# 7th CCP Phenogenomics Conference

## 11–12 September 2025
## Prague & on-line

# ABSTRACT BOOK

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Czech Centre for Phenogenomics

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MINISTRY OF EDUCATION, YOUTH AND SPORTS

Czech Academy of Sciences

STRATEGY AV21
Top research in the public interest

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## WE THANK TO ALL OUR SUPPORTERS AND SPONSORS FOR THEIR CONTRIBUTION TO THE CONFERENCE

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Content

Dear Colleagues,

It is my great pleasure to welcome you to the 7th CCP Phenogenomics Conference.

Similarly to the last year, the conference is devoted to the topic of **rare diseases, gene and cell therapy development, and preclinical modeling with animal systems**, with special focus on **bottom-up approaches to gene therapy development**, integrating basic research with clinical perspectives through sessions featuring not only scientists but also representatives from patient advocacy groups and rare disease foundations.

We believe that the Conference will provide again an excellent opportunity to support networking and interactions among the researchers, CCP staff, users and experts from the commercial sector.

Yours sincerely,

On behalf of the CCP Organizing Committee,
Radislav Sedláček
Director of the Czech Centre for Phenogenomics

Photo © Jana Plavec / Czech Academy of Sciences


## ORGANIZER – CZECH CENTRE FOR PHENOGENOMICS

The Czech Centre for Phenogenomics (CCP) is a large research infrastructure unique in combining genetic engineering capabilities, advanced phenotyping and imaging modalities, SPF animal housing and husbandry, as well as cryopreservation and archiving, all in one central location – at BIOCEV campus.

CCP is the only specialized place in the Czech Republic that, at the level of the world's best centres, creates genetically modified mouse and rat models for indispensable biomedical research and at the same time uses standardized but the most advanced phenotyping to characterize the expression of gene functions. CCP outputs are utilized solving the role of genes in the development and treatment of human diseases. CCP provides unique comprehensive preclinical research services in the Czech Republic. With the quality of service and publication results, CCP has gained a worldwide reputation, it has a strong position in international consortia such as the global IMPC (to determine the role of all genes), the European Infrafrontier, and EuroPDX. CCP is involved in several international scientific projects.

www.phenogenomics.cz

## ACKNOWLEDGEMENTS:

MINISTRY OF EDUCATION, YOUTH AND SPORTS

The Czech Centre for Phenogenomics is supported by the Czech Academy of Sciences RVO 68378050 and by the project LM2023036 Czech Centre for Phenogenomics provided by the Ministry of Education, Youth and Sports of the Czech Republic.

Czech Academy of Sciences

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Top research in the public interest

"Towards precision medicine and gene therapy" research programme of the Strategy AV21 is coordinated by the Institute of Molecular Genetics of the Czech Academy of Sciences.

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Tento projekt je spolufinancován se státní podporou Technologické agentury ČR v rámci Programu Národní Centra kompetence
www.tacr.cz
*Výzkum užitečný pro společnost.*

The project TN02000132/National Centre for New Methods of Diagnosis, Monitoring, Treatment and Prevention of Genetic Diseases is co-financed with state support from the Technology Agency of the Czech Republic under the National Centres of Competence Programme. The Centre aims to improve diagnostic quality beyond the identification of mutations in the genome and to create a base for monitoring of disease progression and therapy effectiveness as well as for testing and development of cell and gene therapies.

| THURSDAY 11TH SEPTEMBER 2025 | |
|---|---|
| 8:15 – 9:00 | Registration |
| **Opening + Session 1 – Models to understand gene function in vivo I (Chair: Radislav Sedláček)** | |
| 09:00 – 09:15 | **Radislav Sedlacek**, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic<br>Welcoming talk: "CCP in 2024-2025 and developing the 'RD-factory' program" |
| **09:15 – 09:50** | **Yann Herault, Institute of Genetics and Molecular and Cellular Biology, France**<br>**"Models to understand gene function in vivo: CNS and disease"** |
| 09:50 – 10:20 | **Alessandra Biffi**, University of Padova and Padova University Hospital, Italy<br>"HSC gene therapy applications in nervous system disorders: from neurometabolic diseases to adult onset dementias" |
| 10:20 – 10:35 | **Shijia Teo**<br>"More than just pretty pictures:<br>Preclinical imaging of in-vivo (animal) and ex-vivo (post-mortem human brain) models" |
| 10:35 – 10:50 | Discussion with speakers |
| 10:50 – 11:15 | Coffee break |
| **Session 2 – Models to understand gene function in vivo II (Chair: Yann Herault)** | |
| 11:15 – 11:45 | **Dierk Niessing**, Helmholtz Zentrum München and Ulm University, Molecular Target and Therapy Center, Germany<br>"PURA syndrome – a rare neurodevelopmental disorder" |
| 11:45 – 12:15 | **Kyuhyung Kim**, Department of Brain Sciences, Daegu Gyeongbuk Institute of Science and Technology, South Korea<br>"Interoceptive regulation of food swallowing in C. Elegans" |
| 12:15 – 12:45 | **Matthew Alexander**, The University of Alabama at Birmingham<br>"Generation and corrective drug screening for models of X-linked myopathy with excessive autophagy (XMEA)" |
| 12:45 – 13:00 | Discussion with speakers |
| 13:00 – 14:30 | Lunch break & Poster session 1 (on site) |
| **Session 3 – Genome programming** | |
| 14:30 – 15:00 | CB Gurumurthy, University of Mississippi Medical Center<br>"RE-CREATING and SCRIPT: emerging technologies for overcoming genome engineering challenges" |
| **15:00 – 15:35** | **Frank Buchholz, Medical Systems Biology, UCC, Faculty of Medicine, TU Dresden, Germany**<br>**"Engineering designer-recombinases for therapeutic genome editing"** |
| 15:35 – 15:50 | Discussion with speakers |
| 15:50 – 16:10 | Coffee break |
| **Session 4 – From genotype to phenotype: disease informatics** | |
| 16:10 – 16:40 | **Damian Smedley**, Queen Mary University of London, United Kingdom<br>"Phenotype-driven approaches to rare disease diagnostics and gene discovery" |
| 16:40 – 17:10 | **Venkata Satagopam**, Luxembourg Centre For Systems Biomedicine, Luxembourg<br>"Translational medicine multi-modal data approaches to investigate complex diseases" |

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|---|---|
| **17:10 – 17:50** | **Gary Peltz, Stanford University, USA**<br>**“AI-Enabled Mouse Genetic Discovery”** |
| 17:50 – 18:05 | Discussion with speakers |
| | Informal part |
| 19:00 – 22:00 | Networking event – informal dinner |

## FRIDAY 12TH SEPTEMBER 2025

### Session 5 – Models to understand gene function as a base for therapy development

| | |
|---|---|
| 09:00 – 09:30 | **Gopal Sapkota**, University of Dundee, United Kingdom<br>“FAM83G/SACK1G Mutations Disrupt CK1α Interaction and WNT Signalling in Palmoplantar Keratoderma” |
| 09:30 – 10:00 | **Jana Balounova**, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic<br>“FAM83H/SACK1H shapes thymic stromal architecture and postnatal lymphopoiesis via CK1 interaction” |
| 10:00 – 10:30 | **Samuele Ferrari**, San Raffaele Telethon Institute for Gene Therapy, Italy<br>“Poisoning of healthy hematopoiesis drives clonal dominance in VEXAS syndrome” |
| 10:30 – 11:00 | **Yonghwan Kim**, Sookmyung Women’s University, Republic of Korea<br>“A rare variant allele of BMPR2 predisposes to the onset of a novel subtype of congenital heterotopic ossification” |
| 11:00 – 11:15 | Discussion with speakers |
| 11:15 – 11:35 | Coffee break |

### Session 6 – Short presentations: Selected poster presentations & technology talks

**FLASH ORAL PRESENTATIONS**

| | |
|---|---|
| 11:35 – 11:45 | **Tanja Sorg**, PHENOMIN – ICS, France<br>“Deciphering the consequences of CLCN4 mutations in rat models for a better understanding of the rare X-linked CLCN4-related neurodevelopmental condition” |
| 11:45 – 11:55 | **Alice Foltýnová**, Institute of Experimental Medicine of CAS, Czech Republic<br>“Reprogramming of glial cells into interneurons using synthetic mRNA” |
| 11:55 – 12:05 | **Chao-Kuen Lai**, Academia Sinica, Taiwan<br>„The Taiwan Mouse Clinic: the first user-friendly platform for high-quality, high-throughput, comprehensive phenotyping and drug testing of mouse models in Asia“ |

**TECHNOLOGIES FOR ANIMAL MODELS**

| | |
|---|---|
| 12:05 – 12:20 | **Dr. Jörg Bantin**, Bio-Rad<br>“Digital PCR is a breakthrough technology that provides ultrasensitive and absolute nucleic acid quantification” |
| 12:20 – 12:35 | **Peter Kesa**, FUJIFILM VisualSonics<br>“HF ultrasound and photoacoustic in phenotyping of animal models – from early embryogenesis to aging studies” |
| 12:35 – 12:50 | **Behdad Pouran**, Milabs, CANBERRA-PACKARD s. r. o.<br>“Unraveling the Biology of Rare and Genetic Diseases with Multi-modal Preclinical Imaging” |
| 12:50 – 14:15 | Lunch break & Poster session 2 (on site) |

## Session 7 – Rare diseases & bottom-up efforts to develop (gene) therapies

| | |
|---|---|
| 14:15 – 14:35 | **Jakub Sikora**, Charles University 1st Medical Faculty, Czech Republic<br>"Pathogenic variants in EHMT2 as a novel cause of Kleefstra syndrome" |
| 14:35 – 15:05 | Foundation 1: Charlie project (www.charlie.science)<br>Research speaker:<br>**Caroline Linster**, University of Luxembourg, Luxembourg<br>"New zebrafish models for lysine metabolism disorders" |
| | Foundation representative speaker:<br>**Albert Carbonell**, Spanish patient association FAMILIA GA1, Spain<br>"Unmet medical and psychosocial needs in glutaric aciduria type 1 and pyridoxine-dependent epilepsy: insights from an international patient survey" |
| 15:05- 15:25 | Coffee break |
| 15:25 – 15:55 | Foundation 2: YWHAG Foundation (www.ywhagfoundation.org) |
| | Scientific speaker:<br>**Helen Chen**, USA<br>"Scientific updates from the YWHAG Research Foundation" |
| | Foundation representative speaker:<br>**Andrew Miner**, YWHAG Foundation, USA<br>"From Heartbreak to Hope: A Father's Journey Mobilizing Global YWHAG Research" |
| 15:55 – 16:25 | Foundation 3: A-T Children's Project (www.atcp.org) |
| | Scientific speaker:<br>**Timothy W. Yu**<br>"Precision genetic intervention and ´N=1 trials´ for Ataxia Telangiectasia" |
| | Foundation/patient representative speaker:<br>**Tomas Pavlicek**, ATAP and A-T Dad, Czech Republic<br>"Global landscape of AT patient organisations" |
| 16:25 – 16:50 | Discussion with speakers |
| **16:50 – 17:25** | **Steve Murray, The Jackson Laboratory, Maine, USA**<br>**"From discovery to treatment: the JAX Center for Precision Genetics"** |
| **CLOSING** | |
| 17:25 – 17:30 | **Radislav Sedlacek**, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic |
| | "Closing remarks" |

## KEYNOTE & FEATURED SPEAKERS

### Gary Peltz, MD, Ph.D.

Professor of Anesthesiology, Perioperative and Pain Medicine, Stanford University, United States of America

### "AI-Enabled Mouse Genetic Discovery"

Dr. Gary Peltz received his MD and PhD from Stanford University, and is certified as a specialist in Internal Medicine and Rheumatology. He was a research executive at a large pharmaceutical company for 17 years, and was selected by Nature Publications as one of the top 10 Pharma research executives worldwide. Dr. Peltz became a full professor in 2008 at the Stanford University Medical School. He has more than 124 peer-reviewed publications.

The Peltz laboratory develops and uses state of the art genomic methods to identify genetic factors affecting disease susceptibility, and to translate these findings into new treatments.

Source: Stanford University, https://biox.stanford.edu/people/gary-peltz

### Yann Herault, Ph.D.

Research Director at the CNRS, the French National Centre for Scientific Research

### "Models to understand gene function in vivo: CNS and disease"

Yann Herault, Ph.D. is a Research Director at the CNRS, the French National Centre for Scientific Research. Biologist and mouse geneticist by training, he is leading the Mouse Clinical Institute, ("Institute Clinique de la Souris", MCI/ICS), and is the leader of a research group at the IGBMC. He has been working on mouse development using genetics approach for more than 20 years. He developed a series of techniques for chromosomal engineering with the aims to study gene regulation at the genomic level in vivo. Now his research interests are focused on evaluating the consequences of gene dosage effect and copy number variation in pathological situation such as in Down Syndrome (or Trisomy 21) to further propose new therapeutic approaches. Y. Herault did his PhD. at the University of Lyon in 1993, and got a post-doctoral training at the University of Geneva from 1993 to 1999 working on Hox gene regulation with Pr. Denis Duboule. He became a PI in 2000 joining the research unit at the Institute de Transgenose in Orleans. Then he was appointed as Director of the infrastructure for Transgenesis and Archiving of Animal Models (TAAM) used by a large number of research groups from various locations from late 2007 to early 2014. He developed CELPHEDIA the National Infrastructure for model animal in the French roadmap for Infrastructure and he is coordinating the PHENOMIN national infrastructure for Biology and Health, laureate of the Investment for the Future in 2011 which is built around the ICS, the TAAM and the Centre for ImmunoPhenomique (CIPHE, head B. Malissen) in Marseille.

