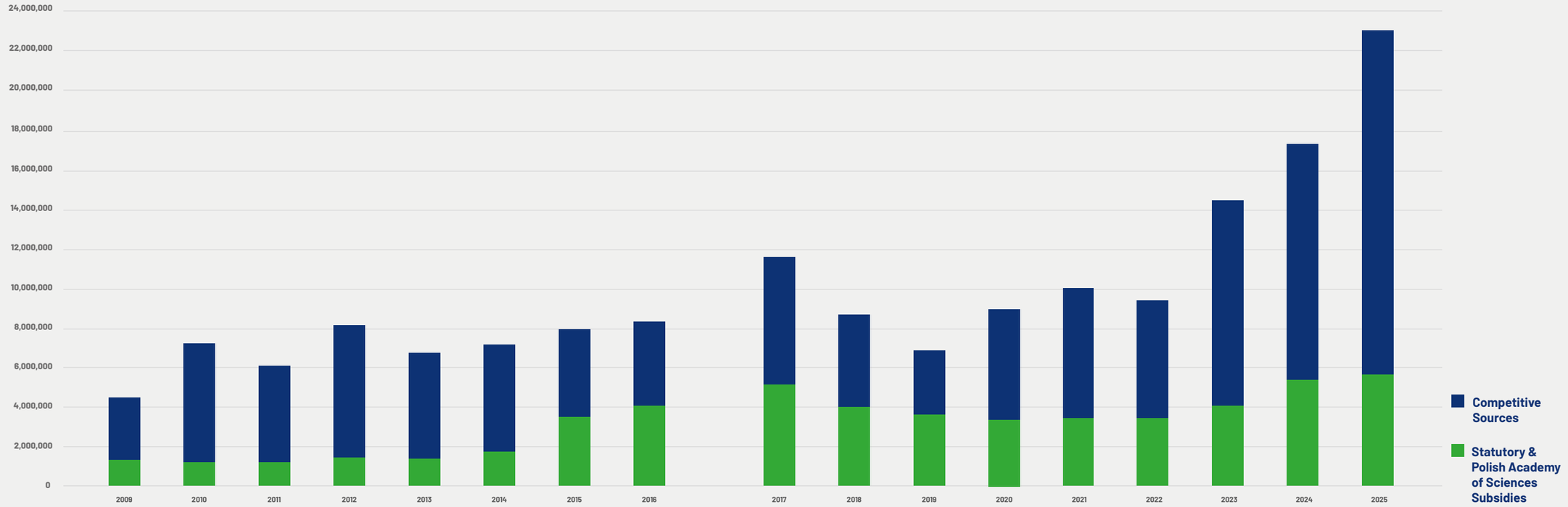
Structure of Funding – 2024



Structure of Funding – 2025



Annual Income 2009-2025 (EUR)



Growth reaching its limits

The International Institute of Molecular and Cell Biology (IIMCB) continues its dynamic development, both in research activity and team size. This growth has brought the Institute to a critical point where the lack of a dedicated, purpose-built headquarters increasingly constrains further expansion.

The Institute currently operates across several locations. Its main scientific facilities at 4 Trojdena Street (approx. 4,000 m²) house laboratories, core facilities, and office space. Due to full utilization of this space, most of the administrative functions have been relocated to separate rented offices, while meetings, seminars, and institute-wide events are held in an external conference space. Such a decentralized operational model poses a challenge that requires increasing effort to maintain organizational integrity.

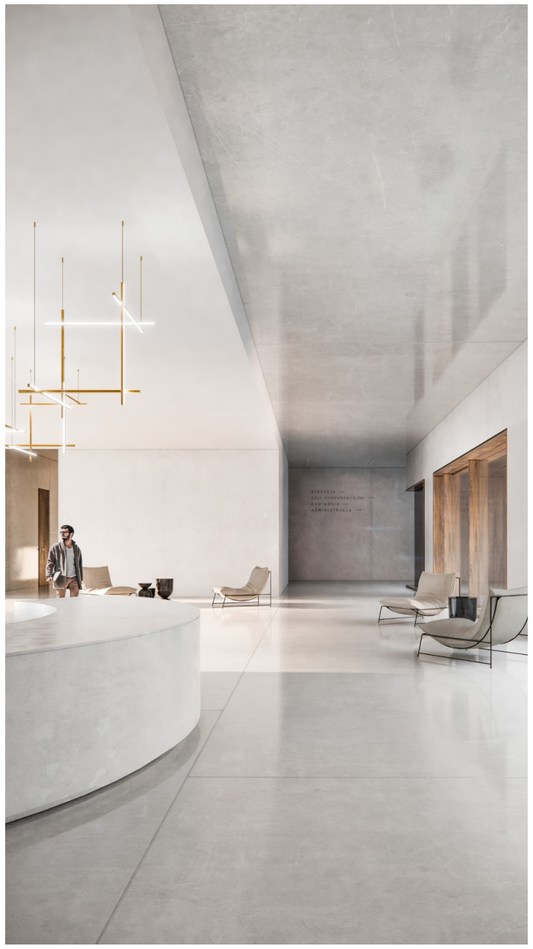
From Critical Mass to the Next Phase of Development

While this distributed model has enabled continued growth in recent years, it is not sustainable in the long term. The current infrastructure limits further development, reduces operational efficiency, and constrains opportunities for integration and collaboration.

