
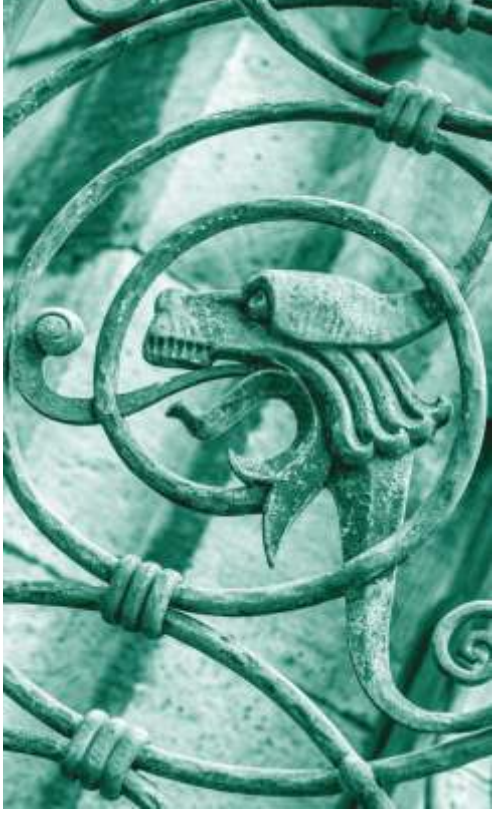


JAGIELLONIAN UNIVERSITY IN KRAKÓW

The latest achievements in biochemistry, biophysics and biotechnology – 50 years of history of the Faculty of Biochemistry, Biophysics and Biotechnology

KRAKÓW, SEPTEMBER 23–24, 2021

JAGIELLONIAN UNIVERSITY IN KRAKÓW

JUBILEE CONFERENCE

The latest achievements in biochemistry, biophysics and biotechnology – 50 years of history of the Faculty of Biochemistry, Biophysics and Biotechnology

KRAKÓW, SEPTEMBER 23–24, 2021

Contents

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The Jubilee Conference "The latest achievements in biochemistry, biophysics, biotechnology – 50 years of the history of the Faculty of Biochemistry and Biotechnology at the Jagiellonian University" is organised under the honorary patronage of the Rector of the Jagiellonian University, Professor **Jacek Popiel**.

JAGIELLONIAN UNIVERSITY
IN KRAKÓW

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Dean's foreword

It is my pleasure and honor to welcome you at the Jubilee Conference organized on the 50th anniversary of the establishment of the Institute of Molecular Biology, which gave rise to the present JU Faculty of Biochemistry, Biophysics and Biotechnology (FBBB).

Over half a century, generations of scientists have successfully secured the FBBB as one of the top scientific centers in Poland in the field of biomolecular research. I am glad that we can celebrate this success together, in the company of former and current employees, our alumni, as well as friends from Poland and abroad.

The 50th anniversary of FBBB is an opportunity to thank our staff, past and present, for their excellence in scientific research, high standards of academic teaching, approaches that support integration of our community and the passion for sharing science. I would also like to thank students and graduates for their support and inspiration in our scientific work. I wish all of us success in our future endeavours.

The Jubilee Conference is also an opportunity to acknowledge the former and present authorities and the entire administration of the Jagiellonian University whose everyday help, support and kindness have been facilitating our work and assisting in achieving the most ambitious goals.

I would like to thank all the participants, our prominent guests including session chairs and invited speakers, who joined the meeting despite the difficult pandemic time to celebrate this anniversary with us.

Last but not least, I would like to thank the Organizers and the Honorary Committee for their efforts to put the meeting together.

I believe the Jubilee Conference will be both a memorable social event and a truly inspiring opportunity to share science, exchange ideas, foster the integration and tighten future collaboration.

I wish you a great time at the conference and in Kraków!

Dean of the FBBB

Jolanta Jura

Organiser's foreword

The unexpected outbreak of the pandemic in 2020 interrupted the Jubilee celebrations of the FBBB, including preparation for the conference. The meeting was postponed to the future, with the hope of coming calmer and safer times.

And so we meet over a year later, in September. It is true that the world around has not returned yet fully to normal, but we have already learned to live in the new reality.

We do hope the lectures on new perspectives of interdisciplinary biological sciences will become the inspiration for our employees, PhD students and students.

The invitation to the conference was accepted by Professor Virginijus Šikšnys from the University of Vilnius – one of the discoverers of CRISPR/Cas9 as a method of gene editing, winner of many awards, including 18 Norwegian Kavli Prize, which he received together with last year's Nobel Prize winners. Professor Šikšnys will give the plenary lecture on September 23.

We also invited our long-time foreign collaborators to participate in the conference, as well as IBM and WBBiB alumni. We will hear their talks on September 24.

Additionally, the Faculty's achievements will be presented during the electronic poster session, showing the latest research conducted at the Faculty.

Both days will end with social gatherings. It will be a unique opportunity to refresh and deepening contacts. We want them to become an opportunity to meet not only among others current employees and doctoral students of the Faculty, but also among our Seniors, to whom we all owe so much, administrative and staff auxiliary and people who started their scientific careers by studying and working at IMB/FBBB.

Head of the Organising Committee

Józef Dulak

Programme

THURSDAY, SEPTEMBER 23, 2021

10.00–15.00 REGISTRATION

14.00–15.00 WELCOME COCTAIL

15.00–15.30 CONFERENCE OPENING, chairperson: Józef Dulak

15.05 Speech by the Dean of the FBBB, professor Jolanta Jura
15.20 Speech by the Rector of the Jagiellonian University

15.30–16.30 HISTORIC OVERVIEW, chairperson: Jolanta Jura

15.30 Wojciech Froncisz, *Rys historyczny*
15.50 Kazimierz Strzałka, *Od Instytutu do Wydziału*
16.10 Zbigniew Madeja, *WBBiB dzisiaj*

16.30–17.00 COFFEE BREAK

17.00–17.40 PLENARY LECTURE, chairperson: Józef Dulak

Virginijus Šikšnys, *Bacterial immunity: from restriction enzymes to CRISPR*

18.15 BUS TRANSFER FOR DINNER

19.00–24.00 DINNER, *Stara Zajezdnia* restaurant, św. Wawrzyńca 12 street

FRIDAY, SEPTEMBER 24, 2021

09.00–10.30 SESSION 1, chairpersons: Claudine Kieda and Patrick Midoux

09.00 Danuta Kozbor, *Reprograming the tumor microenvironment to overcome multiple primary and acquired immune resistance mechanisms in cancer*
09.20 Giulia Fontemaggi, *Non-coding RNA networks control VEGFA expression in breast cancer*
09.40 Paul J. Smith, *Targeting the cancer microenvironment: Insights and translation*
10.00 Marta Miączyńska, *Membrane trafficking and actin dynamics in cancer cell biology*

10.30–11.00 COFFEE BREAK

10.30–11.30 SESSION II, chairpersons: Chantal Pichon and Martyna Elas

10.30 Tomasz Kordula, *New insights into cerebellar astrocyte diversity*
protein-induced cell syncytia
10.50 Luigi Zecca, *Neuromelanins in brain aging and neurodegenerative diseases*
11.10 Jakub Tomasik, *Schizophrenia: From blood biomarkers to repurposed drug candidates*

12.00–13.20 LUNCH

13.20–14.50 SESSION III, chairpersons: Jolanta Jura and Józef Dulak

13.20 Mauro Giacca, *From COVID-19 pathology to therapy: drugs that inhibit SARS-CoV-2 spike*
13.40 Szymon Mańka, *Identification of disease-relevant prion architectures by cryo-EM: can structural biology tell us how prions replicate and kill?*
14.00 Andrzej Joachimiak, *Structural studies of SARS-CoV-2 proteins and their complexes*