Source: Frontiers Media SA, https://loop.frontiersin.org/people/233508/bio

## Prof. Dr. Frank Buchholz

Dean of Research at the Faculty of Medicine Carl Gustav Carus; Professor for Medical Systems Biology and Head of translational research at the University Cancer Center of the TU Dresden

### "Engineering designer-recombinases for therapeutic genome editing"

Prof. Dr. Frank Buchholz is full Professor for medical systems biology and head of translational research at the university cancer center of the TU Dresden since 2010.
As a PhD student till 1997 at the European Molecular Biology Laboratory (EMBL) in Heidelberg, he performed seminal work to implement and improve site-specific recombinases for genome engineering. During his postdoctoral time at the University of California San Francisco (UCSF), he showed for the first time that these enzymes can induce a predefined chromosomal translocation in vivo and he invented substrate-linked directed evolution to breed recombinases with novel specificities. From 2002 to 2010, he perfectionated this approach as an independent group leader at the Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG) in Dresden to develop the Tre recombinase, an enzyme that can eradicate HIV from infected cells. The approach is now developed into a designer-recombinase platform technology and is supported by a number of research grants.
Prof. Dr. Frank Buchholz is also widely known for his development of the esiRNA technology and its implementation as an efficient and specific RNAi screening tool. Employing this tool, he has discovered many new genes relevant for stem cell biology and human diseases. His group has recently extended functional profiling via RNAi and CRISPR/Cas9 technology to primary cells, with the goal to apply this technology to personalized medicine.

Source: TU Dresden, https://tu-dresden.de/med/mf/ucc/medsys/die-professur/inhaber-in?set_language=en

## Steve Murray, Ph.D.

Professor and Senior Director, Genetic Resource Science, The Jackson Laboratory, Bar Harbour, United States of America

### "From discovery to treatment: the JAX Center for Precision Genetics"

The research in his lab is focused on discovering the developmental mechanisms of morphogenesis and structural birth defects using both forward and reverse genetic approaches. We use innovative CRISPR/Cas9 modeling methods to rapidly investigate the function of novel human mutations associated with these conditions to aid in diagnosis and improve our understanding of disease mechanisms. We take advantage of large-scale mutagenesis programs to identify and study novel single gene knockout developmental phenotypes, and diverse mouse genetic backgrounds to explore the systems-level dynamics of embryonic morphogenesis.

His lab also builds large-scale resources for the broader scientific community including the Knockout Mouse Phenotyping Program (KOMP2), which is part of an international effort to create and phenotype a single gene knockout for every protein coding gene in the mammalian genome. For the JAX Center for Precision Genetics (JCPG), we use genome editing technology to engineer precise models of rare disease and, when feasible, explore genome editing strategies for therapeutic intervention.

Source: The Jackson Laboratory, https://www.jax.org/research-and-faculty/faculty/steve-murray

## KEYNOTE & FEATURED LECTURES

**Thursday, 11th September 2025 (17:10 – 17:50)**

**Gary Peltz**, Stanford university, USA
**"AI-Enabled Mouse Genetic Discovery"**

**Thursday, 11th September 2025 (9:15 – 9:50)**

**Yann Herault**, Institute of Genetics and Molecular and Cellular Biology, France
**"Models to understand gene function in vivo: CNS and disease"**

**Thursday, 11th September 2025 (15:00 – 15:35)**

**Frank Buchholz**, Medical Systems Biology, UCC, Faculty of Medicine, TU Dresden, Germany
**"Engineering designer-recombinases for therapeutic genome editing"**

**Friday, 12th September 2025 (16:20 – 16:55)**

**Steve Murray**, The Jackson Laboratory, Maine, USA
**"From discovery to treatment: the JAX Center for Precision Genetics"**

## AI-Enabled Mouse Genetic Discovery

**Gary Peltz [1]**
1. Stanford University School Of Medicine

E-mail of the presenting author: gpeltz@stanford.edu

We have comprehensively characterized SNPs, structural variants, tandem repeats and epigenomic variation in the genomes of 39 inbred mouse strains. AI-based methods were used to characterize the genetic basis for mouse models of human disease-related traits, several of which were described 40 or more years ago. The AI methods used for analysis of mouse models were also used to identify the genetic basis for diseases appearing in human patients.

## SESSION 1 – MODELS TO UNDERSTAND GENE FUNCTION IN VIVO I

### Thursday, 11th September 2025 (9:00 – 10:35)

**9:00 – 9:15**
Radislav Sedlacek, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic
"Welcoming talk: CCP in 2024-2025 and developing the 'RD-factory' program"

**9:15 – 09:50**
Yann Herault, Institute of Genetics and Molecular and Cellular Biology, France "Models to understand gene function in vivo: CNS and disease"

**09:50 – 10:20**
Alessandra Biffi, University of Padova and Padova University Hospital, Italy
"HSC gene therapy applications in nervous system disorders: from neurometabolic diseases to adult onset dementias"

**10:20 - 10:35**
Shijia Teo
"More than just pretty pictures: Preclinical imaging of in-vivo (animal) and ex-vivo (post-mortem human brain) models"

## SESSION 2 – MODELS TO UNDERSTAND GENE FUNCTION IN VIVO II

### Thursday, 11th September 2024 (11:15 – 12:45)

**11:15 – 11:45**
Dierk Niessing, Helmholtz Zentrum München and Ulm University, Molecular Target and Therapy Center, Germany
"PURA syndrome – a rare neurodevelopmental disorder"

**11:45 – 12:15**
Kyuhyung Kim, Department of Brain Sciences, Daegu Gyeongbuk Institute of Science and Technology, South Korea
"Interoceptive regulation of food swallowing in C. Elegans"

**12:15 – 12:45**
Matthew Alexander, The University of Alabama at Birmingham
"Generation and corrective drug screening for models of X-linked myopathy with excessive autophagy (XMEA)"


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## PURA Syndrome – a rare neurodevelopmental disorder

**Dierk Niessing [1,2]**
1. Institute of Pharmaceutical Biotechnology, Ulm University,
2. Institute of Structural Biology at the Molecular Targets and Therapeutics Center, Helmholtz Center Munich

E-mail of the presenting author: dierk.niessing@uni-ulm.de

In recent years, the number of newly identified neurodevelopmental disorders has experienced a significant surge. To date, for only a limited number of these disorders have the underlying pathomechanisms been elucidated, leaving the vast majority of NDDs heavily understudied. Among the latter is PURA syndrome, for which currently about 750 patients have been identified worldwide. First described in 2014, this NDD is caused by sporadic, heterozygous mutations in the PURA gene (5q31.3), resulting in haploinsufficiency of the nucleic acid-binding protein PURA. Individuals with PURA syndrome exhibit intellectual disability, hypotonia, epilepsy, scoliosis, and a spectrum of other, variable symptoms. There is currently no good understanding of the underlying cellular dysregulation upon PURA haploinsufficiency and hence no treatment strategy is available. With the support of patient advocacy groups, we have established a research network to understand the etiology of the PURA Syndrome and develop strategies for therapeutic intervention. My group contributes to these efforts by employing complementing approaches, ranging from structural biology and biochemical studies to multi-omics analyses. Initially, we used immortalized human cell culture to learn that PURA binds to thousands of transcripts and regulates their translation. Subsequently, we transitioned to a more physiological model system by establishing human iPSC-derived 2D and 3D cultures from CRISPR/Cas-generated PURA KO cells in conjunction with their isogenic controls. Already in iPSC-derived 2D neural progenitor cells, we observed dysregulation of neural differentiation markers. Similar abnormalities in expression of differentiation markers were observed in iPSC-derived 3D cerebral organoids, indicating that neural differentiation might be affected upon loss of PURA. Using single-cell RNA sequencing, we found that a loss of PURA and the resulting dysregulation of the afore-mentioned differentiation markers result in an imbalance of neuronal homeostasis. While these observations demonstrate for the first time the importance of PURA for neural and neuronal differentiation, the early timepoint of the observed cellular misdifferentiation holds significant implications for therapeutic interventions in patients with PURA syndrome.

## Interoceptive Regulation of Food Swallowing in C. elegans

**Kyuhyung Kim [1]**
1. Department of Brain Sciences, DGIST, Daegu, Republic of Korea

E-mail of the presenting author: khkim@dgist.ac.kr

Interoception, the process of sensing internal signals from the body, is essential for maintaining homeostasis and survival. Various ion channels, including the PIEZO channel, have been implicated in interoception; however, how different ion channels contribute to this process and interact with cellular signaling pathways remains largely unknown. In C. elegans, the PIEZO channel, encoded by pezo-1 and expressed in the pharyngeal-intestinal valve (PI valve), detects food accumulation in the anterior intestinal lumen and triggers rhythmic pharyngeal plunges — a process that regulates intestinal food movement (Park et al., 2024). However, how PIEZO channels translate mechanical cues into cellular signals remains poorly understood, particularly the mechanisms by which mechanically activated channels regulate downstream signaling events mediating physiological responses. Here, we show that the evolutionarily conserved calcium-activated chloride channels Bestrophins (BESTs) regulate PIEZO-dependent pharyngeal plunge. Among the 26 bestrophin genes in C. elegans, we found that best-1 and best-9 are co-expressed in the PI valve. We also found that best-9 best-1 double mutants, but not best-1 or best-9 single mutants, exhibit prolonged and deep pharyngeal plunges, which are restored by the expression of best-1 or best-9 cDNA under the control of their respective promoters. Furthermore, overexpression of best-1 or best-9 in the PI valve decreases the frequency and depth of pharyngeal plunges, leading to defects in food swallowing. These results indicate that best-1 and best-9 act redundantly to inhibit pharyngeal plunging in the PI valve. Additionally, optogenetic activation of the PI valve in double mutants results in significantly deeper pharyngeal plunges compared to wild-type worms. This study uncovers a mechanistic link between BEST channels and PIEZO-dependent mechanosensation, providing insights into how BEST channels regulate interoceptive processes.

## SESSION 3 - GENOME PROGRAMMING

### Thursday, 11th September 2025 (14:30 – 15:35)

**14:30 – 15:00**
CB Gurumurthy, University of Mississippi Medical Center
“RE-CREATING and SCRIPT: emerging technologies for overcoming genome engineering challenges”

**15:00 – 15:35**
Frank Buchholz, Medical Systems Biology, UCC, Faculty of Medicine, TU Dresden, Germany
“Engineering designer-recombinases for therapeutic genome editing”

## RE-CREATING and SCRIPT: Emerging Technologies for Overcoming Mouse Genome Engineering Challenges

**CB Gurumurthy [1,2]**

1. Professor, Department of Cell and Molecular Biology, University Of Mississippi Medical Center
2. Director, Genome-editing Research, Education, and Animal genome Targeting (GREAT) Core

E-mail of the presenting author: cgurumurthy@umc.edu

Over the past decade, our laboratory has led the development of transformative genome engineering technologies, including Easi-CRISPR and i-GONAD which have become widely adopted for creating genetically engineered mouse models across the globe. While these methods have enabled the generation of thousands of models each year, their efficiency drops significantly when working with large DNA inserts — typically those exceeding a few kilobases. In this presentation, I will introduce two emerging technologies developed in our laboratory that address these limitations: RE-CREATING (RE-engineering using CRISPR of previously Engineered Alleles To Insert New Genes) and SCRIPT (Simultaneous CRISPR and PITT). I will share experimental data demonstrating how these methods enhance the efficiency and accuracy of inserting large DNA fragments, opening new avenues for complex genome engineering in vivo.

## Engineering Designer-Recombinases for Therapeutic Genome Editing

**Frank Buchholz [1]**
1. Medical Systems Biology, Medical Faculty, Technical University Dresden, Germany

E-mail of the presenting author: frank.buchholz@tu-dresden.de

Many genetic mutations that cause human diseases have been identified over the last decades. Recent breakthroughs in the field of genome editing now provide a genuine opportunity to establish innovative gene and cell therapy approaches to repair DNA lesions to replace, engineer or regenerate malfunctioning cells in vitro, or directly in the human body. However, most of the recently developed genome editing technologies introduce double stranded DNA breaks at a target locus as the first step to gene correction. These breaks are subsequently repaired by one of the cell intrinsic DNA repair mechanisms, typically inducing an abundance of random insertions and deletions (indels) at the target locus. Ideally, therapeutic genome editing should, however, be efficient and specific, without the introduction of indels.

Site-specific recombinases (SSRs) allow genome editing without triggering cell intrinsic DNA repair pathways as these enzymes fulfill both cleavage and immediate resealing of the processed DNA, allowing precise, predictable and efficient genome editing in vivo. We use substrate-linked directed evolution coupled with rational design to program SSRs to target therapeutically relevant human genomic sites. Recently, we have improved activity and specificity of designer-recombinases by fusing their coding sequences to zinc-finger DNA-binding domains. I will show that this approach improves the properties of designer-recombinase with therapeutic potential and present and a prototype of a multilateral recombinase that can be programmed to recombine many target sites in a ZFD-dependent manner.

## SESSION 4 - FROM GENOTYPE TO PHENOTYPE: DISEASE INFORMATICS

### Thursday, 12th September 2024 (16:10 – 17:50)

**16:10 – 16:40**
Damian Smedley, Queen Mary University of London, United Kingdom
“Phenotype-driven approaches to rare disease diagnostics and gene discovery”

**16:40 – 17:10**
Venkata Satagopam, Luxembourg Centre For Systems Biomedicine, Luxembourg
“Translational medicine multi-modal data approaches to investigate complex diseases”

**17:10 – 17:50**
Gary Peltz, Stanford university, USA
“AI-Enabled Mouse Genetic Discovery”

## Phenotype-driven approaches to rare disease diagnostics and gene discovery

**Damian Smedley [1]**
1. Queen Mary University of London

Whole genome and exome sequencing (WES/WGS) approaches have revolutionised diagnostics for rare genetic diseases over the last decade. However, identifying the causative variant(s) from amongst the millions of variants in a WGS remains challenging and more than half of patients remain undiagnosed, even after state-of-the-art WGS and analysis. I will describe the work of my team and collaborators in the IMPC and Monarch Initiative to utilise clinical and model organism phenotype data to facilitate this task and open-source software approaches such as Exomiser that we have developed for the rare disease community. Our experiences of translating these approaches with Genomics England for the 100,000 Genomes Project and NHS Genomic Medicine Service will be presented. Finally, I will describe our current approaches to helping the many patients that remain undiagnosed from the 100,000 Genomes Project through a combination of reanalysis, multi-omics approaches and disease-gene association discovery.