At the same time, the Institute has reached a level of scientific quality and scale that justifies a transition to a new phase of development. IIMCB has established a strong international position, secured competitive research funding, and built a critical mass of research activity and talent. In this context, a new headquarters is becoming essential for sustaining growth and fully realizing the Institute's potential.

A Project Ready for Implementation

Significant progress has already been made. The Institute has secured land for the investment and, in 2023, selected an architectural design by Atelier Tektura. The project envisages a modern research facility with four above-ground floors and one underground level, with a total area exceeding 20,000 m², integrating research, administrative, and public functions.



Advanced Readiness: Awaiting Financing

As of March 2026, the building permit application is under review. The project is therefore well advanced from a formal and planning perspective, and construction could begin once financing is secured.

Designing a 21st-century Research Environment

The new headquarters will provide state-of-the-art infrastructure for research in RNA and cell biology, including advanced laboratories and core facilities. It will also improve conditions for interdisciplinary collaboration, strengthen the Institute's translational potential, and support closer interaction with the biotech and pharmaceutical sectors. Importantly, the project has a broader systemic dimension. It would contribute to strengthening Poland's biomedical research and innovation ecosystem, enhancing international competitiveness, and supporting closer links between science and application.

The Remaining Barrier: Infrastructure Financing

The key remaining challenge is securing construction funding. While the Institute has been highly successful in obtaining competitive research grants, such funding cannot be allocated to infrastructure development.

Towards Partnership and Implementation

The Institute therefore continues efforts to engage public and private partners in order to enable the implementation of this strategically important investment.

Scientific Publications, Grants and Seminars

in 2024-2025

146 Peer-reviewed Publications

Authors	Title	Journal
Abu Nahia K, **Sulej A**, **Migdał M**, Ochocka N, Ho R, Kamińska B, Zagorski M, **Winata CL**.	scRNA-seq reveals the diversity of the developing cardiac cell lineage and molecular players in heart rhythm regulation.	iScience. 2024 doi: 10.1016/j.isci.2024.110083
Álvarez L, Haubrich K, Iselin L, Gillioz L, Ruscica V, Lapouge K, Augsten S, Huppertz I, Choudhury NR, Simon B, Masiewicz P, Lethier M, Cusack S, Rittinger K, Gabel F, Leitner A, **Michlewski G**, Hentze MW, Allain FHT, Castello A, Hennig J.	The molecular dissection of TRIM25's RNA-binding mechanism provides key insights into its antiviral activity.	Nat Commun. 2024 doi: 10.1038/s41467-024-52918-x
Badepally NG, **de Moura TR**, **Purta E**, **Baulin EF**, **Bujnicki JM**.	Cryo-EM Structure of raiA ncRNA From Clostridium Reveals a New RNA 3D Fold.	J Mol Biol. 2024 doi: 10.1016/j.jmb.2024.168833
Baranykova S, **Gupta RK**, Kajdasz A, Wasilewska I, **Macias M**, **Szybinska A**, **Węgierski T**, **Nahia KA**, **Mondal SS**, **Winata CL**, **Kuźnicki J**, **Majewski L**.	Loss of Stim2 in zebrafish induces glaucoma-like phenotype.	Sci Rep. 2024 doi: 10.1038/s41598-024-74909-0
Bartak M, Krahel WD, Chodkowski M, Grel H, Walczak J, **Pallepati A**, Komorowski M, Cymerys J.	ATPase Valosin-Containing Protein (VCP) Is Involved During the Replication and Egress of Sialodacryoadenitis Virus (SDAV) in Neurons.	Int J Mol Sci. 2024 doi: 10.3390/ijms252111633
Bharadwaj P, Shet SM, Bisht M, **Sarkar DK**, Franklin G, Kotrappanavar NS, Mondal D.	Suitability of Adenosine Derivatives in Improving the Activity and Stability of Cytochrome c under Stress: Insights into the Effect of Phosphate Groups.	J Phys Chem B. 2024 doi: 10.1021/acs.jpcb.3c05996
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Bochtler M.	Protein memory?	Bioessays. 2024 doi: 10.1002/bies.202400162
Bohdan DR, **Bujnicki JM**, **Baulin EF**.	ARTEMIS - a method for topology-independent superposition of RNA 3D structures and structure-based sequence alignment.	Nucleic Acids Res. 2024 doi: 10.1093/nar/gkae758
Brouze M, **Czarnocka-Cieciura A**, **Gewartowska O**, **Kusio-Kobiałka M**, **Jachacy K**, **Szpila M**, **Tarkowski B**, **Gruchota J**, **Krawczyk P**, **Mroczek S**, **Borsuk E**, **Dziembowski A**.	TENT5-mediated polyadenylation of mRNAs encoding secreted proteins is essential for gametogenesis in mice.	Nat Commun. 2024 doi: 10.1038/s41467-024-49479-4