14.20–14.50 COFFEE BREAK

14.50–15.50 SESSION IV, chairpersons: Artur Sabat and Jan Potempa

14.50 Xavier Gomis-Ruth, *Structural insight into pathogenic potential of periodontal pathogens*
15.10 Rich Lamont, *The oral microbiome in homeostasis and dysbiosis*
15.30 Alistair McCormick, *Developing tools to progress synthetic biology in cyanobacteria*

15.50–16.20 COFFEE BREAK

16.20–17.50 SESSION V, chairpersons: Tomasz Róg and Artur Osyczka

16.20 Vivek Sharma, *Computational modeling of redox-coupled proton pumping by respiratory complex I*
16.40 Jukka Kallijarvi, *Translational studies of mitochondrial complex III deficiency: from sick babies to bacteria*
17.00 Reimund Goss, *Xanthophyll cycles of higher plants and algae*
17.20 Guillem Ylla, *The new FBBB's Laboratory of Bioinformatics and Genome Biology: computational to approaches to study genes, genomes, gene regulatory networks*

17.50 CONFERENCE CLOSING, Jolanta Jura and Kazimierz Strzałka

18.00–20.00 FAREWELL COCTAIL, BUFFET

PLENARY LECTURE

Bacterial immunity: from restriction enzymes to CRISPR

Virginijus Šikšnys

Institute of Biotechnology, Vilnius University, Vilnius, Lithuania

Bacteriophages are major parasites of bacteria. To counter fight viral attacks bacteria developed multiple defense barriers that interfere with nearly every step of virus life cycle. These multiple defense barriers constitute a primitive immune system that protects bacteria against invading viruses. Bacterial immunity provided by restriction-modification and CRISPR-Cas antiviral defense systems resemble innate and adaptive immunity of vertebrates. Basic research aimed to understand molecular mechanisms of innate immunity provided by restriction-modification enzymes triggered a revolution in recombinant DNA technology while recent studies of adaptive bacterial immunity provided by the CRISPR-Cas systems resulted in the development of powerful tools for genome manipulation and revolutionised genome editing field.

SESSION I

Reprograming the tumor microenvironment to overcome multiple primary and acquired immune resistance mechanisms in cancer

Anna Mistarz[1], Marta Winkler[1], Andrzej Wierzbicki[1], Hanna Rokita[2], Danuta Kozbor[1]

[1]Department of Immunology, Roswell Park Comprehensive Cancer Center, Buffalo USA;
[2]Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Kraków, Poland

The goal of our studies is to generate robust tumor-specific T cell responses for durable tumor regression in patients with chemotherapy-resistant ovarian cancer (OC) by targeting immunosuppressive mechanisms using a viral oncotherapy combination. The scientific premise of this project stems from our discovery that blockade of the CXCL12 chemokine/CXCR4 receptor axis in OC by intraperitoneal delivery of an oncolytic vaccinia virus expressing a CXCR4 antagonist in combination with doxorubicin or immune checkpoint blockers yields a significant therapeutic impact by stimulating rigorous T cell responses as well as enhancing T cell migration to tumor sites. The successful execution of this study may lead to a paradigm-shifting immunotherapeutic strategy that overcomes multiple immune resistance mechanisms in patients with OC, and potentially other solid tumors.

BIBLIOGRAPHY
1. Gil M et al. Targeting CXCL12/CXCR4 signaling with oncolytic virotherapy disrupts tumor vasculature and inhibits breast cancer metastases *PNAS*. 2013 April;110(7): E12291-300.
2. Komorowski M et al. Reprograming antitumor immunity against chemoresistant ovarian cancer by a CXCR4 antagonist-armed viral oncotherapy. *Mol Ther Oncolytics*. 2016 Dec; 3:16034-16048.
3. McGray A J R et al. A prime/boost vaccine platform efficiently identifies CD27 agonism and depletion of myeloid-derived suppressor cells as therapies that rationally combine with checkpoint blockade in ovarian cancer. *Cancer Immunol, Immunother*. 2021, Apr;20:1-10.

Supported: NIH/NCI U01CA233085 and NIH/NCI 2P50CA159981.

SESSION I

Non-coding RNA networks control VEGFA expression in breast cancer

Giulia Fontemaggi[1], Chiara Turco[1], Gabriella Esposito[1], Anna Benedetti[2], Alessia Iaiza[2], Francesco Fazi[2], Mattia Forcato[3], Giovanni Blandino[1]

[1]Oncogenomic and Epigenetic Unit, IRCCS Regina Elena National Cancer Institute, Rome, Italy; [2]SAIMLAL Department, Sapienza University, Rome, Italy; [3]Department of Life Sciences, University of Modena and Reggio Emilia, Italy

Solid tumors secrete VEGFA leading to increased formation of blood vessels, reprogramming of tumor-associated macrophages and self-renewal of cancer cells. Production of VEGFA is fine tuned in breast cancer cells through different levels of gene expression and secretion control.

Post-transcriptional control of VEGFA isoforms production, in particular, is exerted by the long non-coding RNA (lncRNA) MALAT1, in complex with ID4 and mutant p53 proteins as well as with the oncogenic splicing factor SRSF1. This ribonucleoprotein complex favors on the one hand the production of the VEGFxxx at the expense of VEGFxxxb isoforms, on the other hand the synthesis of a circular RNA (circVEGF), which in turn controls the synthesis of VEGFA at the translational level.

SESSION I

Targeting the cancer microenvironment: insights and translation

Paul J. Smith[1,2]

[1]Cancer and Genetics Division, School of Medicine, Cardiff University, Cardiff, UK. [2]OncoTherics Poland Sp. z o.o., Kraków, Poland

Understanding the dynamic nature of cancer cell micro-communities presents scientific and technological challenges but is set to lead to improved therapeutic outcomes. Tumor micro-environment hypoxia, due to inadequate or chaotic vascularity, can present a major obstacle for effective treatment with radiotherapy, chemotherapy and immunotherapy. Tumour cells experiencing hypoxia, have impaired drug delivery and present survival-related modifications to phenotype with distinct patterns of genetic divergence – changes that facilitate drug resistance and metastasis. An attractive therapeutic strategy is to target cancer cell responses to hypoxia.

The presentation will focus on the potential for unidirectional hypoxia-activated prodrugs to selectively target aggressive cancer cells, especially when aligned with advanced imaging and biomarker approaches.

BIBLIOGRAPHY

1. Bhandari V, et al. Divergent mutational processes distinguish hypoxic and normoxic tumours. *Nat Commun*. 2020 Feb 5;11(1):737.
2. Rankin EB, Giaccia AJ. Hypoxic control of metastasis. *Science*. 2016 Apr 8;352(6282):175-80
3. Nesbitt H, et al. Targeting Hypoxic Prostate Tumors Using the Novel Hypoxia-Activated Prodrug OCT1002 | Inhibits Expression of Genes Associated with Malignant Progression. *Clin Cancer Res*. 2017 Apr 1;23(7):1797-1808.

SESSION I

Membrane trafficking and actin dynamics in cancer cell biology

Marta Miączyńska

Laboratory of Cell Biology, International Institute of Molecular and Cell Biology, Warsaw, Poland

Accumulating evidence indicates that aberrant membrane trafficking in cancer cells contributes to oncogenesis by affecting intracellular signaling, cytoskeleton dynamics, mechanotransduction and metabolism. I will use two recent studies from my lab to highlight why some proteins regulating membrane trafficking can serve as targets for cancer therapies. First, we discovered the synthetic lethality between VPS4 paralogs and its underlying mechanisms that could be exploited for precision therapy of VPS4B-deficient cancers [1]. Second, we identified intracellular processes induced by stimulation of AXL receptor tyrosine kinase that is frequently overactivated in metastatic or drug-resistant cancers [2].