## Translational medicine multi-modal data approaches to investigate complex diseases

**Venkata Satagopam [1]**
1. Luxembourg Centre For Systems Biomedicine, Luxembourg

E-mail of the presenting author: venkata.satagopam@uni.lu

Neurodegenerative (e.g. PD - Parkinson's disease), immunological (e.g IBD - Inflammatory Bowl Disease, MS - Multiple Sclerosis, RA - Rheumatoid Arthritis) and recent COVID19 diseases are quite complex in their etiology. In order to stratify and discover the signatures, biomarkers for early diagnosis, we need high quality clinical cohort studies. This talk will focus on the clinical and translational medicine informatics approaches developed to build up cohorts and to capture the clinical data using state-of-the-art electronic Case Report Forms (eCRFs) encoded with standard ontologies and controlled terminologies. Secure management and efficient integration of clinical, associated molecular data (multi omics - genomics, transcriptomcis, proteomics, metabolomics, lipidomics, microbiome data), imaging and sensor/mobile data. Interoperability of this heterogeneous data in content and format is another challenge. It involves, mammoth task of data curation, harmonisation and FAIRification (making data Findable, Accessible, Interoperable and Reusable) to facilitate the cross study analysis. Application of statistical and Machine Learning (ML) methods to analyse multi-layered data to stratify the patients into different subgroups based on disease severity and progression and identification of biomarkers representing each subgroup. In addition, application of central and federated knowledge management methods, disease maps, to discover the mechanistic models and co-morbidities of these complex diseases.

## AI-Enabled Mouse Genetic Discovery

**Gary Peltz [1]**
1. Stanford University School Of Medicine

E-mail of the presenting author: gpeltz@stanford.edu

We have comprehensively characterized SNPs, structural variants, tandem repeats and epigenomic variation in the genomes of 39 inbred mouse strains. AI-based methods were used to characterize the genetic basis for mouse models of human disease-related traits, several of which were described 40 or more years ago. The AI methods used for analysis of mouse models were also used to identify the genetic basis for diseases appearing in human patients.

## SESSION 5 - MODELS TO UNDERSTAND GENE FUNCTION AS A BASE FOR THERAPY DEVELOPMENT

### Friday, 12th September 2025 (9:00 – 11:00)

**9:00 – 9:30**
Gopal Sapkota, University of Dundee, United Kingdom
"FAM83G/SACK1G Mutations Disrupt CK1α Interaction and WNT Signalling in Palmoplantar Keratoderma"

**9:30 – 10:00**
Jana Balounova, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic
"FAM83H/SACK1H shapes thymic stromal architecture and postnatal lymphopoiesis via CK1 interaction"

**10:00 – 10:30**
Samuele Ferrari, San Raffaele Telethon Institute for Gene Therapy, Italy
"Poisoning of healthy hematopoiesis drives clonal dominance in VEXAS syndrome"

**10:30 – 11:00**
Yonghwan Kim, Sookmyung Women's University, Republic of Korea
"A rare variant allele of BMPR2 predisposes to the onset of a novel subtype of congenital heterotopic ossification"

## FAM83G/SACK1G Mutations Disrupt CK1 Interaction and WNT Signalling in Palmoplantar Keratoderma

**Sapkota G. [1]**
1. University Of Dundee

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Palmoplantar keratoderma (PPK) is a rare, multifaceted skin disorder characterized by epidermal thickening, painful abrasions on the palms and soles, and abnormal hair morphology. Recent studies, including our own, have identified biallelic pathogenic variants in the FAM83G (also known as SACK1G) gene associated with PPK in both humans and dogs. FAM83G/SACK1G is a member of the poorly characterized FAM83 protein family consisting of eight members (A–H), which we have shown regulate the subcellular localization and substrate specificity of CK1 family of Ser/Thr kinases via their conserved Scaffold Anchor of CK1 (SACK1) domain. We previously demonstrated that FAM83G/SACK1 activates WNT signalling through interaction with CK1α. Strikingly, all known PPK-associated FAM83G/SACK1G variants (A34E, R52P, and R265P) are unable to bind CK1α and consequently fail to activate WNT signalling. Consistent with this, patient-derived cells harbouring the R265P variant show impaired FAM83G–CK1α interaction and diminished WNT signalling. These findings suggest that loss of CK1α recruitment by mutant FAM83G/SACK1G and the resulting attenuation of WNT signalling underlie the molecular pathogenesis of PPK.

## FAM83H/SACK1H shapes thymic stromal architecture and postnatal lymphopoiesis via CK1 interaction

**Jana Balounová [1]**

1. Czech Centre for Phenogenomics, Institute of Molecular Genetics of CAS, Czech Republic

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Family of Sequence Similarity 83H (FAM83H/ SACK1H) is primarily expressed in epithelial cells, where it associates with CK1 and keratins to regulate cytoskeletal organization, cell proliferation, and vesicular trafficking.

To investigate the role of FAM83H in immune system homeostasis, we generated two mouse models: Fam83h-deficient mice (Fam83hem2(IMPC)Ccpcz, Fam83h-/-), and mice lacking a part of the N-terminal CK1-binding domain (Fam83hΔ87/Δ87). Both strains exhibit nearly identical phenotypes, underscoring the essential role of the CK1-binding domain in FAM83H function.

Consistent with other Fam83h-deficient models, these mice are subviable, smaller in size, and display a sparse, scruffy coat, scaly skin, weakness, and hypoactivity. Importantly, both strains exhibit impaired lymphoid cell production during early postnatal development. While fetal hematopoiesis remains intact, B cell and NK cell development in the bone marrow is partially blocked at the pro- and pre-B cell stages and the immature NK cell stage in the absence of FAM83H. In the thymus, Fam83h is expressed by thymic epithelial cells (TECs), and its deficiency in stromal cells results in a severe impairment of DN3 T cell expansion, ultimately leading to insufficient T cell production.

Fam83h-deficient cortical TECs (cTECs) show elevated expression of circadian rhythm genes and reduced expression of the TEC master regulator Foxn1, along with its multiple downstream targets. This suggests a role for FAM83H and CK1 in cTEC maturation.

In summary, FAM83H, together with CK1, is essential for organizing the keratin cytoskeleton in thymic epithelial cells, thereby maintaining thymic stromal architecture and supporting normal T cell development.

## Poisoning of healthy hematopoiesis drives clonal dominance in VEXAS syndrome

**Ferrari S [1,2]**, Molteni R1 [2], Fiumara M [1], Campochiaro C [1,2], Alfieri R [3], Cenci S [1,2], Cavalli G [1], Naldini L [1,2]
1. IRCCS Ospedale San Raffaele
2. Vita-Salute San Raffaele University
3. National Research Council

Clonal dominance characterizes hematopoiesis during aging and increases susceptibility to blood cancers and common non-malignant disorders. VEXAS syndrome is a recently discovered adult-onset autoinflammatory disease burdened by a high mortality rate and caused by dominant hematopoietic clones bearing somatic mutations in the UBA1 gene. However, pathogenic mechanisms driving clonal dominance are unknown. Moreover, the lack of disease models hampers the development of disease-modifying therapies. Here, we performed immunophenotypic characterization of hematopoiesis and single-cell transcriptomics in a cohort of 9 male patients with VEXAS syndrome, revealing pervasive inflammation across all lineages. Hematopoietic stem/progenitor cells (HSPCs) in patients are skewed toward myelopoiesis and acquire senescence-like programs. Humanized models of VEXAS syndrome, generated by inserting the causative mutation in healthy HSPCs through base editing, recapitulated proteostatic defects, cytologic alterations, and senescence signatures of patients' cells, as well as disease hematologic and inflammatory hallmarks. Competitive transplants of human UBA1-mutant and wild-type HSPCs showed that while mutant cells are more resilient to the inflammatory milieu, likely through the acquisition of the senescence-like state, wild-type ones are progressively exhausted and overwhelmed by VEXAS clones, overall impairing functional hematopoiesis and leading to bone marrow failure. Our study unveils the mechanism of clonal dominance, provides models for preclinical investigation of therapeutic strategies, and might have implications for clinical management of VEXAS syndrome.

## A Rare Variant Allele of BMPR2 Predisposes to the Onset of a Novel Subtype of Congenital Heterotopic Ossification

Myung-Jin Kim [1], Tae-Joon Cho [2,3] and **Yonghwan Kim [1]**

1. Department of Biological Sciences & Research Institute of Women's Health, College of Natural Sciences, Sookmyung Women's University, Seoul 04310, Republic of Korea.
2. Division of Pediatric Orthopaedics, Seoul National University Children's Hospital, Seoul 03080, Republic of Korea.
3. Department of Orthopaedic Surgery, Seoul National University College of Medicine, Seoul 03080, Republic of Korea.

Heterotopic ossification, a pathological condition whereby soft tissues transform into skeletal bones, is rare but debilitating disease without any effective treatment. Mutations in ACVR1 or GNAS have been implicated in congenital heterotopic ossification, however, cellular and molecular mechanisms underlying the pathophysiology of heterotopic ossification have not been fully elucidated. Here we report that BMPR2 is a previously unidentified genetic contributor of the congenital heterotopic ossification. We show that a rare gain of function mutation in BMPR2 (c.1126G>A, p.E376K) leads to congenital heterotopic ossification. The pathological features of The BMPR2E376K appear to be reminiscent of previously reported fibrodysplasia ossificans progressiva (FOP), yet manifest a number of distinct hallmarks, including lack of stereotypic malformation of the big toes. The BMPR2E376K appears to function as a neomorph, which displays exaggerated responses toward Activin A stimulation by selectively interacting with ACVR1, supporting the idea that dysregulation of ACVR1-mediated Activin A signaling may serve as a critical contributing factor for heterotopic ossification. Taken together, our data illustrate the complex molecular features underlying the pathophysiology of heterotopic ossification, and highlight the importance of BMPR2 as a nexus for ACVR1 and Activin A interaction. Moreover, our findings provide a theoretical framework for developing a novel therapeutic option for heterotopic ossification.

## SESSION 6 – SHORT PRESENTATIONS: SELECTED POSTER PRESENTATIONS & TECHNOLOGY TALKS

### Friday, 12th September 2025 (11:35 – 12:35)

### FLASH ORAL PRESENTATIONS:

**11:35 – 11:45**
Tanja Sorg, PHENOMIN – ICS, France
“Deciphering the consequences of CLCN4 mutations in rat models for a better understanding of the rare X-linked CLCN4-related neurodevelopmental condition”

**11:45 – 11:55**
Alice Foltýnová, Institute of Experimental Medicine of CAS, Czech Republic
“Reprogramming of glial cells into interneurons using synthetic mRNA”

**11:55 – 12:05**
Chao-Kuen Lai, Academia Sinica, Taiwan
„The Taiwan Mouse Clinic: the first user-friendly platform for high-quality, high-throughput, comprehensive phenotyping and drug testing of mouse models in Asia“

## Deciphering the consequences of CLCN4 mutations in rat models for a better understanding of the rare X-linked CLCN4–related neurodevelopmental condition

**Sorg T [1,2]**, Birling M [1,2], Prevost G [1,2], Riet F [1,2], Hérault Y [1,2]
1. PHENOMIN – ICS
2. Université de Strasbourg, CNRS, INSERM, CELPHEDIA

CLCN4-related neurodevelopmental condition (CLCN4-NDC) is a rare X-linked condition caused by inherited or de novo pathogenic variants of the CLCN4 gene, affecting both sexes and being associated with intellectual disability, epilepsy, gastrointestinal issues, movement and behavioural disorders.

CLCN4 encodes the CIC-4 protein, a 2Cl–/H+ exchanger present in various tissues, more highly expressed in brain and skeletal tissue. The function of CIC-4 is not yet well understood, and how CLCN4 pathogenic variants lead to the observed clinical symptoms remains unclear. The medical needs of CLCN4-NDC patients remain largely unmet with only supportive multidisciplinary therapies available. Thus, there is a need to better understand the pathophysiology of CLCN4-NDC by using an appropriate animal model. Given that the rat Clcn4 gene is on the X chromosome like in humans, in opposite to the mouse, we generated a rat Clcn4 LOF “KO” line and a “KI” line harbouring the A549V GOF variant. We then generated the experimental cohorts of animals to evaluate the suitability of these rat lines as animal models for CLCN4-NDC. We carried out a detailed phenotypic characterisation of CIC-4 LOF and GOF hemizygous males and heterozygous females using a test battery covering learning and memory, coordination, locomotor activity, neuromuscular function, compulsive behavior, anxiety, depression, blood analysis, proteomics and histological analysis of relevant organs. We could show that Clcn4 GOF males display behavioural and neurological phenotypes, while heterozygous females show only a few mild phenotypes. In contrast, Clcn4 LOF rats no not display any phenotype.

Overall, this project will enable us to evaluate how well the rat model fits with the clinical spectrum of CLCN4-NDC in a LOF or GOF context and determine its usability for future research on the CLCN4-NDC pathophysiology and potential therapeutic developments.