Bylinowska J, Wierzbicka E, Białecka-Dębek A, **Mossakowska M**, **Szybalska A**, Pietruszka B.	Association between dietary variety and anthropometric parameters in community-dwelling older adults: results of a population-based PolSenior study.	Ann Agric Environ Med. 2024 doi: 10.26444/aaem/190388
Cappannini A, **Ray A**, **Purta E**, **Mukherjee S**, **Boccaletto P**, **Moafinejad SN**, Lechner A, Barchet C, Klaholz BP, **Stefaniak F**, **Bujnicki JM**.	MODOMICS: a database of RNA modifications and related information. 2023 update.	Nucleic Acids Res. 2024 doi: 10.1093/nar/gkad1083
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Chamera S, **Wycisk K**, **Czarnocki-Cieciura M**, **Nowotny M**.	Cryo-EM structure of rotavirus B NSP2 reveals its unique tertiary architecture.	J Virol. 2024 doi: 10.1128/jvi.01660-23
Chlebus K, Zdrojewski T, Jagiełło K, **Mossakowska M**, Chudek J, Więcek A, Grodzicki T.	Prevalence of hypercholesterolemia in the elderly and very elderly members of the Polish population: results of a national cross-sectional representative survey.	Pol Arch Intern Med. 2024 doi: 10.20452/pamw.16882
Chudek A, Kotyla P, Kozak-Szkopek E, **Mossakowska M**, Wieczorowska-Tobis K, Sulicka-Grodzicka J, Olszanecka-Glinianowic M, Chudek J, Owczarek AJ.	Inflammation in Older Poles with Localized and Widespread Chronic Pain-Results from a Population-Based PolSenior Study.	J Clin Med. 2024 doi: 10.3390/jcm13195870
Czarnocka-Cieciura A, Poznański J, Turtola M, Tomecki R**, Krawczyk PS, Mroczek S, Orzeł W,** Saha U, Jensen TH**, Dziembowski A, Tudek A.**	Modeling of mRNA deadenylation rates reveal a complex relationship between mRNA deadenylation and decay.	EMBO J. 2024 doi: 10.1038/s44318-024-00258-3
Czestkowski W, Krzemiński Ł, Piotrowicz MC, Mazur M, Pluta E, Andryianau G, Koralewski R, Matyszewski K, Olejniczak S, Kowalski M, Lisiecka K, Kozieł R, Piwowar K, Papiernik D, **Nowotny M**, **Napiórkowska-Gromadzka A**, **Nowak E**, Niedziałek D, Wieczorek G, Siwińska A, Rejczak T, Jędrzejczak K, Mulewski K, Olczak J, Zasłona Z, Gołębiowski A, Drzewicka K, Bartoszewicz A.	Structure-Based Discovery of High-Affinity Small Molecule Ligands and Development of Tool Probes to Study the Role of Chitinase-3-Like Protein 1.	J Med Chem. 2024 doi: 10.1021/acs.jmedchem.3c02255
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68 Grants Running

in 2024-2025 with total awarded funding

347 093 880 PLN

EU FRAMEWORK PROGRAMMES

Funded by the European Union

5 projects
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HORIZON EUROPE

- **TEAMING FOR EXCELLENCE** *(RACE) RNA and Cell Biology – from Fundamental Research to Therapies* (101059801); 10 130 508.75 EUR for the IIMCB (total grant budget: 14 993 885 EUR) 2023-2029; **M. Miączyńska** in the consortium with the University of Edinburgh and the Flanders Institute for Biotechnology
- **ERC – Advanced Grant** *ViveRNA Principles of endogenous and therapeutic mRNA turnover in vivo* (101097317); 2 499 875 EUR; 2023-2028; **A. Dziembowski**
- **EIC – Transition Grant** *(INCYPRO) A key technology to enable the broad application of proteins in diagnostics and therapeutics* (101057978); 201 250 EUR for the IIMCB (total grant budget: 2 498 750 EUR); 2022-2025; **J.M. Bujnicki**