BIBLIOGRAPHY

1. Szymańska M, et al. Synthetic lethality between VPS4A and VPS4B triggers an inflammatory response in colorectal cancer. *EMBO Mol Med*. 2020 12(2):e10812.
2. Zdżalik-Bielecka D, et al. The GAS6-AXL signaling pathway triggers actin remodeling that drives membrane ruffling, macropinocytosis and cancer cell invasion. *Proc Natl Acad Sci U S A*. 2021 118(28):e2024596118.

SESSION II

New insights into cerebellar astrocyte diversity

Karli Mockenhaupt, Katarzyna M. Tyc, Alexandra Gonsiewski, Adam McQuiston, Tomasz Kordula

Department of Biochemistry and Molecular Biology, Virginia Commonwealth University, Richmond, VA, USA

Distinct astrocyte subpopulations tile different brain regions to accommodate local requirements of neurons and associated neuronal circuits. Nevertheless, mechanisms responsible for generation of astrocyte diversity remain mostly elusive. Although a zinc finger transcription factor Yin Yang 1 (YY1) is highly expressed in astrocytes, its astrocyte-specific functions and mechanisms of action are unknown. We will discuss novel findings uncovering functions of YY1 during generation of specific astrocyte subpopulations in developing cerebellum. We will also present data indicating a critical role of YY1 in the maintenance of mature phenotypes of astrocytes in the adult cerebellum.

SESSION II

Neuromelanin in brain aging and neurodegenerative diseases

Luigi Zecca[1], Ioannis Isaias[2], Guillermo Horga[3], Clifford Cassidy[4], David Sulzer[5], Tadeusz Sarna[6], Fabio A. Zucca[1]

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We have demonstrated that neuromelanins are compounds occurring in many regions of human brain. They particularly accumulate in catecholamine neurons of substantia nigra and locus coeruleus that are selectively susceptible to degeneration accompanying Parkinson disease. We have shown that neuromelanin can play either a protective or toxic role in Parkinson depending on cellular context. Synthesis of neuromelanin is a protective mechanism since the melanic component is generated by removing reactive quinones that are neurotoxic. Neuromelanin can bind redox/toxic metals to form stable non toxic complexes thus being neuroprotective. Metals accumulated by neuromelanin include highly toxic Pb and Hg, in addition to Fe, Zn, Cu, Al, Cr and Mo. On the other hand, extracellular neuromelanin released by degenerating neurons of substantia nigra can activate microglia which release H_2O_2, NO and pro-inflammatory factors causing further neurodegeneration. The loss of neurons containing neuromelanin in Parkinson induces 40–60% decrease of neuromelanin content in substantia nigra, which can be shown by MRI and this method for imaging neuronal loss is becoming a new tool to confirm Parkinson diagnosis.

REFERENCES

1. Cassidy CM, et al. Neuromelanin-sensitive MRI as a noninvasive proxy measure of dopamine function in the human brain. *Proc Natl Acad Sci U S A.* 2019 Mar 12;116(11):5108-5117.
2. Zucca FA, et al. Interactions of iron, dopamine and neuromelanin pathways in brain aging and Parkinson's disease. *Prog Neurobiol.* 2017 Aug;155:96-119.
3. D'Ischia M, et al. Melanins and melanogenesis: from pigment cells to human health and technological applications. *Pigment Cell Melanoma Res.* 2015 Sep;28(5):520-44.
4. Zecca L. Neuromelanin can protect against iron-mediated oxidative damage in system modeling iron overload of brain aging and Parkinson's disease. *J. Neurochem.* Aug 2008; 106(4):1866-1875.
5. Shima T, et al. Binding of iron to neuromelanin of human substantia nigra and synthetic melanin: an electron paramagnetic resonance spectroscopy study. *Free Radic. Biol. Med.* 1997; 23(1):110-119.
6. Zecca L, et al. Interaction of neuromelanin and iron in substantia nigra and other areas of human brain. *Neuroscience.* Jul 1996; 73(2):407-415.
7. Zareba M. The effect of a synthetic neuromelanin on yield of free hydroxyl radicals generated in model systems. *Biochim. Biophys. Acta.* 9 Jun 1995; 1271(2-3):343-348.

SESSION II

Schizophrenia: From blood biomarkers to repurposed drug candidates

Jakub Tomasik[1*], Santiago G. Lago[1*], Geertje F. van Rees[1], Hannah Steeb[1], David A. Cox[1], Nitin Rustogi[1], Jordan M. Ramsey[1], Joshua A. Bishop[2], Tracey Petryshen[3,4,5], Stephen J. Haggarty[2], Javier Vázquez-Bourgon[6,7,8], Sergi Papiol[9,10,11], Paula Suarez-Pinilla[6,7], Benedicto Crespo-Facorro6,7,8, Nico J. van Beveren[12,13,14], Sabine Bahn[1†]

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Psychiatric disorders are increasingly recognised as disorders of the whole body. Previous research has demonstrated a strong link between cells in our blood and the way our central nervous system operates. In this work, we explore primary blood cell function as a model for psychiatric disease. We show that live T lymphocytes from patients with schizophrenia can be used to identify functional disease biomarkers and potential drug targets. Furthermore, they lend themselves to compound library screening and drug repurposing, and can predict treatment efficacy for individual patients. Our approach has the potential to discern new drug targets and accelerate drug discovery and personalized medicine for schizophrenia and other neuropsychiatric conditions.

BIBLIOGRAPHY

1. Lago SG, at al. Drug discovery for psychiatric disorders using high-content single-cell screening of signaling network responses ex vivo. *Sci Adv.* 2019 May;5(5):eaau9093.
2. Lago SG, et al. Exploring the neuropsychiatric spectrum using high-content functional analysis of single-cell signaling networks. *Mol Psychiatry.* 2020 Oct;25(10):2355-2372.

SESSION III

From COVID-19 pathology to therapy: drugs that inhibit SARS-CoV-2 spike protein-induced cell syncytia

Mauro Giacca

King's College London, British Heart Foundation Centre of Research Excellence, School of Cardiovascular Medicine & Sciences, London UK

My laboratory aims to develop new biotherapeutics for cardiac protection and repair after myocardial infarction. We have pioneered the concept that cardiac regeneration can be achieved through the stimulation of the endogenous capacity of cardiomyocytes to proliferate and have identified a series of microRNAs that stimulate this process in both small and large animals [1,2]. Starting from March 2020, we have redeployed our screening expertise to elucidate the mechanisms that regulate SARS-CoV-2 infection. We found that the lungs of patients with COVID-19 contain infected pneumocytes with abnormal morphology and frequent multinucleation. Generation of these syncytia results from activation of the SARS-CoV-2 Spike protein at the plasma membrane level. Based on these observations, we performed two high-content microscopy-based screenings with over 3000 approved drugs to search for inhibitors of Spike-driven syncytia. One of the most effective molecules was niclosamide, which suppressed the activity of TMEM16F/Anoctamin6, a calcium-activated ion channel and scramblase responsible for phosphatidylserine exposure on the cell surface. These findings suggest a potential mechanism or COVID-19 disease pathogenesis and support the repurposing of niclosamide for therapy [3]. A clinical trial with niclosamide in hospitalized COVID-19 patients in ongoing in India.