## Reprogramming of glial cells into interneurons using synthetic mRNA

**Foltýnová A [1,3]**, Koblas T [2], Knotek T [1,3], Kriška J [1], Turečková J [1], Janečková L [4], Vaňátko O [1,3], Anděrová M [1]
1. Institute Of Experimental Medicine
2. Institute for Clinical and Experimental Medicine
3. Second Faculty of Medicine, Charles University
4. Institute of Molecular Genetics

Parvalbumin GABAergic interneurons are important players in stabilizing neuronal networks as they prevent excessive neuronal firing. They are vital for cognitive processes, such as learning and memory and their loss is associated with neurological disorders, including epilepsy, Alzheimer's disease, and schizophrenia. Given the extremely limited neurogenesis in the adult human brain, neuronal reprogramming has emerged as a promising strategy for replenishing neuronal loss. Focusing on reprogramming glial cells in the brain into parvalbumin GABAergic interneurons could partially restore impaired neuronal networks and therefore save other neuronal subtypes which would otherwise not survive. The most common approach in neuronal reprogramming of glial cells is to upregulate pro-neuronal genes using viral vectors, preferentially retroviruses. However, challenges remain regarding the conversion efficacy, neuronal maturity, and slow conversion rates observed in these methods. Recent advancements suggest that synthetic mRNA may enhance the efficiency of neuronal reprogramming by facilitating rapid protein translation upon entry into target cells. Another advantage of using synthetic mRNA is uptake of all used transcription factors by transfected target cells which cannot be guaranteed using viral vectors. To date, no studies have explored the use of synthetic mRNA of Ascl1, Sox2, Dlx5, Lhx6, and FoxG1 to generate PV+ interneurons from glial cells in vitro. Our preliminary findings indicate successful optimization of transfection protocols using syn-mRNA in NG2 glia cultures, and significant upregulation of key GABAergic genes within 24-48 hours post-transfection. This study aims to accelerate the differentiation of PV+ interneurons from NG2 glia and astrocytes, offering innovative therapeutic strategies in neurological disorders.

## The Taiwan Mouse Clinic: the first user-friendly platform for high-quality, high-throughput, comprehensive phenotyping and drug testing of mouse models in Asia

**Lai C [1]**, Fong S [2], Chiang W [1], Yang I [2], Chen Y [1], Liu Y [2], Hung H [1], Chen C [1,2]

1. Taiwan Mouse Clinic-National Comprehensive Phenotyping and Drug Testing Center, Biomedical Translation Research Center, Academia Sinica
2. Institute of Biomedical Sciences, Academia Sinica

The Taiwan Mouse Clinic (TMC) is a specific pathogen-free (SPF) animal facility designed for comprehensive mouse phenotyping and drug testing, as well as specialized customized services in disease model studies and exploratory safety pharmacology. To facilitate user-friendly services, TMC has developed a unique and straightforward Standard Operating Procedure (SOP) for the easy check-in of mice. This SOP allows researchers' SPF mice to be admitted directly into the facility without a quarantine period. In addition, mice are housed in separate individually ventilated cage (IVC) carts or rooms based on user groups, ensuring proper health monitoring and care. This practice has helped TMC maintaining a 17-year record free from twelve specific pathogens. Notably, TMC has developed a highly effective method for “cleaning” mice that circumvents the need for re-derivation through embryo transfer or cesarean hysterectomy. In-depth studies have shown that environmental effects and assay interactions would affect mouse phenotyping. Furthermore, TMC has observed strain-specific phenotypic differences in drug responses. For instance, the open field test demonstrated significantly high activity in C57BL/6J mice, and telemetry ECG indicated the presence of T waves in CD-1 and C57BL/6J strains but not in the C57BL/6N strain. TMC operates under a contract research organization (CRO)-style business model, demonstrating continued user base and revenue growth. The TMC model has become a valuable resource in preclinical research, aiding drug candidate selection within new drug development programs.

## TECHNOLOGIES FOR ANIMAL MODELS:

**12:05 – 12:20**
Jörg Bantin, Bio-Rad
“Digital PCR is a breakthrough technology that provides ultrasensitive and absolute nucleic acid quantification”

**12:20 – 12:35**
Peter Kesa, FUJIFILM VisualSonics
“HF ultrasound and photoacoustic in phenotyping of animal models – from early embryogenesis to aging studies”

**12:35 – 12:50**
Behdad Pouran, Milabs, CANBERRA-PACKARD s. r. o.
“Unraveling the Biology of Rare and Genetic Diseases with Multi-modal Preclinical Imaging“

## Digital PCR is a breakthrough technology that provides ultrasensitive and absolute nucleic acid quantification.

**Bantin J [1]**
1. Bio-rad

Digital PCR is a breakthrough technology that provides ultrasensitive and absolute nucleic acid quantification. This technique is particularly useful for low abundance targets, targets in complex backgrounds, allelic variants (SNPs) and for monitoring of subtle changes in target levels.

In the Droplet Digital™ PCR (ddPCR™) System, each PCR sample is partitioned into a large number of microscopic droplets prior to amplification. Each droplet is an individual PCR reaction. After end-point amplification, fluorescence is detected in the droplets in which target sequence was amplified. These droplets are scored as positive. Droplets not containing the target sequence show little or no fluorescence and are scored as negative. Using the Poisson distribution law, the fraction of positive droplets is converted to the number of molecules in the starting sample, without the need for standard curves (absolute quantification).

Applications for digital PCR cover different areas of biology. The following describes some of the most popular fields of application: : Liquid biopsy, Copy number variation (CNV), Rare sequence detection, Gene expression and miRNA analysis, Single-cell analysis, Contaminant testing in cell and gene therapy and Pathogen detection.

Bio-Rad has more than 14 years experience in digital PCR and there are more than 12.000 peer-reviewed publications featuring droplet digital PCR technology. Furthermore Bio-Rad offers also more than 1895 wet-lab validated assays for target mutations among other applications.

Bio-Rad offers the most comprehensive line of digital PCR products. With the addition of four new instruments, our portfolio sets a new benchmark in providing advanced Droplet Digital PCR (ddPCR) solutions with world-class expertise to support your research.

## SESSION 7 – RARE DISEASES & BOTTOM-UP EFFORTS TO DEVELOP (GENE) THERAPIES

### Friday 12th September 2025 (14:15 – 16:55)

**14:15 – 14:35**
Jakub Sikora, Charles University 1st Medical Faculty, Czech Republic
"Pathogenic variants in EHMT2 as a novel cause of Kleefstra syndrome"

**14:35 – 15:05**
Foundation 1: Charlie project (www.charlie.science)
Research speaker: Caroline Linster, University of Luxembourg, Luxembourg
"New zebrafish models for lysine metabolism disorders"
Foundation representative speaker: Albert Carbonell, Spanish patient association FAMILIA GA1, Spain
"Unmet medical and psychosocial needs in glutaric aciduria type 1 and pyridoxine-dependent epilepsy: insights from an international patient survey"

**15:05 – 15:25**
coffee break

**15:25 – 15:55**
Foundation 2: YWHAG Foundation (www.ywhagfoundation.org)
Scientific speaker: Helen Chen, USA
"Scientific updates from the YWHAG Research Foundation"
Foundation representative speaker: Andrew Miner, YWHAG Foundation, USA
"From Heartbreak to Hope: A Father's Journey Mobilizing Global YWHAG Research"

**15:55 – 16:25**
Foundation 3: A-T Children's Project (www.atcp.org)
Scientific speaker: Timothy W. Yu
"Precision genetic intervention and ´N=1 trials´ for Ataxia Telangiectasia"
Foundation/patient representative speaker: Tomas Pavlicek, ATAP and A-T Dad, Czech Republic
"Global landscape of AT patient organisations"

**16:25 – 16:50**
Discussion with speakers

**16:50 – 17:25**
Steve Murray, The Jackson Laboratory, Maine, USA
"From discovery to treatment: the JAX Center for Precision Genetics"

**17:25 – 17:30**
Radislav Sedlacek, Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Rep.
"Closing remarks"

## Pathogenic variants in EHMT2 as a novel cause of Kleefstra syndrome

**Sikora J [1]**, Nosková L, Hnízda A, Kmoch S
1. First Faculty Of Medicine - Charles University

Kleefstra syndrome (OMIM 610253) is a rare genetically heterogeneous autosomal dominant neurodevelopmental disorder characterized by delayed psychomotor development and mild dysmorphic features.

EHMT1 and EHMT2 genes encode human euchromatin histone lysine methyltransferase 1 (GLP) and 2 (G9a), respectively. GLP and G9a proteins form heteromeric complexes with essential roles in epigenetic regulation of gene expression. While EHMT1 haploinsufficiency was established as the cause of Kleefstra syndrome twenty years ago, the pathogenesis of G9a dysfunction in human disease remains largely unknown.

We report clinical and molecular correlates of six de novo EHMT2 (G9a) variants in an international cohort of patients with clinical presentation, episignatures, histone modifications and transcriptomic profiles similar to those of Kleefstra syndrome. In contrast to GLP Kleefstra syndrome-causing mutants, these G9a variants encode for structurally stable proteins that are catalytically incompetent due to aberrant interactions either with histone H3 tail or with S-adenosylmethionine. Moreover, heterozygous mice carrying a patient-derived variant (Ehmt2 c.3385_3396del) exhibited growth retardation, facial/skull dysmorphia and aberrant behavior.

EHMT2 variants described here likely exert dominant-negative effect on GLP/G9a complexes and thus genocopy the EHMT1 haploinsufficiency causing Kleefstra syndrome via a distinct molecular mechanism. Our studies not only established a novel genetic cause of Kleefstra syndrome and therefore allow effective clinical and molecular diagnostics and family counseling, but also set stage to develop and test specific therapies for this rare medical condition.


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## Unmet medical and psychosocial needs in glutaric aciduria type 1 and pyridoxine-dependent epilepsy: insights from an international patient survey

Dekker H [1], van Muilekom M [2,3], Coughlin C [4], van Karnebeek C [5,6], **Carbonell A [7,8]**

1. VKS, The Dutch patient association for Inherited Metabolic Diseases
2. Amsterdam UMC location University of Amsterdam, Emma Children's Hospital, Department of Child and Adolescent Psychiatry & Psychosocial Care
3. Emma Center for Personalized Medicine, Amsterdam UMC
4. Section of Clinical Genetics and Metabolism, Department of Pediatrics, University of Colorado Anschutz Medical Campus
5. Department of Pediatrics, Emma Children's Hospital and Amsterdam. Gastroenterology Endocrinology Metabolism, Amsterdam UMC, University of Amsterdam
6. On behalf of United for Metabolic Diseases
7. Familias GA y PDE, Patient Advocacy Organization
8. Institute of Molecular Biology of Barcelona, IBMB-CSIC

**Background**: Glutaric Aciduria Type 1 (GA1) and Pyridoxine-Dependent Epilepsy (PDE-ALDH7A1) are rare neurometabolic disorders caused by enzymatic deficiencies in the lysine catabolic pathway. Early diagnosis and management are critical to preventing severe neurological outcomes. However, significant knowledge gaps exist, making disease management challenging for physicians, patients, and caregivers. This study, conducted by the CHARLIE consortium, aimed to identify the unmet medical and psychosocial needs of patients and caregivers to improve their quality of life. It also sought to identify key patient priorities to guide future therapeutic research.

**Methods**: An online survey with 70 questions was distributed to GA1 and PDE-ALDH7A1 patients and caregivers. Responses were analysed using descriptive statistics in SPSS and thematic analysis in MAXQDA for open-ended questions.

**Results**: A total of 129 respondents from 17 countries completed the survey. Patient and caregiver needs extended beyond medical aspects, affecting all areas of life and highlighting disease complexity. Psychological support was a major unmet need, with 74% of respondents lacking access despite recognizing its importance. Additionally, 54% had not been referred to patient organizations, limiting community support. Another key challenge identified was difficulty in accessing specialized healthcare services. Dietary adherence in PDE-ALDH7A1 was low (48%), while GA1 adherence was generally higher, though outdated protocols were still followed. In PDE-ALDH7A1, 76% of respondents emphasized that the absence of newborn screening caused diagnostic delays and suboptimal early treatment. Regarding future treatments, 74% preferred single-dose over maintenance therapies, indicating that the burden of long-term treatment impacts decision-making. Furthermore, 74% expressed willingness to participate in clinical trials, underscoring the demand for innovative therapies addressing both disease outcomes and long-term management challenges.

**Conclusion**: This study provides real-world evidence of the complex psychosocial and clinical challenges faced by patients and caregivers. Findings highlight key areas for improvement, including early diagnosis, specialized medical care, psychosocial support, and day-to-day disease management. The results emphasize the urgent need to develop better therapies that enhance quality of life of GA1 and PDE-ALDH7A1 patients and caregivers.

## Scientific updates from the YWHAG Research Foundation

**Chen H [1]**
1. YWHAG Research Foundation

De novo pathogenic variants or deletions of the YWHAG leads to DEE-56 (OMIM 617665), presented as early-onset seizures, intellectual disability (ID), motor deficit, autism spectrum disorders (ASD) and global developmental delays. The YWHAG gene encodes for tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma isoform, a member of the 14-3-3 protein family. 14-3-3 proteins form homo-and hetero-dimers to bind to phosphorylated sites on target proteins, influencing protein activity, stability and localization to facilitate signal transduction. While YWHAG plays a vital role in neurodevelopment and neuronal homeostasis, we do not know why pathogenic variants of YWHAG result in DEE-56. Better understanding of how YWHAG pathogenic variants result in cellular defects and neurodevelopment will allow us to formulate disease-modifying precision therapies.