HORIZON 2020

- **INFRAIA** *(iNEXT-Discovery) Infrastructure for transnational access and discovery in structural biology* (871037); 47 500 EUR for the IIMCB (total grant budget: 9 987 756.50 EUR); 2020-2024; **M. Nowotny**
- **ITN-MSCA** *(ROPES) ROles of ePitranscriptomic in diseasES* (956810); 227 478.6 EUR for the IIMCB (total grant budget: 3 095 829 EUR); 2020-2025; **J.M. Bujnicki**

EUROPEAN MOLECULAR BIOLOGY ORGANIZATION

EMBO

4 projects
3 570 000 PLN

- **EMBO Instalation Grants** *Spatial organisation of protein quality control in neurodegenerative diseases* (IG-6019-2025); 250 000 EUR 2025-2029; **L. Wróbel**
- **EMBO Instalation Grants** *Role of microbiota in progression of liver disease* (5685); 250 000 EUR 2024-2029; **A. Kołodziejczyk**
- **EMBO Instalation Grants** *From dynamics of bacterial RNA degradation to gene expression manipulation tools* (5730); 250 000 EUR 2024-2029**; E. Małecka**
- **EMBO Postdoctoral Fellowship**; *Exploring RNA folds and remote evolutionary relationships with an improved structural similarity search method* (ALTF 525-2022); 96 000 EUR; 2022-2024; **E. Baulin**

AMERICAN FEDERATION FOR AGING RESEARCH

afar american federation for aging research

1 project
178 096 PLN

- **New Investigator Award**; *Red vs. white: Does failure in red blood cell recycling drive T cell aging?* (2032952); 178 096 PLN for the IIMCB (total grant budget: 375 000 USD); 2023-2025; **K. Mleczko-Sanecka**

FOUNDATION FOR POLISH SCIENCE

FNP Foundation for Polish Science

1 project
36 293 600 PLN

- **International Research Agenda** *(RACE-PRIME) RNA and Cell Biology Platform for Research and Innovation in Medicine* (FENG.02.01-IP.05-T003/23); 36 293 600 PLN 2024-2029; **M. Miączyńska**

European Funds for Smart Economy | Republic of Poland | Co-funded by the European Union | FNP Foundation for Polish Science

National Information Processing Institute

NATIONAL INFORMATION PROCESSING INSTITUTE

1 project
100 251 697.12 PLN

- **KPO – The National Recovery and Resilience Plan** *(IBMiK) Molecule and Cell Research Infrastructure* (KPOD.01.18-IW.03-0006/23); 100 251 697.12 PLN; 2024-2025; **M. Miączyńska**

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Łukasiewicz Research Network – PORT Polish Center for Technology Development

WIB ŁUKASIEWICZ – PORT Wirtualny Instytut Badawczy

1 project
28 398 800 PLN

- **Virtual Research Institute**; *(HERO) Horizon for Excellence in messenger RNA applications in immunoOncology*; (UoF/01-WIB-1/2020-011) in partnership with the University of Warsaw, the Medical University of Warsaw, the Institute of Physical Chemistry of the Polish Academy of Sciences; 28 398 800 PLN for the IIMCB (total grant budget: 69 160 450 PLN); 2022-2027; **A. Dziembowski** (Leader), **M. Miączyńska**, **M. Nowotny**

Medical Research Agency (ABM)

MEDICAL RESEARCH AGENCY

1 project
5 244 375 PLN

- *Identification of Biomarkers of Metabolic Dysfunction–Associated Steatotic Liver Disease* (4/ABM/03/KPO/ KPOD.07.07-IW.07-0158/24-00); 5 244 375.00 PLN; 2025-2026; **A. Kołodziejczyk**

NATIONAL RECOVERY PLAN | Republic of Poland | Funded by the European Union NextGenerationEU | MEDICAL RESEARCH AGENCY

NATIONAL SCIENCE CENTRE

NATIONAL SCIENCE CENTRE POLAND

47 projects
112 420 794 PLN

DIOSCURI

- *The Dioscuri Centre for RNA-Protein Interactions in Human Health and Disease* (2019/02/H/NZ1/000020); 13 120 884.00 PLN; 2021-2030; **G. Michlewski**

MAESTRO

- *TENT5A Poly(A) Polymerase: A Key Regulator in the Hypothalamus-Pituitary hormonal axis in humans* (2024/54/A/NZ4/00403); 4 806 800 PLN; 2025-2030; **A. Dziembowski**
- *The role of mTOR-Brg1 interaction in normal and aberrant neuronal activity* (2020/38/A/NZ3/00447); 4 092 140 PLN; 2021-2026; **J. Jaworski**
- *Structural and mechanistic studies of bacterial DNA repair* (2017/26/A/NZ1/01098); 4 228 500 PLN; 2018-2024; **M. Nowotny**
- *Integrative modeling and structure determination of macromolecular complexes comprising RNA and proteins* (2017/26/A NZ1/01083); 3 500 000 PLN; 2018-2025; **J.M. Bujnicki**
- *Oncogenic mechanisms of DIS3 mutations* (2016/22/A/NZ4/00380); 3 490 750 PLN; 2017-2025; **A. Dziembowski**