BIBLIOGRAPHY

1. Eulalio A, et al. 2012. Functional screening identifies miRNAs inducing cardiac regeneration. *Nature*. 492, 376- 81.
2. Gabisonia K, et al. 2019. MicroRNA therapy stimulates uncontrolled cardiac repair after myocardial infarction in pigs. *Nature*. 569, 418-422.
3. Braga L, et al. 2021. Drugs that inhibit TMEM16 proteins block SARS-CoV-2 spike-induced syncytia. *Nature*. 594, 88-93.

SESSION III

Identification of disease-relevant prion architectures by cryo-EM: can structural biology tell us how prions replicate and kill?

Szymon W. Mańka, Adam Wenborn, Jemma Betts, Susan Joiner, Helen Saibil, John Collinge and Jonathan D.F. Wadsworth

MRC Prion Unit at UCL, Institute of Prion Diseases, University College London, 33 Cleveland Street, London W1W 7FF, UK

Prions are infectious misfolded protein assemblies causing acute and rapidly fatal neuro-degenerative diseases such as Creutzfeldt-Jakob disease (CJD) in humans, scrapie in sheep and bovine spongiform encephalopathy (mad cow disease) in cattle, also transmittable to humans (variant CJD). Prions propagate by recruiting a host protein called prion protein (PrP) into a pathogenic rod-like assembly, but the details of this process are not known. Protective mutations in human PrP sequence have been discovered, but it is still enigmatic how these single amino acid substitutions render PrP resistant to prionogenic conversion. Moreover, prions come in various strains that show distinct biochemical properties and disease profiles and the structural basis of strain differentiation and selection is of great interest. We use cryogenic electron microscopy (cryo-EM) to study structures of the authentic infectious ex-vivo rodent-adapted scrapie prions at high-resolution. We observed two distinct populations of fibrils representing a single prion strain: one is a single-protofilament amyloid fibril and the other comprises two protofilaments. What is the meaning of the two architectures? Do paired fibres represent the mechanism of replication? Or is it just a purification artefact? What structural components confer or mediate toxicity? Our efforts are now focused on achieving atomic-resolution structures of these and other prion assemblies to gain further insight into the prion replication mechanism, the mechanistic roles of protective mutations and inter-species transmission barriers.

SESSION III

Structural studies of SARS-CoV-2 proteins and their complexes

Andrzej Joachimiak[1,2,3], Karolina Michalska[1,2]

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[3]Department of Biochemistry and Molecular Biology, University of Chicago, Chicago, IL 60367, USA

The COVID-19 pandemic, caused by SARS-CoV-2, is creating huge social and economic damage to local communities, whole countries, and the entire world. At present only vaccines and monoclonal antibodies are available as effective medical countermeasures, small-molecule antiviral drugs do not exist. Although this virus is similar to SARS- and MERS-CoVs, the detailed information about SARS-CoV-2 proteins structures and functions is urgently needed to help develop effective therapeutics. We applied high-throughput protein production and structure determination pipeline at the Center for Structural Genomics of Infectious Diseases to produce SARS-CoV-2 proteins and determine high resolution crystals structures. We focused on nonstructural proteins (Nsps) expressed as polypeptides 1a and 1ab and processed into 15 functional proteins. Several Nsps assemble into a large membrane-bound replicase-transcriptase complex and exhibits multiple enzymatic and binding activities. Thus far at CSGID we have determined over 60 structures for 14 CoV-2 proteins. These structures include: Nsp1 virulence factor suppressing host gene expression by mRNA degradation and interaction with the 40S ribosomal subunit, several Nsp3 components – Ubl1 (ubiquitin-like domain), ADRP (ADP-ribose phosphatase domain, also known as macrodomain), NAB (nucleic acid biding domain) and PLpro (papain-like protease), Nsp5 (main protease, Mpro), Nsp7/Nsp8 primase complex, Nsp9 (RNA-binding protein), Nsp10/Nsp16 (2'-O-ribose methyltransferase complex) and Nsp15 (uridylate-specific endoribonuclease). We compare these structures with previously reported homologs from SARS and MERS coronaviruses and point to similarities and differences. We also determined structures of complexes with proteins, ligands and inhibitors, including FDA approved drugs. We deposited all structures to the Protein Data Bank and released the coordinates to scientific community prior publication. We also shared all reagents and protocols. This collection of structures details inhibitors recognition and interactions providing fundamental molecular and mechanistic insight into these proteins' functions. Our findings can accelerate structure-based drug design efforts targeting essential SARS-CoV-2 proteins to identify high-affinity inhibitors of clinical value.

SESSION IV

Structural insight into pathogenic potential of periodontal pathogens

Danuta Mizgalska[2], Theodoros Goulas[1], Arturo Rodríguez-Banqueri[1], Florian Veillard[2], Mariusz Madej[2], Ewelina Małecka[2], Katarzyna Szczęśniak[2], Mirosław Książek[2], Magdalena Widziołek[2,3], Tibisay Guevara[1], Ulrich Eckhard[1], Maria Solà[4], Jan Potempa[2,5], F. Xavier Gomis-Rüth[1]

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Porphyromonas gingivalis is a keystone pathogen of the human dysbiotic oral microbiome that causes severe periodontitis. It employs a type-IX secretion system (T9SS) to shuttle proteins across the outer membrane (OM) for virulence. Uniquely, T9SS cargoes carry a C-terminal domain (CTD) as secretion signal, which is cleaved and replaced with anionic lipopolysaccharide by transpeptidation for extracellular anchorage to the OM. Key elements for this transport have been analysed by structural biochemistry and will be presented.

SESSION IV

Porphyromonas gingivalis interactions with epithelial cells in the community context

Richard J. Lamont

Department of Oral Immunology and Infectious Diseases, University of Louisville, Louisville, KY, USA

Oral epithelial cells are central to the maintenance of homeostasis. *Porphyromonas gingivalis* induces dysbiotic epithelial responses which contribute to disease. *P. gingivalis* virulence, however, is expressed in the context of heterotypic communities. We explored whether organisms that are commensal individually can modulate pathogenicity in a community. We used RNA-Seq to define epithelial pathways regulated in response to *P. gingivalis* alone, but restored toward homeostasis by *S. gordonii*. Pathways included those involved in proliferation, migration, epithelial mesenchymal transition (EMT), apoptosis, and inflammation; and many of these revolved around the FOXO1-ZEB2 signaling axis. The results suggest that on epithelial surfaces a relative decrease in the proportion of *S. gordonii* to *P. gingivalis* would promote phonotypes which are hallmarks of cancer.

SESSION IV

Developing tools to progress synthetic biology in cyanobacteria

Alistair McCormick

SynthSys and Institute of Molecular Plant Sciences, School of Biological Sciences, University of Edinburgh, Edinburgh, UK

Cyanobacteria are key organisms in the global ecosystem and have significant biotechnological potential. Nevertheless, our molecular understanding and capacity to engineer cyanobacteria remains underdeveloped. Even in model species, such as *Synechocystis* sp. 6803, many proteins and pathways have not been fully characterized [1]. Recently several new fast-growing strains have been identified, which show promise for advancing cyanobacterial research and biotechnology applications [2]. Here I will discuss our work to develop tools to advance cyanobacteria into the synthetic biology age, including the development of rapid plasmid assembly and transformation/transconjugation systems [3], a standardised mutant library for *Synechocystis* sp. 6803, and our recent success in producing a thermotolerant variant of the high value blue pigment-protein phycocyanin [4].