The YWHAG Research Foundation was founded in 2023 with the goal of raising awareness, accelerating research and finding a cure for patients. To date, we have established multiple research projects with partners across academia, industry and other non-profit foundations. 1) Dr. David Bearden, M.D. (University of Rochester, New York, USA) is conducting a two-year long natural history study to better understand disease progression in patients with YWHAG-associated DEE. 2) Dr. Joao Pereira, Ph.D. (University of Alabama, Birmingham, USA) is investigating and correcting the neuronal mechanisms underlying YWHAG pathology. Specifically, the Pereira lab generated cortical neurons from induced pluripotent stem cells (iPSC) to measure neuronal hyperexcitability to model seizure phenotypes as observed in patients. 3) Dr. Laura Civiero, Ph.D. (University of Padova, Padua, Italy) is investigating how the R132C variant impacts the interaction between YWHAG and potential binding partners, and how perturbation of this interaction can result in epilepsy. 4) Dr. Kazuhito Toyooka, Ph.D. (Drexel University College of Medicine, Philadelphia, USA) and Dr. Yi Zhou (Florida State University, Tallahassee, USA) are in collaboration to better understand the role of YWHAG during early stage of development, specifically neuronal migration and morphology.

Lastly, we are in partnership with the Rare Disease Translational Center at the Jackson Laboratory and the Czech Center for Phenogenomics to generate and characterize a novel Ywhag  mouse model for our research community.

## From Heartbreak to Hope: A Father's Journey Mobilizing Global YWHAG Research

**Miner A [1]**
1. Ywhag Research Foundation

As a father, there a few times that are forever engrained in your memory, unfortunately for us it was when James five-and-a-half months old, suddenly he became pail, went rigid, and slipped into a wordless seizure. In those seconds the room closed in, the clock froze, and all I could do was beg him to take a breath. Eighteen months of E.R. and doctor visits, countless tests, and sleepless nights later, a single line of text from genetic testing finally named our fear: an ultra-rare YWHAG mutation. At the time of the diagnosis, the mutation was discovered just a few years prior with no real information known and no active research being done. The gravity of the situation began to sink in for our family: no treatments, no clinical trials, and no hope. Just the cold comfort of "It is what it is."
My wife and I refused to accept a future defined by that phrase. We built the YWHAG Foundation out of equal parts determination and stubborn hope. Never again did we want another family to have to face this diagnosis alone or without a path forward. In two short years we have:

- Global Community Engagement: Through the foundation, more than 40 families in more than a dozen countries now share stories, de-identified data, and encouragement in a private Facebook group and regular Zoom meetups. This laid the groundwork for the first YWHAG natural history study and a global patient registry.
- Quickly developed research assets: In the first few months of the foundation forming iPSC lines were made available and shared with labs across the USA. Following a successful grant application, a partnership with Jackson Labs was also formed and the first of its kind YWHAG mouse model was started in early 2025 with expected completion in the coming months.
- Rallied experts who see our kids first, publications second: Neurologists, geneticists, and research partners meet regularly to discuss grant opportunities and collaboration efforts all while moving swiftly to push for experiments with real potential to help our kids.
- Ever Expanding Website and Resource Hub: Our Foundation's website is continually updated with plain-language research, new resources, and actionable how-tos. We are constantly striving to empower families and clinicians worldwide to stay informed and engaged.

Early research findings are providing valuable insight and hope that targeted interventions are within reach. Yet progress hinges on collaboration: our foundation provides patient access, biologic tools, and an energized advocacy network; we seek partners with complementary expertise in structural biology, RNA therapeutics, and precision epilepsy trials.

James's first seizure stole one peaceful morning; it also ignited a movement. By presenting this work, I aim to bridge the lived experience of caregivers with the rigor of academia, spurring a collective effort toward the first disease-modifying therapy for the YWHAG mutation. Together, we can convert rare into understood and ultimately, into treatable.

## SESSION 8 – CLOSING

### Friday, 12th September 2025 (16:55 – 17:00)

**16:55 – 17:00**
Radislav Sedlacek, Czech Centre for Phenogenomics Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic
“Closing remarks”



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## A) POSTER SESSION

**Poster session 1 (on-site) - Thursday 11th**
10:50 -11:15
13:00 -14:30
15:50 – 16:10

**Poster session 2 (on-site) –Friday 12th**
11:15 – 11:35
12:50 – 14:15
15:05 – 15:25

**A) Research poster presentations**

(PO-1) **Federica Gambini:** New mouse model for inducible hACE2 expression enables to dissect SARS-CoV-2 pathology beyond the respiratory system

(PO-2) **Michaela Prochazkova:** Insig1, a regulator of lipid metabolism, impacts ciliogenesis and brain development

(PO-3) **František Špoutil:** Preclinical in-vivo imaging at CCP

(PO-4) **Dominik Arbon:** Biosafety Level 3 facility for Preclinical Testing and Efficacy Studies of antivirals against infectious pathogens

(PO-5) **Michaela Šímová:** Mapping Yolk Sac-Derived Hematopoietic Lineages: A Hemato-Endothelial Perspective

(PO-6) **Marcel Bochin:** ICV Intracerebroventricular infusion in mice

(PO-7) **Miles Joseph Raishbrook:** The significance of Lratd2 in retinal homeostasis

(PO-8) **Volodymyr Porokh:** Mouse models as tools to study possible genetic causes of infertility

(PO-9) **Jana Boháčová:** Automated Differentiation of Tumor and Healthy Tissue Using Spectral X-ray Imaging and Artificial Intelligence

(PO-10) **Simon Trcka:** Intellicage data analysis pipeline

(PO-11) **Alena Kadukova:** Cognitive Impairment in the Remote Period after Fractionated Irradiation of the Mice Head

(PO-12) **Rodolfo Favero:** SPINK5/LEKTI IS A CRITICAL MEDIATOR OF EPITHELIAL INTEGRITY: IMPLICATIONS FOR NETHERTON SYNDROME

(PO-13) **Lukas Kucera:** 15N Ammonia tracing with MALDI-FTICR imaging in regenerating liver – re-directing of toxic product into de novo pyrimidine synthesis and cell proliferation

## (PO–01) New mouse model for inducible hACE2 expression enables to dissect SARS-CoV–2 pathology beyond the respiratory system

**Gambini F [1]**, Arbon D [2], Nickl P [2], Zatecka V [2], FEDOSIEIEVA O [2], Labaj J [2], Novosadova V [2], Tryl'cová J [3], Weber J [3], Procházka J [1,2], Balounová J [2], Sedláček R [1,2]

1. Institute of Molecular Genetics, Czech Academy of Sciences, Laboratory of Transgenic Models of Diseases
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Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) infection, primarily affecting the respiratory tract, is also recognized for impacting multiple organ systems. This broad effect is due to the expression of angiotensin-converting enzyme 2 (ACE2), the primary receptor for SARS-CoV-2, which is present in various tissues. Understanding how the virus affects these systems is essential for developing therapeutic strategies. In this study, we used a conditional mouse model, Rosa26creERT2/chACE2, which enables the expression of human ACE2 (hACE2) across several organs, allowing us to investigate the multisystemic effects of SARS-CoV-2 infection. Our findings show that Rosa26creERT2/chACE2 mice are susceptible to SARS-CoV-2 infection in a dose- and sex-dependent manner. Notably, male mice exhibited more severe disease outcomes, including significant weight loss, severe lung pathology, and impaired pulmonary function, with higher mortality rates compared to females. These results suggest that sex differences may modulate disease severity, underscoring the importance of considering these factors in studies. We also compared two routes of viral inoculation: intratracheal and intranasal administration. While intratracheal infection mainly affects the lungs, intranasal inoculation allowed viral spread to the brain, highlighting the role of the nasal route in neurological manifestations. This route also led to increased activation of the innate immune system, although both routes triggered a robust adaptive immune response. This suggests that the route of infection influences immune system activation and shapes disease outcomes. Our study emphasizes the importance of a multisystemic approach to understanding SARS-CoV-2 infection. The Rosa26creERT2/chACE2 model is a valuable tool for examining the impact of the virus across multiple organs and has potential for preclinical evaluation of antiviral therapies and vaccines, providing deeper insights into viral mechanisms and targeted interventions.

## (PO–02) Insig1, a regulator of lipid metabolism, impacts ciliogenesis and brain development

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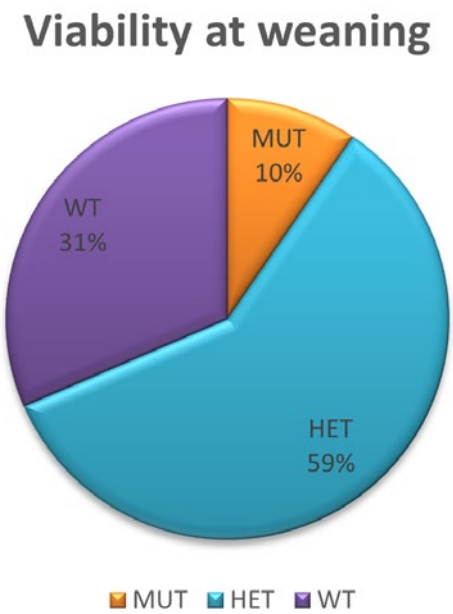
INSIG1 (Insulin Induced Gene 1) is classically known as a feedback regulator of lipid and cholesterol biosynthesis, predominantly studied in hepatic contexts. However, its function beyond metabolic regulation remains poorly understood. Here, we uncover a novel role for Insig1 in brain development, with direct implications for ciliogenesis.

We show that Insig1 is strongly expressed in the embryonic central nervous system (CNS), contrasting with its limited postnatal expression profile. Insig1 knockout (KO) mice are subviable, with fewer weaned pups than expected from Mendelian ratios. Prenatal assessment at E18.5 reveals a subset of KO embryos with hydrocephalus, growth retardation, and cardiac malformations.
Histological and cellular analyses reveal defects in primary cilia architecture in the embryonic brain and in cultured Insig1 KO MEFs. Within the developing brain, Insig1 is highly expressed in multiple regions, including specific populations of the choroid plexus (ChP), a specialized ciliated epithelium responsible for cerebrospinal fluid production.In mutants, ChP morphology is disrupted, providing a likely basis for hydrocephalus.

These findings point to an unexpected developmental function of Insig1 in cilia formation and CNS morphogenesis, likely mediated through membrane and lipid-related mechanisms. Our work extends the relevance of lipid metabolic regulators into the domain of neurodevelopmental biology.



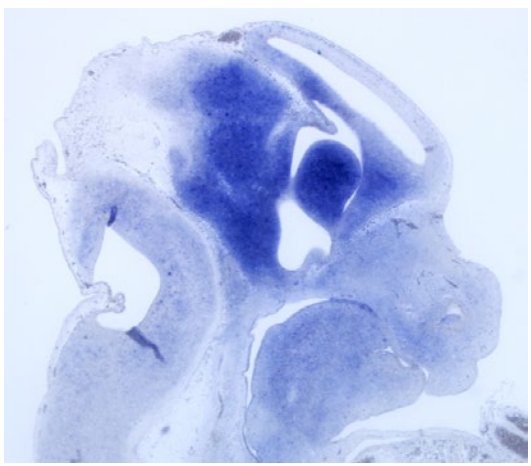



Image1: Subviability of Insig1 KO mice at weaining
Image2: Insig1 expression in brain at E12.5

## (PO–03) Preclinical in-vivo imaging at CCP

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The Czech Centre for Phenogenomics offers broad portfolio of standardized assays useful for preclinical studies on rodents. Our experiences enable us to run very comprehensive experiment and thus answer key questions for drug development. Furthermore, participating in the services of the Centre for Preclinical Testing we can offer usual preclinical tests in GLP mode. In-vivo imaging is a crucial part of the analysis, as we can visualize the structure of our interest and observe changes over time. There four main areas of our expertise are: vision, echocardiography, cancerogenesis, and skeletal development.

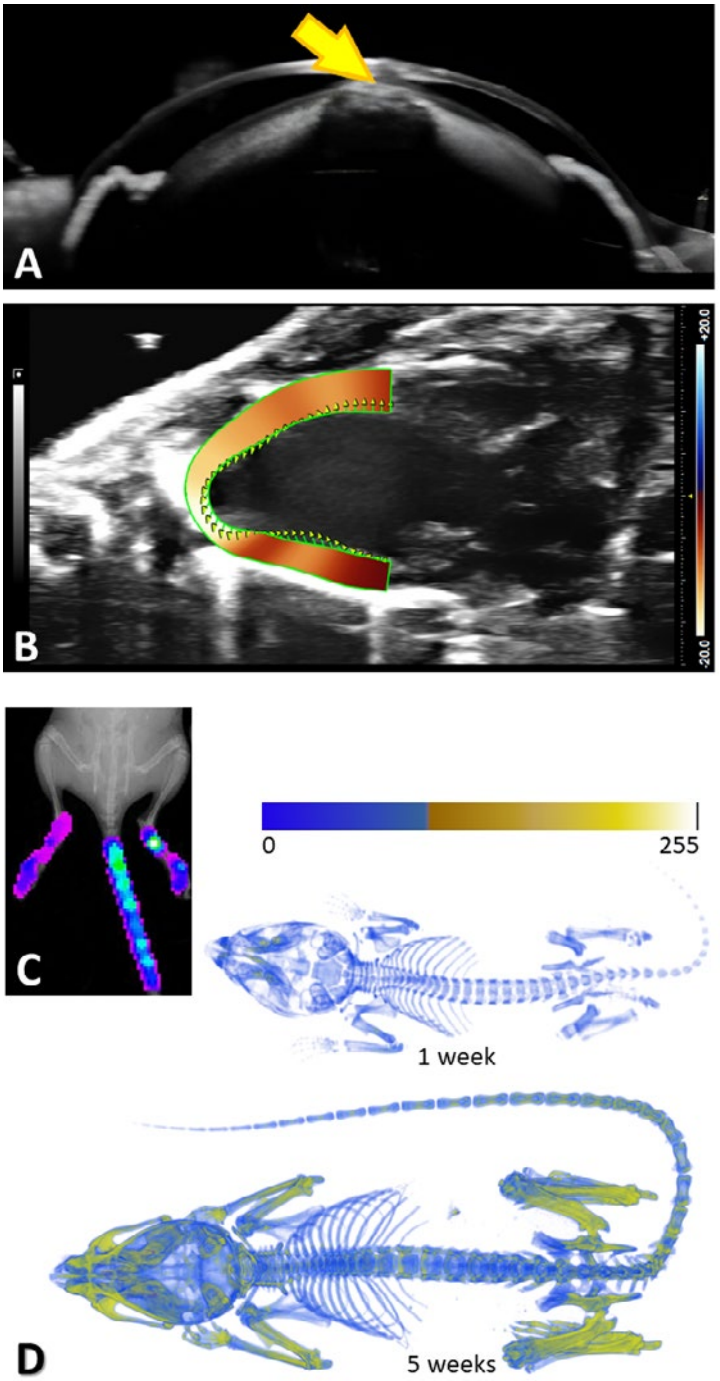
For vision, Pentacam high-resolution imaging device based on Scheimpflug photography is used to image and examine anterior eye segment. With optical coherence tomography, we are able to examine retina and its blood vessels. AngioTool software enables to quantify blood vessels.