SONATA BIS

- *Unravelling the Mechanisms of Gene Expression of Hepatitis A Virus* (2024/54/E/NZ6/00119); 4 778 740 PLN; 2025-2030; **S. Bresson**
- *Dynamics of RNA degrading complexes in bacteria* (2022/46/E/NZ1/00462); 3 218 840 PLN; 2023-2028; **E. Małecka**
- *Adaptation of Proteins to Evade Premature Degradation by the Ubiquitin-Proteasome System* (2021/42/E/NZ1/00190); 3 686 840 PLN; 2022-2027; **W. Pokrzywa**
- *Identifying unique adaptive responses of red pulp macrophages to iron deficiency* (2020/38/E/NZ4/00511); 3 613 374 PLN; 2021-2026; **K. Mleczko-Sanecka**

GRIEG (EEA and Norway Grants)

- *Cellular adaptation to cold* (2019/34/H/NZ3/00691); 3 834 426 PLN; 2021-2024; **W. Pokrzywa**; Partner: University of Oslo, Norway
- *The impact of cytoplasmic polyadenylation on local translation in neurons* (2019/34/H/NZ3/00733); 1 935 625 PLN; 2020-2024; **A. Dziembowski**; Partner: University of Bergen, Norway; University of Warsaw, Poland

OPUS

- *Mechanistic and structural studies of adenoviral DNA replication* (2024/55/B/NZ1/02607); 3 174 698 PLN; 2025-2029; **M. Nowotny**
- *Targeting Proteinopathies: Understanding and Mitigating the Effects of Pathogenic Mutations in Cullin-RING Ubiquitin Ligase Receptor* (2024/53/B/NZ3/02882); 3 295 220 PLN; 2025-2029; **W. Pokrzywa**
- *"Stealth" asparaginases as improved protein drugs for the treatment of childhood acute lymphoblastic leukemia (ALL)* (2024/53/B/NZ1/01841); 2 875 400 PLN; 2025-2029; **M. Bochtler**
- *Finding molecular mechanisms behind the activation of stellate cells* (2023/51/B/NZ2/02649); 4 191 920 PLN; 2024-2028; **A. Kołodziejczyk**
- *How inactivation of Mitochondrial Calcium Uniporter protects dopaminergic neurons* (2023/49/B/NZ4/02744); 2 917 239 PLN; 2024-2028; **J. Kuźnicki**
- *Biological control and pharmacological regulation of RNAs implicated in aetiology of Parkinson's disease* (2023/49/B/NZ1/02456); 2 999 834 PLN; 2024-2028; **G. Michlewski**
- *Structural studies of herpesvirus proteins involved in DNA replication* (2022/45/B/NZ1/02456); 2 047 255 PLN; 2023-2027; **M. Figiel**
- *Elucidating the contribution of non-coding genomic elements to heart development and disease at single-cell resolution* (2022/47/B/NZ2/02926); 3 040 240 PLN; 2023-2027; **C.L. Winata**
- *Structural and mechanistic studies of (+)RNA virus replication* (2021/41/B/NZ1/03620); 2 684 000 PLN; 2022-2026; **M. Nowotny**
- *Building a genomic atlas of human inner ear malformations: focus on novel genes and functional non-coding regions* (2021/41/B/NZ5/04390); 845 460 PLN for the IIMCB (total grant budget: 2 986 560 PLN); 2022-2026; **V. Korzh**; coordinated by the Institute of Physiology and Pathology of Hearing
- *AXL receptor signaling in cancer cell growth and drug resistance* (2020/39/B/NZ3/03429); 2 482 764 PLN; 2021-2027; **M. Miączyńska**
- *Rac1 contribution to brain connectivity impairments and neuropsychiatric disorders in Tuberous Sclerosis Complex* (2020/37/B/NZ3/02345); 2 251 260 PLN; 2021-2025; **J. Zmorzyńska**
- *Identification of novel vulnerabilities of VPS4B-deficient cancers cells* (2020/37/B/NZ3/02991); 1 878 854 PLN; 2021-2027; **E. Szymańska**
- *Experimental analysis of molecular determinants involved in epilepsy* (2020/39/B/NZ3/02729); 1 780 590 PLN; 2021-2026; **V. Korzh**
- *Unraveling the influence of posttranscriptional modifications on RNA 3D structure formation and its dynamics, with the integrated use of theoretical and experimental approaches* (2020/37/B/NZ2/02456); 1 650 000 PLN; 2021-2026; **J.M. Bujnicki**
- *The new methodology for better understanding of ligand-RNA interactions* (2020/39/B/NZ2/03127); 671 000 PLN; 2021-2026; **F. Stefaniak**