BIBLIOGRAPHY

1. Mills LA, et al. Current knowledge and recent advances in understanding metabolism of the model cyanobacterium Synechocystis sp. PCC 6803. *Biosci. Rep.* 2020 40: BSR20193325.
2. Gale GAR, et al. Emerging species and genome editing tools: future prospects in cyanobacterial synthetic biology. *Microorg.* 2019 7:409.
3. Vasudevan R, et al. CyanoGate: A Golden Gate modular cloning suite for engineering cyanobacteria based on the plant MoClo syntax. *Plant Physiol.* 2019 180: 39-55.
4. Puzorjov A, et al. Production of thermostable phycocyanin in a mesophilic cyanobacterium. M*et. Eng. Comm.* 2021 13:e00175.

SESSION V

Computational modeling of redox-coupled proton pumping by respiratory complex I

Vivek Sharma[1,2]

[1]Department of Physics, University of Helsinki, Finland. [2]HiLIFE Institute of Biotechnology, University of Helsinki, Finland

The first electron-acceptor in the bioenergetic chains of many organisms is respiratory complex I. This massive enzyme weighs ca. 500 kDa to 1 MDa, transfers two electrons from NADH to a quinone (Q) molecule, and transfers the free energy of the reaction to proton pumping. The proton electrochemical gradient established across the bacterial or mitochondrial membrane enables the synthesis of ATP. The respiratory complex I plays a key role in mitochondrial function and dysfunction by coupling energy production to NADH/Q recycling and ROS production. However, despite extensive structural, biophysical and biochemical investigations, the redox-coupled proton pumping mechanism of complex I remains unknown. We performed free energy simulations and microseconds of atomistic molecular dynamics (MD) simulations on bacterial and mitochondrial complexes, which led to the identification of Q binding sites in the ~35 Å Q tunnel of complex I [1,2]. Building upon high resolution cryo electron microscopy data and site directed mutagenesis studies on yeast complex I, our multiscale computer simulations revealed novel substrate and pumped proton routes [3,4], led to a revised role of one supernumerary subunit [4] and yielded new mechanistic insights into long-range electron-proton coupling [5,6] and function of complex I [7].

BIBLIOGRAPHY

1. Warnau J, et al. Redox-coupled quinone dynamics in the respiratory complex I. *Proc. Natl. Acad. Sci. USA* 2018 115(36):E8413-E8420.
2. Haapanen O, et al. Role of second quinone binding site in proton pumping by respiratory complex I. *Front. Chem.* 2019 7:221.
3. Parey K, et al. High-resolution structure and dynamics of mitochondrial complex I–insights into the proton pumping mechanism. *Biorxiv.* 2021.
4. Yoga EG, et al. Essential role of accessory subunit LYRM6 in the mechanism of mitochondrial complex I. *Nat. Comm.* 2020 11(1):1-8.
5. Parey K, et al. High-resolution cryo-EM structures of respiratory complex I: mechanism, assembly, and disease. *Sci. Adv.* 2019 5(12): eaax9484.
6. Djurabekova A, et al. Proton motive function of the terminal antiporter-like subunit in respiratory complex I. *BBA Bioener.* 2020 1861(7):148185.
7. Haapanen O, Sharma V. Redox-and protonation-state driven substrate-protein dynamics in respiratory complex I. *Curr. Opin. Electrochem.* 2021 29:100741.

SESSION V

Translational studies of mitochondrial complex III deficiency: from sick babies to bacteria

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Mutated *BCS1L* is the most common cause of respiratory chain (RC) complex III deficiency, resulting in defective assembly of the RISP subunit into CIII. Knock-in mice carrying a homozygous *Bcs1l*$^{p.S78G}$ patient mutation [1] display juvenile-onset growth restriction, hypoglycemia, hepatopathy, kidney tubulopathy, making this an excellent experimental model [2]. The CIII deficiency is further exacerbated in a genetic background carrying a spontaneous *mt-Cyb*$^{p.D254N}$ variant [3]. Bypassing the CIII-CIV segment with transgenic alternative oxidase (AOX) is dramatically beneficial to the mutant mice, preventing lethal late-onset cardiomyopathy[4]. Here, I will present an overview of the mutant mouse model and some of our latest interventional and mechanistic studies.

BIBLIOGRAPHY

1. Fellman, V. et al. Iron-overload disease in infants involving fetal growth retardation, lactic acidosis, liver haemosiderosis, and aminoaciduria. *Lancet.* 1998 Feb 14;351(9101):490-3.
2. Levéen, P. et al. The GRACILE mutation introduced into Bcs1l causes postnatal complex III deficiency: a viable mouse model for mitochondrial hepatopathy. *Hepatology.* 2011 Feb;53(2):437-47.
3. Purhonen, J. et al. A spontaneous mitonuclear epistasis converging on Rieske Fe-S protein exacerbates complex III deficiency in mice. *Nat Commun.* 2020 Jan 16;11(1):322.
4. Rajendran, J. et al. Alternative oxidase-mediated respiration prevents lethal mitochondrial cardiomyopathy. *EMBO Mol Med.* 2019 Jan;11(1):e9456.

SESSION V

Xanthophyll cycles of higher plants and algae

Reimund Goss

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The short personal review summarizes interesting results on the violaxanthin cycle of higher plants and the diadinoxanthin cycle of diatoms, many of which have been obtained in collaboration with the Department of Plant Physiology and Biochemistry in Krakow. With respect to the violaxanthin cycle of higher plants I will show that the mode of zeaxanthin synthesis, i.e. synthesis by a light-driven proton gradient versus synthesis in the dark in a reaction medium adjusted to the pH-optimum of the enzyme violaxanthin de-epoxidase, influences the capacity of zeaxanthin to induce non-photochemical quenching of chlorophyll a fluorescence (NPQ).

A second major point concerning the violaxanthin cycle of higher plants will be the presentation of results about the lipid dependence of xanthophyll cycling, which finally led to the direct isolation of a functional violaxanthin cycle domain consisting of the light-harvesting complex of photosystem II (LHCII), the enzyme violaxanthin de-epoxidase, the main thylakoid membrane lipid MGDG and the substrate violaxanthin. With regard to the diadinoxanthin cycle of diatoms the focus will be on the different properties of the diadinoxanthin cycle enzymes compared with the enzymes of the violaxanthin cycle of higher plants, with a special emphasis on the fast epoxidation of diatoxanthin to diadinoxanthin.

The fast diatoxanthin epoxidation in diatoms has to be seen in conjunction with the direct quenching capacity of diatoxanthin in the absence of a transmembrane proton gradient. I will also point out that diatoxanthin plays an important role in the aggregation of the light-harvesting complexes of diatoms, the fucoxanthin chlorophyll proteins (FCPs). This aggregation is thought to represent the basis for NPQ. Speaking of the diadinoxanthin cycle I will finally address the lipid dependence of xanthophyll cycling in diatoms and point out similarities and differences to higher plants.

SESSION V

The new FBBB's Laboratory of Bioinformatics and Genome Biology: computational approaches to study genes, genomes, gene regulatory networks

Guillem Ylla[1,2]

[1]Department of Organic and Evolutionary Biology, Faculty of Arts and Sciences, Harvard University, Cambridge, MA, USA. [2]Faculty of Biology, Jagiellonian University, Kraków, Poland

The "Bioinformatics and Genome Biology Laboratory" will open its doors at the Faculty of Biochemistry, Biophysics and Biotechnology of the Jagiellonian University in November. The aim of this laboratory is to develop and use computational approaches to broadly study genomes, their regulation, and their evolution. The number of species with an available genome assembly has grown exponentially in recent years and will likely keep growing. These genomes are not only extremely valuable tools to facilitate the development of molecular techniques, but also, a very rich source of information that we can exploit to gain relevant biological information. An example of that is the recently published genome of the cricket *Gryllus bimaculatus*, which gave us new insights into the genome size evolution, the roles of DNA methylation and putative genes involved in their characteristic chirping. While the price of generating "omics" data keeps decreasing, there are still many bottlenecks on processing, analyzing, and interpreting the data. In an ongoing project, we generated 57 transcriptomes of different cell types, in different stages, and different treatments of *Drosophila melanogaster* ovaries. The integration of our large and complex dataset with publicly available data allowed us to identify new genes and their regulatory mechanisms that could play a relevant role in determining the number of progeny in insects. These are just two examples of the type of projects we are excited about at the "Bioinformatics and Genome Biology Lab", and we encourage you to reach out to us if you have, or plan to have, any kind of omics data.