The Vevo F2 Lazr-X High-Frequency Ultrasound Imaging System with photoacoustics (Fujifilm) is primarily used for echocardiography. It enables the observation of wall thickness, visualization of vessel wall movement, and detection of vascular pathologies. The system allows assessment of blood flow too. It is suitable for various applications including general imaging, neurobiology, oncology, developmental studies, image-guided injections, ischemia assessment, and biomarker and molecular imaging. We are able to apply these techniques also on mice fetuses in-situ.

Whole body fluorescence and bioluminescence detection compared with 2D X-ray images of mice are the main tool for observation of tumor progression and invasivity. With sensitive detectors of Lago X (Bruker) small metastasis can be detected and measured exactly. The system can be used also for detection of inflammation.

The main focus of our microCT systems (MILabs U-CTUHR and Bruker SkyScan 1278) is to detect changes in skeletal development and mineralization in high resolution (up to 4 µm/vx), which is already suitable e.g. for arthrosis or tooth enamel. MicroCT can be used as additional modality e.g. for metabolomics to localize fat deposition, for cancerogenesis by usage of contrast agents implied to blood stream, or for changes in lung functionality in lung fibrosis model. Optical Imaging ad-on unit of MILabs U-CTUHR can be used as back-up for the Lago X system.

Figure:
OPT (A): corneolenticular fusion (yellow arrow). Echocardiography (B): heart ventricle with EKV. Bioluminescence
(C): inflammation in tail and paws over 2D X-ray. MicroCT of mouse skeleton
(D): blue – yellow shift corresponds to changes in mineralization; 50 µm/vx resolution.



## (PO–04) Mapping Yolk Sac-Derived Hematopoietic Lineages: A Hemato-Endothelial Perspective

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During embryogenesis, blood cell production is sustained by three independent hematopoietic waves. The first two originate in the yolk sac (YS), while the third arises intra-embryonically and is driven by hematopoietic stem cells (HSCs), which later establish lifelong hematopoiesis. However, HSCs are dispensable prenatally, highlighting the importance of YS-derived progenitors for early development and potential prenatal therapies.

Our study aims to map YS-derived hematopoietic lineages, investigate their origins, and assess their contribution to myeloid cell production. Using single-cell RNA sequencing (scRNA-Seq), we identified a common hemato-endothelial ancestor for YS-derived waves. We show that the first wave generates cells with megakaryocyte-erythrocyte (MkE) potential, while the second wave, driven by erythro-myeloid progenitors (EMPs), gives rise to both MkE progenitors and the first myeloid cells. To further characterize EMP-derived blood production, we identified differentially expressed genes and searched for potential surface marker candidates. Notably, we found complement receptor CD88 to be a marker of the early EMP subset, which could enhance flow cytometry-based identification. Additionally, we are developing a novel lineage-tracing model to distinguish between hematopoietic waves across different niches.
Our findings suggest that YS-derived waves share a hemato-endothelial ancestor and that EMPs are responsible for the first myeloid cells in embryogenesis. Ongoing in vivo validation of this model will provide deeper insights into early hematopoietic development and its clinical implications.

## (PO–05) ICV Intracerebroventricular infusion in mice

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Intracerebroventricular (ICV) administration is a widely employed technique in preclinical neuroscience research that enables direct access to the central nervous system (CNS) by delivering substances into the cerebrospinal fluid (CSF) within the brain ventricles. In mouse models, this approach has become indispensable for studying disease mechanisms, testing novel therapies, and overcoming the significant challenge posed by the blood–brain barrier (BBB) which restricts the passage of most large or hydrophilic molecules. ICV administration bypasses this limitation, allowing precise and localized delivery of compounds to the brain parenchyma. Applications of ICV delivery are diverse and span several areas of neuroscience and translational medicine. One major use is the evaluation of molecules that poorly cross the BBB, such as neuropeptides, proteins, antisense oligonucleotides, and viral vectors.

In neurodegenerative or diabetes disease models, ICV injection of amyloid-β peptides or streptozotocin is employed to mimic pathological hallmarks. ICV delivery of adeno-associated virus (AAV) vectors enables widespread gene transfer within the brain, supporting the development of gene therapies for conditions such as spinal muscular atrophy and mucopolysaccharidoses.

Beyond molecular interventions, ICV injection has also been adapted for the delivery of living cells, including neural progenitor cells and engineered stem cells. These cells may migrate from the ventricular system into the brain parenchyma, secrete trophic factors, or provide enzyme replacement in models of metabolic and neurodegenerative diseases. Although cell survival and integration remain challenging, such strategies highlight the potential of ICV routes for regenerative medicine.

Pharmacokinetic and pharmacodynamic studies also benefit from ICV administration, as direct access to the CSF permits controlled dosing, sampling, and monitoring of drug distribution. Coupled with techniques such as stereotaxic surgery and chronic infusion using osmotic pumps, ICV allows both acute and long-term experimental designs. Nevertheless, the technique has inherent limitations: it is invasive, technically demanding, and associated with risks such as infection, tissue damage, and variability in drug distribution within the ventricles. Moreover, translation to clinical use requires careful consideration, as systemic or less invasive delivery routes are typically preferred in human patients unless direct CNS access is essential.

In summary, ICV administration in mouse brain research represents a powerful and versatile tool for probing CNS function, modeling disease, and testing innovative therapeutic strategies. It continues to play an important role in bridging basic neuroscience and clinical application. Its capacity to bypass the BBB, deliver a wide range of therapeutic agents, and enable mechanistic studies underscores its importance in the ongoing development of treatments for neurological disorders.

During autumn 2024 we established ICV application technique using software-controlled Neurostar Stereotaxic Device. Since then, the technique has been effectively used in a number of preclinical studies for pharmacodynamic and toxicity assessment of cellular or genetic therapies for rare diseases, including work conducted in accordance with the stringent GLP mode rules. Recently, we added also the ICV application method using a permanently implanted cannula, which is utilized for repeated delivery. The Czech Centre for Phenogenomics currently routinely employs these methods, which we provide to the scientific community as a standard service.

## (PO–06) The significance of Lratd2 in retinal homeostasis

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Lratd2 is an incompletely characterised protein. Despite reports associating its overexpression with breast, oesophageal and prostate cancer, its function is still unclear. The first LRATD2 knockout mouse line was developed at CCP using CRISPR/Cas9 to create an indel in exon 2.

LRATD2-/- mice display a degenerative retinal phenotype that becomes more severe with age. This phenotype, which bears similarities to the human retinal disease age-related macular degeneration, has been extensively characterised in our lab. LRATD2-/- mice show thinner and more disorganised retinal morphology from 12 weeks of age, as well as reducing electrical responses to light. Transmission electron microscopy revealed a presence of membrane-filled vacuole-like structures and a loss of basal infoldings in the retinal pigmented epithelial cells (RPE) of LRATD2-/- retinas, in addition to drusen-like deposits at the RPE-Bruch's membrane boundary.

We show evidence of a decreased rate of autophagic processes and reduced lysosomal activity following autophagy induction in RPE cells lacking the Lratd2 protein. We hypothesise that reduced autophagy and lysosomal efficiency results in the retinal phenotype shown in LRATD2-/- retinas.

## (PO–07) Mouse models as tools to study possible genetic causes of infertility

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Infertility represents a significant clinical challenge, with genetic factors contributing to its etiology in many cases. However, the mechanisms linking specific gene mutations to impaired reproductive outcomes remain poorly defined. In this study, conducted in collaboration with the Czech Centre for Phenogenomics, we investigated the reproductive consequences of mutations in two candidate genes, Uox and Coa6, previously associated with early embryonic lethality in transgenic mouse models.

From an initial panel of 18 candidates, heterozygous females for Uox (het Uox) and Coa6 (het Coa6) were selected based on availability and experimental feasibility. Breeding experiments demonstrated that both het Uox and het Coa6 females produced significantly fewer offspring compared to wild-type (WT) controls, confirming a reduction in reproductive capacity.

To explore the underlying causes, we performed histological analyses of ovarian sections. Both het Uox and het Coa6 ovaries displayed a reduced number of primary and secondary follicles, with the decrease in primary follicles reaching statistical significance. These findings point to defects in germ cell formation or early oogenesis as the likely origin of reduced fertility. Importantly, later stages of follicle development (antral and preovulatory) were still present, indicating that folliculogenesis was not completely blocked.

To determine whether oocyte meiotic maturation was affected, we carried out time-lapse imaging of isolated oocytes. Key parameters, including timing of germinal vesicle breakdown (GVBD), anaphase onset, and extrusion of the first polar body, were evaluated.

Finally, we explored whether RNA knockdown could serve as a rapid and versatile approach to model gene loss of function in oocytes. Our goal was to establish a workflow using the RfxCas13d system to selectively degrade maternal transcripts, thereby mimicking the functional consequences of gene disruption. Since oocyte development and early embryogenesis depend heavily on maternally stored mRNAs, targeted transcript depletion has the potential to reproduce phenotypes otherwise obtained only through genome editing. This strategy offers several advantages: it is faster, less resource-intensive, and can be applied as a screening step to identify which candidate genes warrant the effort of generating stable transgenic lines—a process that is both time-consuming and sometimes unfeasible when essential genes are involved. In proof-of-concept experiments, transient inhibition of Uox in WT oocytes did not alter meiotic maturation dynamics compared to controls, consistent with findings in het Uox. Importantly, in the case of Coa6, we observed a similar trend between het Coa6 oocytes and those subjected to Cas13d-mediated knockdown, further supporting the utility of this approach. These results validate Cas13d-based transcript knockdown as a complementary tool for functional studies in reproductive genetics.

In summary, our findings demonstrate that reduced reproductive capacity in het Uox and het Coa6 females is primarily attributable to impaired formation of primary follicles, while meiotic maturation of established oocytes remains intact. Moreover, we introduce an RNA-targeting workflow that can accelerate the functional screening of candidate genes in fertility research and guide decisions about investment into genome editing.

## (PO–08) Automated Differentiation of Tumor and Healthy Tissue Using Spectral X-ray Imaging and Artificial Intelligence

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The diagnosis of lesions on mammographic images is considered a difficult task due to the variable sizes and shapes of lesions, problematic boundary definition, and the presence of extremely small lesions that are hard to detect. Standard mammography, based on differences in X-ray absorption of breast tissues, produces grayscale images that often fail to provide sufficient contrast. Since healthy and malignant soft tissues share very similar elemental composition, their attenuation characteristics are nearly identical, making them difficult to distinguish. Automated diagnostics using machine learning, when combined with novel imaging methods that capture a broader spectral range, can improve the detection of suspicious lesions.

Rapid and accurate identification of malignant tissue during surgery is particularly critical, as it directly impacts the completeness of tumor removal and patient outcomes. Despite continuous improvements in digital mammography, distinguishing small, irregular, or poorly defined lesions remains a significant challenge, which may lead to underdiagnosis or unnecessary invasive procedures. Our project addresses these limitations by combining novel spectral X-ray imaging with artificial intelligence (AI)-based data analysis.
Spectral X-ray imaging, enabled by advanced photon-counting detectors, captures energy-resolved data and provides unique tissue-specific signatures. While this technology's potential is clear with high-contrast materials such as specimens with clearly different chemical composition, its true clinical value lies in distinguishing biological tissues where spectral differences are far more subtle. This study aimed to leverage advanced machine learning to aggregate these subtle differences and develop an automated tool for biological tissues differentiation and differentiation between tumor and healthy soft tissue, even when their absorption characteristics are nearly identical.

To validate this approach, spectral datasets from both small-animal and large-animal models are being acquired and analyzed. Ex-vivo resection samples from genetically engineered mice and pigs, containing both healthy and carcinoma tissue, are used to train and test AI algorithms in conditions closely resembling human pathology. These preclinical experiments represent an essential step before applying the methodology to human breast specimens.

Building on these preclinical findings, clustering algorithms such as k-means and Gaussian Mixture are examined using dimension reduction with e.g. Principal Component Analysis or Uniform Manifold Approximation, and Projection to classify spectral data and accurately identify tumor margins directly. Both 2D and 3D spectral X-ray scans are used including scans of artificial phantoms and implants, ex vivo analysis of various mice and pigs' organs, containing both healthy tissue and carcinoma. This combination of spectral imaging and machine learning could provide a powerful, automated framework for non-invasive tissue characterization. This innovation enables the delivery of rapid and reliable intraoperative information, supporting surgeons in real time and reducing the risk of incomplete tumor removal.