- *Reconstructing cardiovascular cell lineage evolution, one cell at a time* (2019/35/B/NZ2/02548); 2 631 552 PLN; 2020-2025; **C.L. Winata**
- *Linking abnormal Ca2+ signaling and the unfolded protein response with Huntington's disease pathology in both YAC128 mouse model and iPSCderived neurons from HD patients* (2019/33/B/NZ3/02889); 1 857 550 PLN; 2020-2024; **M. Czeredys**
- *Analysis of the role of cytoplasmic polyadenylation in the regulation of the innate immune response* (2019/33/B/NZ2/01773); 2 324 800 PLN; 2020-2024; **A. Dziembowski**

POLISH RETURNS (research component funded by NCN)

- *Gut-liver axis in liver cirrhosis* (2023/02/1/NZ5/00003); 200 000 PLN; 2023-2025; **A. Kołodziejczyk**

SONATA

- *Nuclear protein quality control in neurodegeneration* (2023/51/D/NZ3/01939); 2 514 102 PLN; 2024-2027; **L. Wróbel**
- *The role of gut-liver axis in Amanita species mushroom poisoning* (2022/47/D/NZ5/03438); 2 515 560 PLN for the IIMCB (total grant budget: 2 544 840 PLN; 2023-2026; **A. Kołodziejczyk**; in consortium with the Medical University of Warsaw
- *A framework for de novo modeling of RNA structures using restraints derived from experimental data* (2021/43/D/NZ1/03360); 691 252 PLN; 2022-2026; **S. Mukherjee**
- *3D Structure determination of key regulatory regions at the 5' and 3' termini of pathogenic Flaviviruses RNA* (2020/39/D/NZ6/02528); 895 358 PLN; 2021-2026; **T. Rocha de Moura**
- *Discovery and characterization of RNA structure motifs conserved in positive-sense single-stranded RNA viruses and in other functional RNAs* (2020/39/D/NZ2/02837); 825 330 PLN; 2021-2025; **T. Wirecki**
- *Elucidating the role of TENT5C-mediated polyadenylation in erythropoiesis* (2019/35/D/NZ3/04253); 1 482 000 PLN; 2020-2024; **M. Kusio-Kobiałka**

SONATINA

- *Lipid-Proteasome Interplay in Aging and Proteostasis* (2025/56/C/NZ1/00427); 1 196 173 PLN; 2025-2028; **P. Thapa**
- *Targeting nucleic acid-protein complexes with small molecules using a deep- learning framework* (2023/48/C/NZ1/00122); 645 136 PLN; 2023-2026; **R. Nikalayeu**

PRELUDIUM

- *Decoding the molecular mechanisms behind indole-3-acetic acid's influence on liver cells* (2024/53/N/NZ2/03338); 209 960 PLN; 2025-2028; **A. Uryga**
- *Looking for mechanisms responsible for the retinal ganglion cell loss in zebrafish stim2 knockout* (2023/49/N/NZ3/02921); 209 352 PLN; 2024-2027; **S. Baranykova**
- *Exploring the role of Ferroportin-mediated Ca2+ influx in the functional rewiring of macrophages* (2023/49/N/NZ3/04232); 69 540 PLN; 2024-2025; **P. Kumar Mandal**
- *Living on the edge: evolutionary adaptation of substrate-recruiting subunits of the cullin-RING ubiquitin ligase complexes to avoid premature degradation* (2021/41/N/NZ1/03473); 190 770 PLN; 2022-2025; **N. Szulc**
- *Deciphering the molecular mechanism of activity switch of the ubiquitin ligase CHIP* (2021/41/N/NZ1/03086); 132 126 PLN; 2022-2025; **P. Thapa**

PRELUDIUM BIS

- *Chilling resilience: Decoding phosphatases in cold adaptation* (2023/50/O/NZ4/00179); 688 080 PLN; 2024-2028; **W. Pokrzywa**

MINIATURA

- *Study of functional variability of the Lactobacillus strains and their impact on hepatocytes* (2024/08/X/NZ2/01013); 49 500 PLN; 2024-2025; **K. Szczepaniak**