Giulia Fontemaggi

Giulia Fontemaggi is a researcher at the IRCCS Regina Elena National Cancer Institute, Oncogenomic and Epigenetic Unit in Rome. She studied biology at the Sapienza University of Rome, Italy and received her Ph.D. degree in Oncology from the University of Perugia.

Doctor Fontemaggi's research focuses mainly on the functional characterization of non-coding RNA networks in breast and head/neck cancer. The aim of the research is the exploitation of ncRNAs as potential biomarkers and targets for anticancer therapy.

Mario Giacca

Mauro Giacca received his degree in medicine from the University of Trieste, Italy in 1984 and his Ph.D. in Microbiology and Virology from the University of Genoa in 1989. He is a Professor of Cardiovascular Sciences at the School of Cardiovascular Medicine & Sciences, King's College London. Until 2019, he served as the Director-General of the International Centre for Genetic Engineering and Biotechnology (ICGEB). Since 2005, he has held the position of Full Professor of Molecular Biology at the University of Trieste.

Professor Giacca is President of the International Society for Heart Research (ISHR)-European Section. He is considered an expert in the generation of viral vectors for cardiovascular applications and the development of novel biologics for cardiac repair and regeneration. He has published over 370 papers, book chapters and textbooks. His research has been funded by numerous international grants, including two consecutive ERC Advanced Investigator grants.

Since March 2020, he has redeployed part of his group's research to elucidate the mechanisms that regulate SARS-CoV-2 infection. These studies have led to the discovery of a new mechanism that regulates the function of the coronavirus spike protein and is involved in COVID-19 pathogenesis.

F. Xavier Gomis-Rüth

F. Xavier Gomis-Rüth graduated in 1989 from the Universitat Ramon Llull in Barcelona where he studied chemical engineering. From 1989 to 1992, he worked in the protein crystallography laboratory at the Max-Planck Institute of Biochemistry (MPIB) in Martinsried, Germany, mainly on proteolytic enzymes, under the supervision of professors Wolfram Bode and Robert Huber.

In 1992, he obtained a Ph.D. degree from the Ludwig-Maximilian University of Munich. As a PostDoc, he continued his structural studies on proteases at the Autonomous University of Barcelona, MPIB, and at the Molecular Biology Institute of Barcelona (IBMB), a part of Spain's Higher Scientific Research Council (CSIC). In 2000, he became an assistant professor at the IBMB and founded the Proteolysis Laboratory. Since 2008, he has been a full professor at the CSIC and, since 2014, he has been a Director of the Department of Structural Biology at the IBMB.

Professor Gomis-Rüth is an author of over 140 publications. His scientific interests focus on the function and structure of proteins, mostly proteolytic enzymes and their inhibitors.

Reimund Goss

Reimund Goss studied biology. In 1996, he received his Ph.D. degree from the Institute of General Botany, Johannes Gutenberg-University, Mainz, Germany. In 2005, he obtained his habilitation based on a thesis entitled Role of carotenoid molecules in the regulation of photosynthetic light utilization. He works at the Institute of Biology of Leipzig University.

Andrzej Joachimiak

Andrzej Joachimiak studied chemistry at the University of Adam Mickiewicz in Poznań. He received a Ph.D. degree in 1980 from the Institute of Bioorganic Chemistry in Poznań. In 1991, he received his habilitation from the Institute of Biochemistry and Biophysics, Warsaw.

From 1980 to 1993, he held a PostDoc position at the University of Chicago, USA, worked at the Institute of Bioorganic Chemistry in Poznań, and spent 3 years at Yale University. In 1993, he moved to the Argonne National Laboratory where he is currently a director of the Structural Biology Center, a group of the X-ray Science Division. Since 2004, he has also been connected with the University of Chicago, where he is a professor and co-director of the Center for Structural Genomics of Infectious Diseases.

Professor Joachimiak's research interests include enzyme specificity, protein-ligand interactions, protein-nucleic acid interactions, and molecular chaperones. He is a world-renowned expert in the field of synchrotron-based X-ray crystallography and structural biology.

Professor Joachimiak is an author of 400 publications and book chapters (> 29,000 total citations, H-index 84, > 2,700 structures in the PDB). He is an Associate Editor of Protein Science and Protein & Cell, a member of the European Academy of Sciences and the Polish Society of Arts and Sciences, a recipient of the University of Chicago Award for Distinguished Performance and the Arthur H. Compton Award, Advanced Photon Source.

Jukka Kallijarvi

Jukka Kallijarvi is a principal investigator on the Stem Cells and Metabolism Research Program at the Faculty of Medicine, University of Helsinki and an administrative group leader at Folkhälsan Research Center. He studied biochemistry. In 2006, he received his Ph.D. degree in medical genetics from the Faculty of Medicine, University of Helsinki. His group investigates mitochondrial respiratory chain complex III (CIII) deficiencies, particularly GRACILE syndrome, a severe multiorgan metabolic disease in newborn infants. As the main model, they use a patient mutation knock-in mouse and do pharmacological, dietary, and gene therapy interventions to find novel treatments and to understand mechanisms of pathogenesis.

Tomasz Kordula

Tomasz Kordula received both M.Sc. (1988) and a Ph.D. (1992) degrees from the Jagiellonian University. He completed postdoctoral training at the University of Georgia in Athens, USA. His first independent position was at Cleveland State University. He moved his laboratory to Virginia Commonwealth University in 2004 and currently holds the position of Professor and Graduate Program Director.

Dr. Kordula is studying molecular mechanisms regulating both tissue-specific and inflammatory responses of astrocytes.

Danuta Kozbor

Danuta Kozbor is Professor of Oncology in the Department of Immunology at Roswell Park Comprehensive Cancer Center (RPCCC) in Buffalo, NY, USA. She is a basic scientist with expertise in pre-clinical studies specializing in novel immunotherapeutic approaches to target the suppressive tumor microenvironment in platinum-resistant cancers.

She has pioneered the development of oncolytic vaccinia viruses expressing therapeutic proteins to target the CXCL12 chemokine/CXCR4 receptor signaling pathway in combination with checkpoint inhibitors and elucidated their mechanisms of action for a broad applicability in the treatment of solid tumors.

Richard Lamont

Richard Lamont graduated with a BSc (Honours) from the University of Edinburgh in 1982 and completed his PhD in Bacteriology from the University of Aberdeen in 1985.

He has held academic appointments at various universities in the USA, and currently holds the position of Endowed Professor and Chair of the Department of Oral Immunology and Infectious diseases at the University of Louisville.

He is also a recipient of various awards, including IADR Distinguished Scientist Awards (1995, 2006), the MERIT award from NIH (2009), and the University of Louisville President's Award for distinguished research (2016). He has authored over 200 publications in peer-reviewed journals and 5 books. He has been editor-in-chief of the journal Molecular Oral Microbiology since 2015.