The project is being implemented by a consortium of Radalytica a.s., Carebot s.r.o., and Czech Centre for Phenogenomics, combining expertise in imaging systems, artificial intelligence, and preclinical modeling. The expected outcome is a validated methodology and software tool that integrates spectral X-ray imaging with AI-driven diagnostics. By enhancing sensitivity and specificity, this solution has the potential to shorten surgical decision-making and reduce the number of repeated or unnecessary procedures.

## (PO–09) Intellicage data analysis pipeline

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The Intellicage system provides a high-throughput and automated platform for assessing cognitive, motivational, and behavioral flexibility in group-housed mice. Thus, the complexity of its multiphase protocols requires structured data analysis to extract meaningful behavioral metrics. We present an integrated analytical pipeline that generates comprehensive reports with data visualizations and statistical summaries for each Intellicage protocol.

In this pipeline, we use the statistical programming language R to compare mutant mice carrying combined CRISPR-modified alleles in multiple target genes with wild-type C57Bl/6NCrl. Each dataset consists of a specific number of mice, depending on the experiment, which are then categorized based on strain and gender. Animals are tested across the full sequence of Intellicage protocols, including Free and Nosepoke Adaptation, Shaping, Place Preference and Reversal, Memory Flexibility, Competition, Serial Reaction Time, and Delay Discounting.

For each protocol, the report includes an initial exploratory data analysis followed by statistical evaluation of the behavioral tasks. We plot the number of visits and corner preferences for each group, alongside visualizations of nosepokes and licks at each corner. For protocols that involve learning, we calculate the success rates of each individual mouse and assess their learning curves. These descriptive analyses are followed by statistical evaluation using linear mixed models, which enables direct comparison of wild-type and mutant mice across tasks. The models incorporate session and day effects, allowing for a detailed examination of behavioral trajectories over time.

## (PO–10) Cognitive Impairment in the Remote Period after Fractionated Irradiation of the Mice Head

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Purpose: to investigate the effect of fractionated irradiation of the mice head on the behavior and cognition in remote stages after exposure.

Material and methods: the work was performed on female mice of the inbred line C57Bl/6 aged 2.5 months at the beginning of irradiation. The animals were kept in controlled conditions of the vivarium of the Institute of Radiobiology of the National Academy of Sciences of Belarus under a light regime (12 h day / 12 h night) in a group of 5-6 animals per cage, with free access to a standard diet of food and water. All experimental work with laboratory animals was carried out in accordance with the requirements of the Ethics Committee of the Institute of Radiobiology and Directive 86/609/EEC. The animals were divided into two groups: "Irradiation" and "Sham irradiation". Irradiation of the mice head was performed on an X-Rad 320 Precision X-ray Inc. biological X-ray system at a dose of 4 Gy (dose rate 0.98 Gy/min), once a day for 5 consecutive days (total dose of 20 Gy).
Behavior and cognitive functions were studied using the Open Field, Novel Object Recognition (NOR) test and Puzzle box test in the remote period after irradiation (10 months).

Results: irradiation mice demonstrated the anxiety-like behavior and impaired spatial memory in the NOR test in the 10 months after exposure to X-rays.

Ten months after irradiation, during the first presentation of the puzzle box test (stage T1) to mice, the latency of entering the dark compartment was 180 [167; 180] s and was significantly reduced compared to the value in the Sham Irradiation group – 82 [79; 94] s ($p < 0.05$). No differences were recorded between the compared groups for this indicator, when the animals were presented with stages T3, T4, T5 and T6. As well as stage T7 (the entrance to the hole was covered with shavings), in which the ability to learn (assessment of long-term memory) was examined: the median value of the latency of entering the dark compartment was 35 [29; 51] s in the Sham Irradiation group and 162 [144; 173] s in the Irradiation group, respectively ($p < 0.01$). Also after irradiation, cognitive abilities in solving stage T8 (a difficult task) were impaired. Thus, in the remote period after exposure to X-ray radiation at a dose of 20 Gy, female C57Bl/6 mice showed a deterioration in solving a number of stages of the puzzle box test.

## (PO–11) SPINK5/LEKTI IS A CRITICAL MEDIATOR OF EPITHELIAL INTEGRITY: IMPLICATIONS FOR NETHERTON SYNDROME

**Favero R [1]**, Lábaj J [1], FEDOSIEIEVA O [1], Balounová J [1], Žatečka V [1], Kašpárek P [1], Procházka J [1], Sedláček R [1]
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Netherton syndrome (NS) is a rare genodermatosis caused by loss-of-function mutations in the SPINK5 gene. Deficiency of its product, LEKTI, leads to the overactivation of kallikrein-related peptidases (KLKs) promoting a multisystemic disease. While NS is primarily characterized by severe skin barrier dysfunction, patients often present with systemic manifestations such as respiratory complications, infections, and allergies, whose underlying mechanisms remain poorly understood.

To investigate the multisystemic effects of SPINK5/LEKTI deficiency, we generated a tamoxifen-inducible whole-body conditional Spink5 knockout (wb-cSpink5 KO) mouse model. A single i.p. dose of tamoxifen (TAM) at 0.25 mg/40 g body weight was administered to induce Spink5/LEKTI recombination. Three weeks after induction we performed a comprehensive molecular, histopathological, and functional characterization of the skin, lung, and immune system.

Spink5/LEKTI expression was detected in epithelial compartments of several organs in wild-type mice, including the lungs, gastrointestinal tract, pancreas, kidneys, bone marrow, and thymus. Accordingly, Spink5/LEKTI deletion caused tissue damage in these organs, showing a close correlation with clinical manifestations in patients with NS. Skin of wb-cSpink5 KO mice exhibited main features of NS, including inflammation, epidermal thickening due to increased keratinocyte proliferation, hyperkeratosis, and increased desquamation. A disrupted skin barrier, as evaluated by transepithelial water loss (TEWL) measurement, was associated with altered expression of keratinocyte differentiation and barrier markers. In the lungs, Spink5/LEKTI deficiency triggered an intense inflammatory response, disrupted the extracellular matrix (ECM), and induced airway remodeling, resulting in functional impairments in pulmonary mechanics.

Inflammatory infiltration of the skin and lungs was accompanied by alterations in immune organs, indicative of a systemic inflammatory state. The spleen and lymph nodes were enlarged, with evidence of extramedullary hematopoiesis in the spleen. Flow cytometry revealed decreased frequencies of B cells and $CD4^+$ and $CD8^+$ T cells in the spleen. In the lymph nodes, reduced frequencies of $CD4^+$ T cells and increased frequencies of B cells, neutrophils, and monocytes were detected. The thymus displayed defective T-cell maturation, while the bone marrow showed impaired NK- and B-cell differentiation. Peripheral blood analyses demonstrated neutrophilia, monocytosis, and reduced levels of NK cells, B cells, and $CD4^+$ and $CD8^+$ T cells, indicative of impaired lymphopoiesis and skewed myelopoiesis.

In conclusion, Spink5/LEKTI is a critical mediator of epithelial integrity, barrier maintenance, and immune homeostasis. Our wb-cSpink5 KO model provides a robust platform to dissect the pathogenesis of NS, suggesting that respiratory complications are caused by combined local pulmonary alterations and severe systemic immune dysfunction.

## (PO–12) 15N Ammonia tracing with MALDI-FTICR imaging in regenerating liver – re-directing of toxic product into de novo pyrimidine synthesis and cell proliferation

**Kucera L [1]**, B Beduya E [2], Luptáková D [3], Klíma K [1], Vladimír Havlíček V [3], Sedláček R [1], Procházka J [1], Berridge M [4], Neužil J [2]

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Liver is endowed with high regenerative activity, such that the tissue will regrow in the mouse after partial hepatectomy within days. We reasoned that this requires de novo pyrimidine synthesis to support rapid progression via the cell cycle. With MALDI imaging technique we revealed that suppression of de novo pyrimidine synthesis prevents proliferation in regenerating liver, suppressing liver regrowth. Tracing studies and spatial metabolomics revealed a metabolic shift such that ammonia, normally detoxified to urea in the periportal region under homeostasis, is redirected for generating aspartate and carbamoyl phosphate periportally, and glutamine pericentrally, and these products are utilized as precursors by the de novo pyrimidine synthesis pathway. This study uncovers a metabolic reprogramming leading to utilization of a toxic byproduct for anabolic pathways that are essential for liver regeneration.

## B) INFRASTRUCTURE POSTER PRESENTATIONS

(PO-13) **Lucie Dufkova:** Transgenic and Archiving Module: Implementation and Enforcement of the 3Rs Principle

(PO-14) **Libor Kopkan:** Advanced Technological Upgrade of the Washing Center at CCP-AFM Vestec

(PO-15) **Juraj Labaj:** Histopathology Unit

(PO-16) **Juraj Labaj:** Biochemistry and Haematology Unit

(PO-17) **Marcela Pálková:** Vision screen

(PO-18) **Sylvie Cervenkova:** Bioimaging & Embryology Unit

(PO-19) **David Pajuelo Reguera:** Metabolism Unit

(PO-20) **Silvia Magalhaes Novais:** PDX and Cancer Models Unit

(PO-21) **Dominik Arbon:** Biosafety Level 3 facility for Preclinical Testing and Efficacy Studies of antivirals against infectious pathogens

(PO-22) **Kateryna Pysanenko:** Neurobiology & Behaviour Unit

(PO-23) **Gizela Koubkova:** Preclinical testing at the Czech Centre for Phenogenomics

(PO-24) **Jiri Lindovsky:** Hearing & Electrophysiology Unit

(PO-25) **Eva Nekvindová:** Cardiovascular Unit

(PO-26) **Vendula Novosadová:** Bioinformatics Unit

(PO-27) **Jana Balounova:** Immunology Unit

(PO-28) **Lukas Kucera:** Metabolomics Unit

(PO-29) **Maximilian Golena:** Phenolyze-2: Interactive Software for Statistical Analysis and Data Exploration of IMPC Pipeline Data at the Czech Centre for Phenogenomics

## (PO–13) Transgenic and Archiving Module: Implementation and Enforcement of the 3Rs Principle

**Dufkova L [1]**, Nickl P [1], Krupkova M [1], Michalikova C [1], Dostalova P [1], Vikhrova E [1], Zelena K [1], Kolihova A [1], Machalova E [1], Sedlacek R [1]

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Transgenic and Archiving Module (TAM) is a key part of the Czech Centre for Phenogenomics (CCP). TAM provides complete service, from the initial gene-targeting design, generation of the rodent model, to the genotyping, breeding and archiving.

Implementation and enforcement of the 3R concept for each step of the whole process, from planning the experiment, selection of technology, harm-benefit analysis, husbandry conditions, colony management of genetically modified lines to actual procedures, are crucial for all three modules of CCP, except TAM also Animal Facility Module (AFM) and Phenotyping Module (PM).

TAM is responsible for the generation of novel genetically modified mice and rats using state-of-the-art technologies that allow the reduction of animal consumption in line with 3R principles. For example, CRE/FLP mediated allele conversions using AAV vectors enables the conversion from tm1a to tm1d in a single animal during IVF-based reanimation/rederivation from sperm, resulting in 80% of fully converted animals. Furthermore, mouse/rat model generation using programmable nucleases (TALEN, CRISPR/Cas9) using electroporation instead of microinjection reduces the number of donors animals, more than 90% of murine embryos continue their development.

In conclusion, before starting a new project a harm - benefit analysis is performed and also knowledge of veterinarians of AFM and scientists from TAM and PM of CCP is incorporated. The health and well-being of newly generated genetically modified lines are effectively monitored for clinical abnormalities, the number of animals used are continuously analyzed and measures that can enhance animal welfare are implemented.

## (PO–14) Advanced Technological Upgrade of the Washing Center at CCP-AFM Vestec

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The Animal Facility Module (AFM) of the Czech Centre for Phenogenomics (CCP) at the BIOCEV provides advanced infrastructure for laboratory animal husbandry under strict health and welfare standards. To optimize workflows and maintain these conditions, the washing center was modernized. The main washing units were replaced with high-performance systems, enhancing efficiency in processing cages, bottles and racks. This upgrade supports compliance and secures the long-term sustainability of the CCP's operations.

The Arcadia tunnel washer is a high-capacity hydro-spray system capable of processing up to 1,500 mouse cages per hour. In comparison with previous Tecniplast models, it introduces significant innovations in resource consumption and maintenance. Compact round tanks with tangential suction enable operation with a reduced water volume, thereby lowering the energy demand for heating and decreasing detergent use. A self-cleaning wedge filter with automatic backflush eliminates the need for manual cleaning and ensures higher operational continuity. In addition, a newly developed plastic conveyor belt minimizes noise and the risk of damage to IVC components, while providing optimal water drainage through the inclined presentation of lids. Arcadia has been validated according to FELASA AK KAB and AAALAC standards and is equipped with the Polaris HMI interface, which allows remote monitoring, diagnostics, and consumption tracking. Compared to the previous generation of tunnel washers, it delivers both higher capacity and efficiency as well as markedly lower operational costs.

The Alpha cage and rack washer represents the latest generation of batch-type systems and is distinguished from earlier models by its patented Adaptive Cleaning Technology (ACT). This approach employs rotational-vertical movement of the spray arms, delivering 39% greater mechanical washing force and complete surface coverage, including drinking bottles. In combination with new high-density presentation racks, Alpha achieves a capacity of up to 154 GM500 cages per cycle, corresponding to more than 1,200 cages per hour at eight cycles. This performance is comparable to tunnel-based solutions, yet in a more compact format. Compared with previous Tecniplast rack washers, Alpha reduces water consumption by up to 75% (300 ml per cage) and energy use by more than 13%. Ergonomics are further enhanced by a 30% reduction in rack weight, while safety is improved through tempered glass doors with inflatable seals and integrated safety sensors. Like Arcadia, Alpha is equipped with the Polaris HMI interface, enabling remote monitoring and integration with automated systems. Both systems fully comply with European directives (2006/42/EC, 2014/35/UE, 2014/30/UE) and international standards (UNI EN ISO 12100:2010, CEI EN 60204-1:2006, UNI EN ISO 13849-1:2016, UNI EN ISO 13732-1:2009), ensuring mechanical, electrical, and ergonomic safety during long-term use.