POLISH NATIONAL AGENCY FOR ACADEMIC EXCHANGE

6 projects
4 846 788 PLN

- **Welcome to Poland 2024** *Comprehensive Support for Foreign Nationals at IIMCB – An Essential Element of Conducting High-Quality Research* (BPI/WTP/2024/1/00046); 544 408 PLN; 2025-2027; **K. Fiedorowicz**
- **NAWA-EURAXESS** *Establishment of a regional NAWA-EURAXESS network in the Mazowieckie Voivodeship* (BPI/EUR/2024/1/00008/U/00001); coordinated by the National Centre for Nuclear Research, 306 852 PLN for the IIMCB (total grant budget: 1 115 472 PLN); 2025-2028
- **IMPRESS-U** *Supplement: Structure and function of plastid nucleoid* (BPN/NSF/2023/1/00011); 967 180 PLN; 2024-2026; **M. Nowotny**
- **Polish Returns Programme** *Gut-liver axis in liver cirrhosis* (BPN/PPO/2022/1/00023/U/00001); 1 123 200 PLN; 2023-2026; **A. Kołodziejczyk**
- **STER Programme** *Internationalisation of the Warsaw Doctoral School in Natural and BioMedical Sciences* (BPI/STE/2021/1/00034/U/00001); coordinated by the Nencki Institute of Experimental Biology; 142 000 PLN for the IIMCB (total grant budget: 1 968 030 PLN); 2022-2024; **U. Białek-Wyrzykowska**
- **Polish Returns Programme** *Regulation of microRNAs for the treatment and understanding the etiology of Parkinson's disease* (PPN/PPO/2020/1/00006/U/00001); 2 070 000 PLN; 2021-2025; **G. Michlewski**

POLISH ACADEMY OF SCIENCES

1 project
874 878 PLN

- **PASIFIC** *Targeted single-cell gene expression analysis of mRNA vaccine response* (847639); 874 878 PLN; 2022-2025; **E. Poniecka**

50 Seminars in 2024–2025

Date (YYYY-MM-DD)	Speaker	Title	Affiliation
2024-02-01	**Katie Berry**	Molecular genetic dissection of bacterial RNA-protein interactions	Mount Holyoke College
2024-02-08	**Wojciech Galej**	Structural and biochemical studies of the intron recognition by the human spliceosome	EMBL Grenoble
2024-02-22	**Noga Ron-Harel**	Metabolism in T cell activation and aging	Technion - Israel Institute of Technology
2024-02-29	**Pavel Dvorak**	Synthetically primed adaptation of bacterial metabolism to renewable sugar substrates	Masaryk University
2024-03-07	**Pierre Alexandre Kaminski**	Bacteriophages with a ZTGC DNA alphabet, a proof of concept for the synthetic biology of non-canonical nucleic acids	Institut Pasteur
2024-03-14	**Jens Puschof**	Modelling cancer-microbe interactions with organoids and organs-on-a-chip	German Cancer Research Center
2024-03-21	**Jan Löwe FRS**	Prokaryotic cytoskeletons - filaments organising small cells	MRC Laboratory of Molecular Biology in Cambridge
2024-04-04	**Mario Pende**	mTOR role in seizure-prone genetic diseases and the metabolic control of senescence	Institut Necker Enfants Malades
2024-04-11	**Natalia Szulc**	Best Papers Seminar: Lysine deserts and cullin-RING ligase receptors: Navigating untrodden paths in proteostasis	International Institute of Molecular and Cell Biology in Warsaw
2024-04-18	**Sebastian Glatt**	tRNAslational control of eukaryotic gene expression	Małopolska Centre of Biotechnology
2024-05-09	**Barbara Di Ventura**	Right here. Right now. Spatio-temporal control of gene expression	University of Freiburg
2024-05-16	**Axel Methner**	Iron-sulfur cluster loss in mitochondrial CISD1 mediates PINK1 loss-of-function phenotypes	University Medical Center of Johannes Gutenberg University Mainz
2024-05-23	**Guoliang Xu**	Enzymatic DNA Modifications Controlling Development and Adaptation	Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences
2024-06-05	**Vasili Hauryliuk**	Bioinformatics-driven discovery of novel antiphage immunity systems	Lund University
2024-06-06	**Eran Meshorer**	Paleo-epigenetics: Reconstructing DNA methylation of archaic humans reveals ancient and recent evolutionary adaptation	Hebrew University
2024-06-13	**Lynne Maquat**	Nonsense-mediated mRNA decay in human health and disease	University of Rochester
2024-06-19	**Antoni Wróbel**	Molecular mechanisms of viral entry underlying viral evolution and host change	The Francis Crick Institute
2024-06-20	**Magdalena Winiarska**	Searching for mechanisms of resistance to immunotherapies	Mossakowski Medical Research Institute of the Polish Academy of Sciences
2024-06-27	**Gunther Hartmann**	Innate immune sensing of nucleic acids and its use for prevention and treatment	University Hospital Bonn
2024-08-28	**Kelly M. Zatopek**	Life at the extremes: Nucleic acid maintenance in hyperthermophilic archaea	New England Biolabs
2024-10-03	**Chinmoy Patra**	Extracellular matrix in Heart Regeneration	Agharkar Research Institute
2024-10-15	**Włodek Minor**	Artificial Intelligence in Biomedical Research: The Good, The Bad and The Ugly	University of Virginia
2024-10-24	**Jakub Sędziński**	Cell fate and mechanics of developing mucociliary epithelium	The Novo Nordisk Foundation Center for Stem Cell Medicine, reNEW
2024-10-31	**Yugi Sugita**	Enhanced sampling simulations of biomolecules using multiscale models	RIKEN