His latest projects focus on: periodontal disease pathogenesis, molecular and cellular interactions between *Porphyromonas gingivalis* and gingival epithelial cells, communications between microorganisms formulating plaque and *Porphyromonas gingivalis*.

Szymon Mańka

Szymon W. Mańka graduated with M.Sc./M.Res. from the Faculty of Biochemistry, Biophysics and Biotechnology (WBBiB) at the Jagiellonian University in 2005, where he studied proteomes of S. aureus mutants in the laboratory of Professor Jan Potempa. In 2010, he was awarded a Ph.D. from Imperial College London. In his thesis, Szymon proposed a mechanism of collagen degradation by prototypic human collagenase. In 2011–2019 he worked at the University of Oxford and at Birkbeck College London, where he specialised in structural biology and biophysics.

Szymon collaborated with numerous laboratories in Europe and the US and presented his work on prestigious conferences around the World. He published a number of high-impact papers that shed light on molecular mechanisms of fundamental processes of multicellular life, such as cell division and organ development. In 2019, Szymon established a cryo-electron microscopy (cryo-EM) laboratory at the UCL Institute of Prion Diseases (University College London). His current research focuses on near-atomic structure determination of authentic, highly infectious ex vivo prions.

Biograms

Alistair McCormick

Alistair McCormick is a Reader in Plant Molecular Physiology and Synthetic Biology and the Director of Edinburgh Plant Science.

His group focuses on enhancing photosynthetic efficiencies in plants and the development of cyanobacteria as bio-platforms for producing high value products. A standardized MoClo system developed by his group for rapidly engineering cyanobacteria (CyanoGate) is the basis of an ambitious, collaborative 'big data' project to generate the first genome knockout library of the model cyanobacterium *Synechocystis* sp. 6803.

Marta Miączyńska

Marta Miączyńska is the Director and the head of Laboratory of Cell Biology at the International Institute of Molecular and Cell Biology in Warsaw. She graduated in molecular biology from the Jagiellonian University and received her PhD in genetics from the University of Vienna. She did postdoctoral work at the EMBL Heidelberg and at the Max Planck Institute for Molecular Cell Biology and Genetics in Dresden.

As a cell biologist she studies the molecular mechanisms integrating membrane transport, in particular endocytosis, with intracellular signaling pathways, also in the context of oncogenesis. She discovered a distinct population of early endosomes in the cell, so called APPL endosomes. Co-author of over 50 publications cited >3000 times. She received fellowships from Austrian Science Fund, Human Frontier Science Program Organization and L'Oreal Poland for Women in Science. Laureate of prestigious national and international grants. Panelist of granting agencies, including ERC. Member of European Molecular Biology Organization (EMBO), Academia Europaea, Polish Academy of Sciences, EMBO Council and Council of the National Science Center (2016–2018).

Biograms

Vivek Sharma

Vivek Sharma is Sigrid Jusélius senior researcher and principal investigator at the Department of Physics, University of Helsinki, Finland. He completed his doctoral degree in the group of Mårten Wikström studying cbb3-type cytochrome oxidases, and received postdoctoral training in Ilpo Vattulainen's group at Tampere University, Finland.

His research focuses on the molecular mechanism of respiratory complexes, which he studies with multiscale computational methods.

Virginijus Šikšnys

Virginijus Šikšnys graduated in chemistry from the University of Vilnius in 1978. In 1983, he obtained a doctoral degree at the Lomonosov Moscow State University, where he studied enzyme kinetics. After returning to Lithuania, he worked for ten years at the Institute of Applied Enzymology in Vilnius. In 1993, he completed an internship at the laboratory of the Nobel laureate Robert Huber at the Max-Planck Institute in Martinsried, Germany. Since 1995, Professor Šikšnys has been working at the Institute of Biotechnology of the Vilnius University, where he heads the Department of Protein-DNA Interactions.

He is an author of over 100 scientific articles. He has received several awards for his achievements, including the Lithuanian State Science Award (2001), St. Christopher Award for the merits in science from the Vilnius City Council (2015), the Warren Alpert Foundation Award (2016) and the Kavli Prize in nanoscience (2018).

The research interests of Virginijus Šikšnys focus on the relationship between the structure and function of enzymes involved in the metabolism of nucleic acids. For nearly twenty years, he studied restriction endonucleases and solved about 15 tertiary structures of these enzymes. Since 2007, Professor Šikšnys has focused on the mechanistic research of CRISPR-Cas, the newly discovered bacterial antiviral systems, and was one of the first to show programmable DNA cleavage by the Cas9 protein.

Paul J. Smith

Paul J. Smith studied medical microbiology at Bristol University and received his Ph.D. from Manchester University in 1977.

Professor Smith has been active in the fields of DNA repair, drug development, cytometry and imaging technologies for more than 30 years. After postdoctoral National Engineering Council fellowships positions in Canada at the Chalk River Nuclear Laboratories, including support by the US National Cancer Institute, he returned to the UK becoming a senior non-clinical scientist with the UK Medical Research Council in Cambridge. There he developed a programme focused on anticancer drug resistance and co-established the Hoechst dye spectral shift methodology, later exploited by others for stem cell isolation. In 1995 he was appointed to the Chair of Cancer Biology at Cardiff University (Emeritus Professor July 2013 to present).

His research expertise and patents encompass the cell cycle, DNA topoisomerases, biophotonics and anticancer drugs – deploying imaging and flow cytometry technologies. He is a Past President of the International Society for Advancement of Cytometry. Professor Smith is a co-founder and director of the molecular probe company Biostatus Ltd and the spin-out Oncotherics Ltd currently developing novel hypoxia targeting anticancer drugs.

Jakub Tomasik

Jakub Tomasik holds a M.Sc. degree in Biotechnology from the Jagiellonian University and a Ph.D. in Neuroscience from the Erasmus Medical Centre in Rotterdam. He worked at the Max Planck Institute of Psychiatry in Munich, and for the diagnostics company Psynova Neurotech Ltd. He is currently a Senior Research Associate at the University of Cambridge.

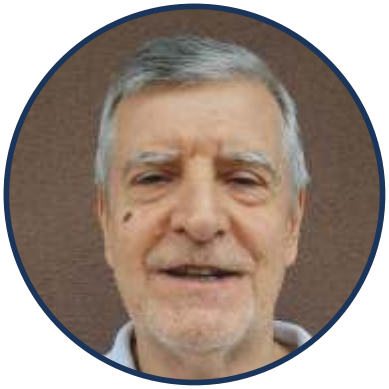
His research focuses on improving current approaches in the diagnostics and treatment of major neuropsychiatric conditions such as bipolar disorder, major depression and schizophrenia using biomarkers and digital data.

Biograms

Guillem Ylla

Guillem Ylla received his bachelor's degree in Biotechnology and a master's degree in Omics Data Analysis from the University of Vic (Barcelona). Guillem did his Ph.D. studying the genomic and transcriptomic basis of the origin and evolution of insect metamorphosis in the Institute of Evolutionary Biology of the Pompeu Fabra University and Spanish Research Council. Subsequently, he moved to the USA as a postdoctoral researcher at the University of Florida where he worked developing computational tools to study microRNAs and alternative splicing. Then, he moved to Harvard University, to study arthropod genomics and evolution in the Extavour lab.

Currently, he is establishing his laboratory on "Bioinformatics and Genome Biology" at the Faculty of Biochemistry, Biophysics and Biotechnology of the Jagiellonian University where he will use bioinformatics approaches to study multiple aspects of genomes and their regulation.



Luigi Zecca

Luigi Zecca heads the Laboratory of Aging and Neurodegeneration at the Institute of Biomedical Technologies in Milan, Italy and is currently a Visiting Professor of Neurobiology at Columbia University (New York, NY, USA).

From 2001 to 2007, Professor Zecca was a Director of Research at the Institute of Biomedical Technologies, before subsequently being appointed Director of this Institute (from 2008 to 2015). Since 2018, he has been a Member of the Steering Committee of the National Institute of Research and Care of Aging in Ancona, and a Committee Member of the Department of Biomedical Sciences, National Research Council of Italy.

Professor Zecca is recognized as a leading scientist in neuromelanin research. Together with his coworkers, he described the key aspects of neuromelanin structure, synthesis, and interaction with metals. He also showed that neuromelanins are ubiquitous in the human brain, occur in special autolysosomes, accumulate with aging, and affect neurodegeneration.

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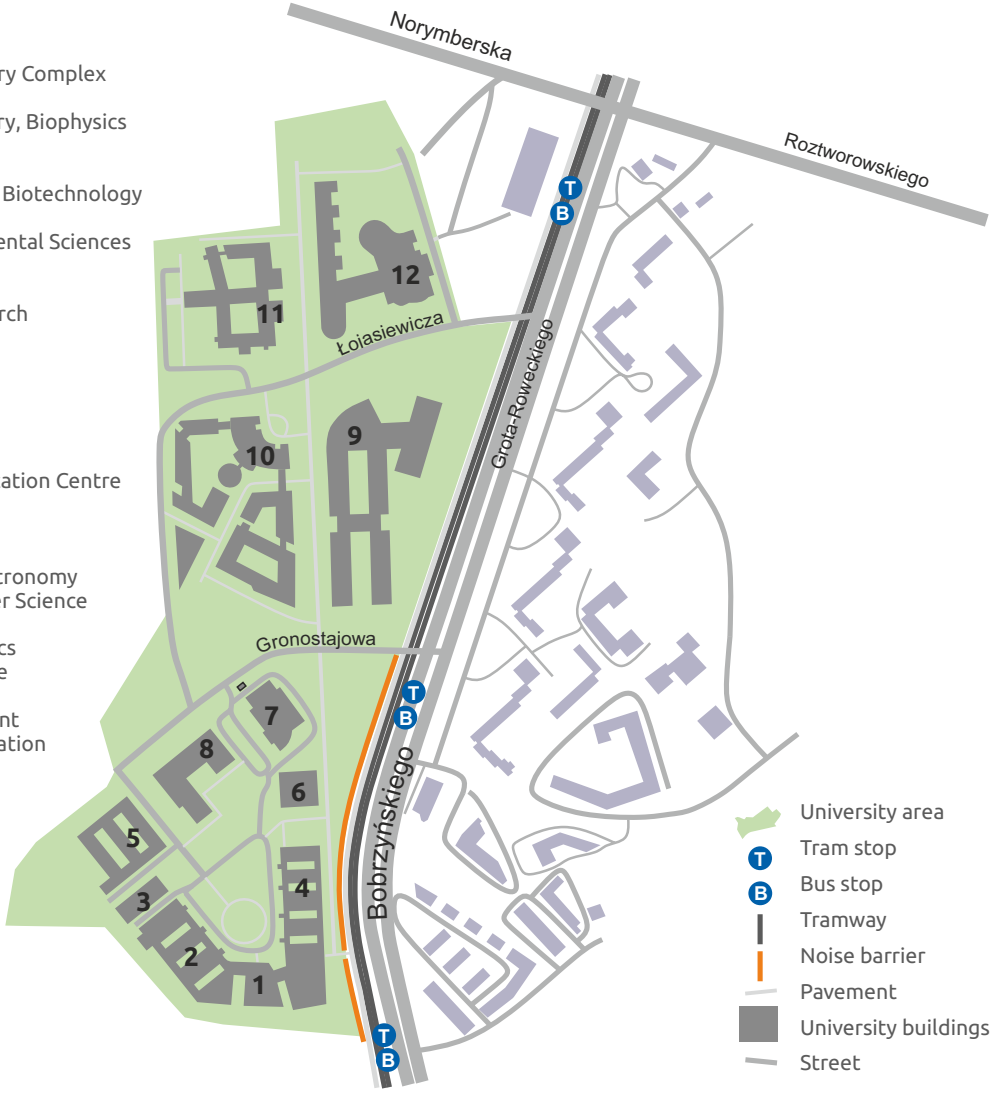

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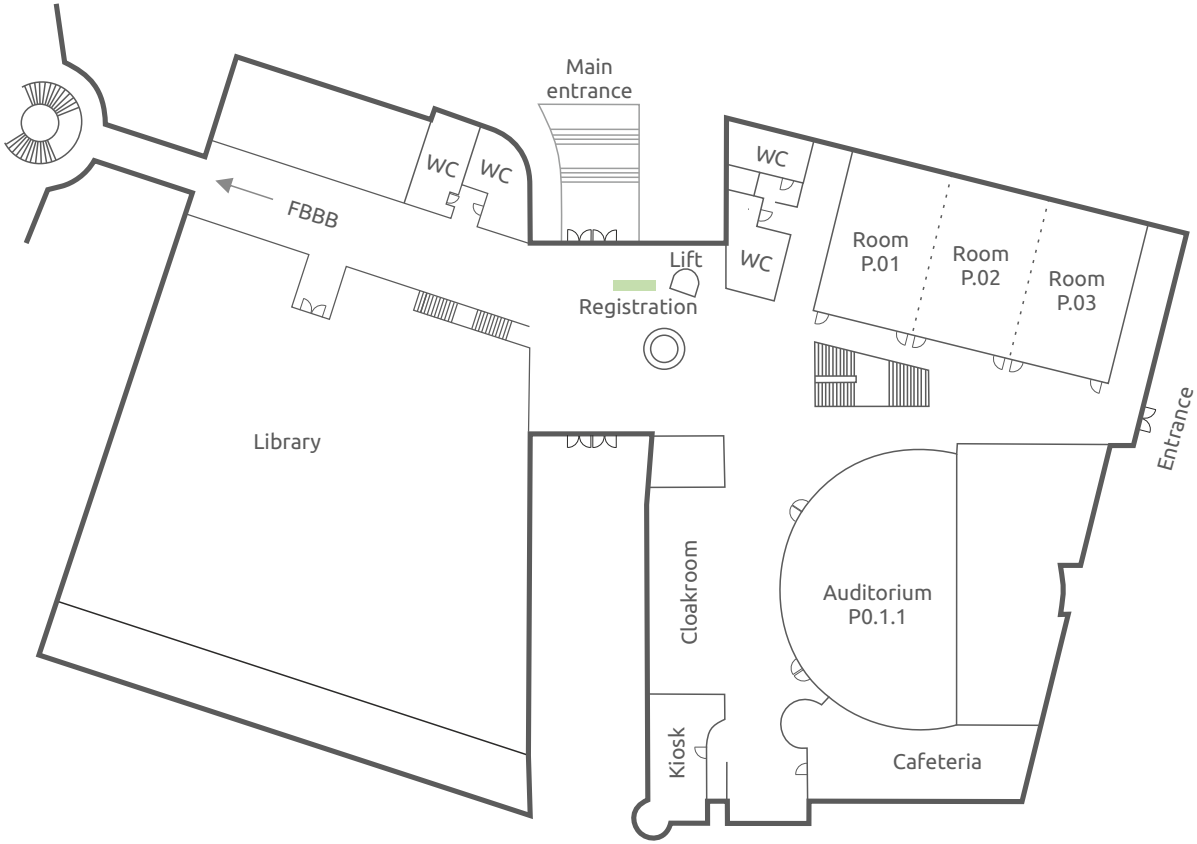

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