2024-11-07	**Ulrich J. Lorenz**	Microsecond Time-Resolved Cryo-EM	École Polytechnique Fédérale de Lausanne (EPFL)
2024-11-28	**Björn Schumacher**	Genome Stability in Aging and Disease: New Insights from C. elegans	University of Cologne
2024-12-05	**Jakub Godlewski**	Viral Upgrade of Brain Tumor Vesicles to Amplify Tumor Immunity	Mossakowski Medical Research Institute of the Polish Academy of Sciences
2024-12-12	**Ashwin Chari**	Why worry about accurate protein structures?	Max-Planck-Institute for Multidisciplinary Sciences
2025-01-09	**Mateusz Sikora**	Integrative modeling of glycoproteins	Malopolska Centre of Biotechnology, Max Planck Institute of Biophysics
2025-01-22	**Daniel Mertens**	Chances and Challenges of Implementing Large Language Models into Clinical Information Processes	University Hospital Ulm, and German Cancer Research Center DKFZ
2025-01-23	**Jens Hör**	Bacterial Antiviral Defense by a Ubiquitin-like System	Helmholtz Institute for RNA-based Infection Research
2025-03-20	**Aleksandra Pękowska**	RNA and RNA binding proteins mediate maturation of chromatin topology during embryonic stem cell differentiation	Nencki Institute of Experimental Biology of the Polish Academy of Sciences
2025-04-10	**Lidia Wróbel and Tomasz Turowski**	Career Journeys and Challenges: Perspectives from Young Group Leaders	International Institute of Molecular and Cell Biology in Warsaw and Institute of Biochemistry and Biophysics of the Polish Academy of Sciences
2025-05-09	**Jørgen Kjems**	Design and delivery of RNA therapeutics	Aarhus University
2025-05-13	**Utz Fischer**	Making mRNA in the wrong compartment: how poxviruses express their genes in the cytoplasm of a host	Theodor-Boveri Institute, University of Würzburg
2025-05-22	**Salim Seyfried**	Biomechanical signaling in zebrafish models of vascular anomalies	University of Potsdam
2025-05-29	**Vineet Gaur**	Nature’s precision - specialized molecular scissor in plant DNA repair and recombination	National Institute of Plant Genome Research
2025-06-05	**Oliver Hobert**	Regulatory Logic of Cell Type Specification in the Nervous System	Columbia University
2025-06-06	**Patrick Paush**	Of DNA making and RNA breaking in bacterial immunity against phage	Vilnius University, Life Sciences Center – European Molecular Biology Laboratory (LSC-EMBL)
2025-07-02	**Thomas Müller-Reichert**	Application of correlative light and electron microscopy (CLEM) to quantitatively analyse spindle organisation during mitosis	TUD Dresden University of Technology
2025-09-11	**Santiago Ramón Maiques**	Portrait of a Diseased Protein: Pathogenic Mutations in the Multienzymatic CAD Complex	Instituto de Biomedicina de Valencia
2025-10-16	**Magdalena Winiarska**	Resistance to CD19 CAR-T immunotherapies in B-cell malignancies	Mossakowski Medical Research Institute of the Polish Academy of Sciences
2025-10-23	**Bożena Kamińska-Kaczmarek**	Tumor microenvironment at single-cell resolution and its modulation	Nencki Institute of Experimental Biology of the Polish Academy of Sciences
2025-11-06	**Agnieszka Chacińska**	Regulatory checkpoints in biogenesis of mitochondrial proteins	International Institute of Molecular Mechanisms and Machines of the Polish Academy of Sciences
2025-11-13	**Edith Marcial Juarez**	Cellular and molecular mechanisms regulating follicular dendritic cell expansion across the lifespan	Babraham Institute
2025-11-20	**Ewelina Knapska**	Emotional echoes: neural mechanisms by which others’ emotions shape adaptation	Nencki Institute of Experimental Biology of the Polish Academy of Sciences
2025-11-27	**Mykhailo Batiuk**	From Cellular Diversity to Epigenetics of Psychiatry: A Single-Cell Perspective	École Polytechnique Fédérale de Lausanne (EPFL)
2025-12-03	**David Balchin**	How the ribosome solves difficult folding problems	The Francis Crick Institute
2025-12-04	**Kacper Rogala**	Molecular mechanisms of mTOR signaling pathways	Stanford University School of Medicine
2025-12-18	**Jesper Velgaard Olsen**	Single-cell proteomics of protein abundance and turnover	Novo Nordisk Foundation Center for Protein Research (CPR), University of Copenhagen

Notes

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