**PRODUCT PROFILE**

Together, the Arcadia tunnel washer and the Alpha washer represent a major step forward compared to earlier IWT Tecniplast models. Arcadia demonstrates excellence in large-scale cage processing with minimal operational costs, while Alpha provides high throughput in a compact format, making it an ideal solution for medium to large laboratories. Both systems address current requirements for efficiency, validation, ergonomics, and sustainability in laboratory operations, while fully complying with the latest European and international safety standards.

## (PO–15) Biochemistry and Haematology Unit

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Clinical Chemistry (the study of the chemical composition of the blood plasma/serum), haematology (the study of the blood cellular components and acid-base balance), and urinalysis (analysis of chemical and cellular composition of urine) are integral part of clinical pathology which provides a quantifiable way to assess animal health and to diagnose disease and toxicity. Clinical chemistry analyses of plasma/serum and urine comprise of metabolites, ions, enzymes, and serological quantifications that could be used to assess metabolic and functional abnormalities of different organs of the body. Examination of whole blood for haematology may reveal pathologies or treatments that affect blood cell populations and coagulation.

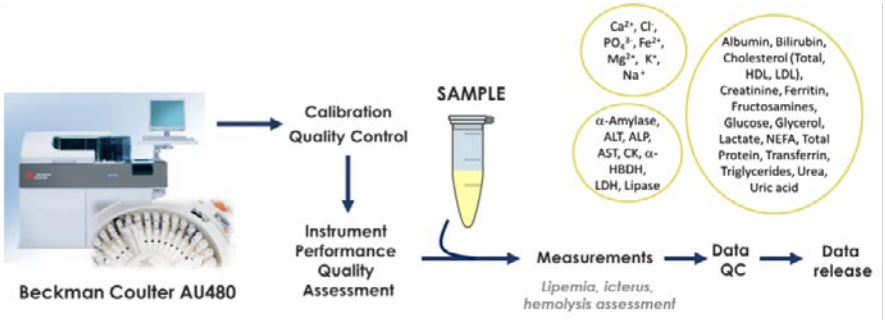
We use advanced analytical platforms maintained at high standards with methodologies following robust screening protocol by the International Mouse Phenotyping Resource of Standardized Screens (IMPReSS). Furthermore, the Biochemistry and Haematology Unit is a GLP (Good Laboratory Practice) – certified, SUKL (State Institute for Drug Control, ČR) – audited laboratory capable of analyzing samples from pre-clinical studies. The Unit can likewise measure multitude of biomolecules from a single sample using different panels for multiplex immunoassays and tested kits for individual analytes. Multiplexing is done by a bead- and flow cytometry-based assay utilizing Luminex® xMAP® technology in a flexible analyzer.

More information at www.phenogenomics.cz/phenotyping/biochemistry-and-haematology/.

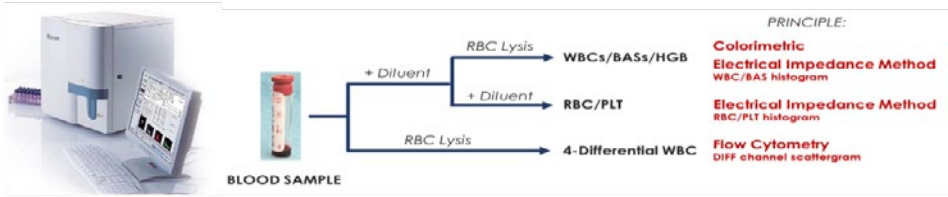
Instrumentation and Technologies:
**CLINICAL CHEMISTRY PLATFORMS:**
The Beckman Coulter AU480 Clinical Chemistry Analyzer - Electrolytes, enzymes, and organic analytes can be measured as part of a clinical chemistry panel. Available panels include: liver, kidney, pancreas, inflammation, lipid, cardiac & muscle, anemia, bone and IMPC.
The Siemens CLINITEK Advantus® Urine Chemistry Analyzer - utilizes reflectance spectrophotometry to semiquantitatively analyze urine test strips.

**HAEMATOLOGY PLATFORMS:**
The Mindray BC-5300 Vet or BC-30 Vet analyzers - for measurement of veterinary complete blood count and WBC differentials.
The Siemens Sysmex® CA-560 Automated Blood Coagulation Analyzer - for measuring different blood coagulation parameters via coagulation, chromogenic, or immunoassay methodology (bottom).
The ABL90 FLEX PLUS blood gas analyzer - acid-base balance cassette analyzer for determination of internal environment parameters, electrolytes, metabolites, total hemoglobin and its derivatives

**IMMUNOASSAY PLATFORMS:**
Singleplex ELISA assays or multiplexing using spectrophotometer or the Bio-Plex® 200 Luminex. Samples that can be analyzed include serum/plasma, lavages, urine, milk, culture media, and cell/tissue culture supernatants.




The Beckman Coulter AU480 Clinical Chemistry Analyzer



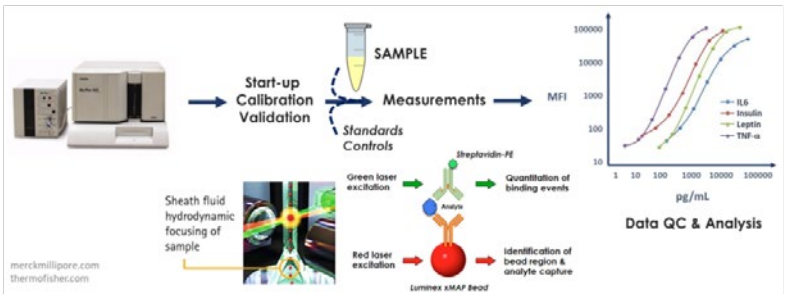

The Mindray BC-5300 Vet and BC-30 Vet Analyzer



Parameters measured:

**Blood gases:** pH , $pCO_2$ , $pO_2$
**Metabolites:** cGlu , cLac , cCrea , cUrea
**Electrolytes:** $cCa^{2+}$ , $cCl^-$ , $cK^+$ , $cNa^+$
**Oximetry:** FCOHb , ctBil , ctHb , FHbF , FHHb , FMetHb , $sO_2$ , $FO_2Hb$

The ABL90 FLEX PLUS Blood Gas Analyzer




The Bio-Plex® 200 Luminex

## (PO–16) Histopathology Unit

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The Histopathology unit is one of the largest units of the CCP Phenotyping Module and provides service for a broad range of research community including users working with non-rodent material. The unit is particularly engaged in experimental pathology. The work flow of the histopathology laboratory covers all procedures from gross morphology through various staining techniques and fluorescent slide scanning to pathology description. Complete necropsy of mouse/rat is performed by veterinary pathologist and all macroscopic findings are documented. Almost all steps in tissue processing and slide preparation are automatized to achieve the highest levels of reproducibility and quality. The lab offers H&E staining done by automated stainer, wide range of special stains and immunohistochemistry. The microscopic evaluation of histological samples is done by pathologist and complex report with picture documentations is a standard. Most of activities are conformed to Good Laboratory Practices (GLP).

**Instrumentation & technologies:**
Tissue processing: Leica ASP6025 - The most modern vacuum tissue processor

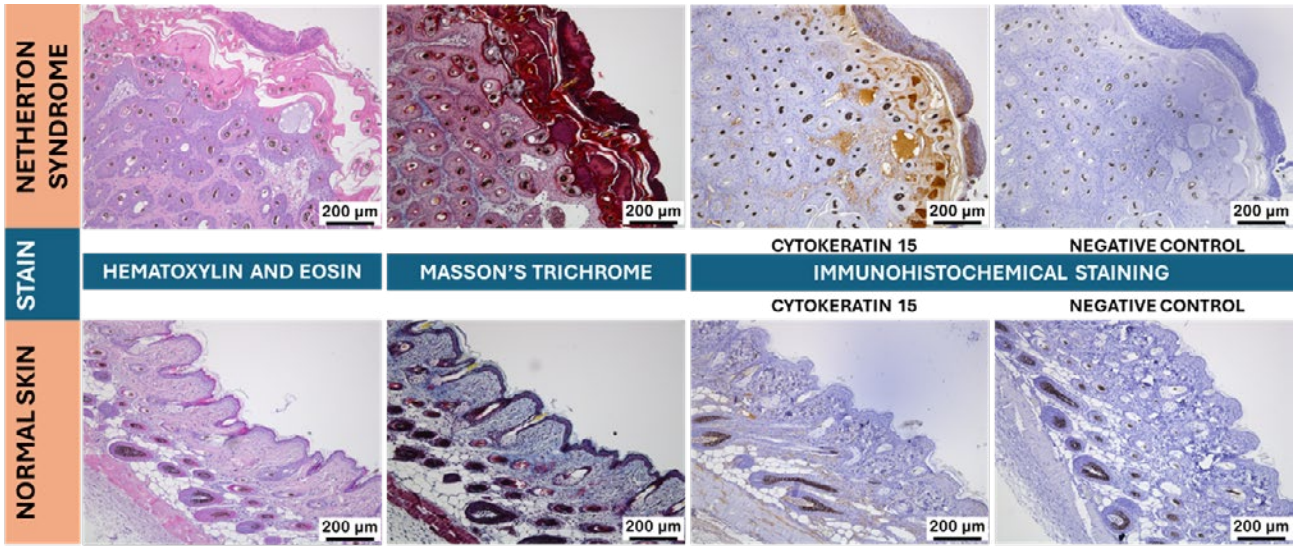
Sectioning fresh specimens: Vibratom Leica 1200 - automated vibrating blade microtome

Slide staining: MultistainerLeica ST5020 in conjunction with Leica CV5030 Coverslipper - an exceptionally versatile stainer-coverslipper workstation; Ventana Benchmark Speial Stains - Automated slide stainer for special stains; Ventana Discovery ULTRA - Automated stainer for immunohistochemistry and in situ hybridization

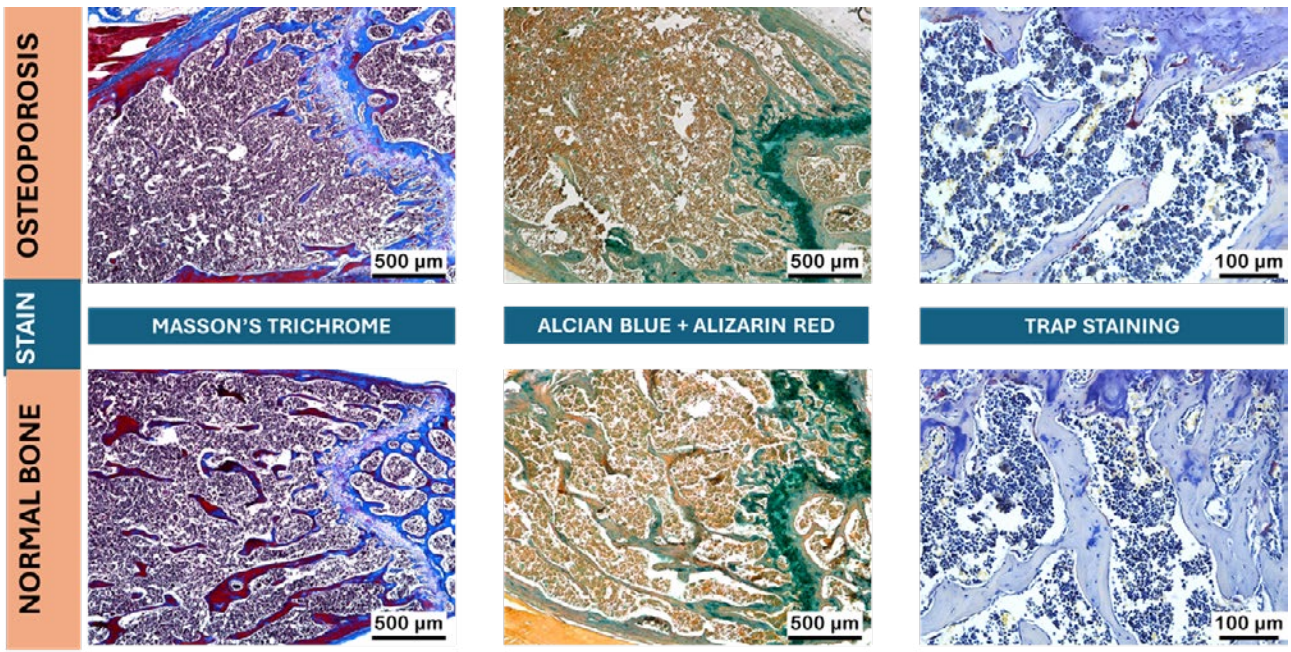
Microscopy and analysis: Carl Zeiss Axio Imager.Z2 - motorized microscope imaging station, capable of both brightfield and fluorescence capture; Leica DM3000 - Semi automated high-throughput brightfield microscope system

Slide scanning: Carl Zeiss Axio Scan.Z1 - Combined brightfield and fluorescence slide scanner with ability to also scan histotopograms. Equiped with ultra-fast LED fluorescent module and 7 different excitation/emission filters.

ConaPat - Tracking system.




**Netherton Syndrome**




**Osteoporosis**

## (PO–17) Vision screen

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Vision unit is a part of phenogenomic center and it is mainly focused on imaging, analyzing morphological structures and assessing morphological abnormalities in rodent eyes. These primary examinations are routinely performed in all mice coming to our unit. In special cases such as obvious morphological pathology of retina or special requests (e.g. mouse model for the retinopathy, diabetic disease etc.), the function of the retina is proved by electroretinography (ERG).

Additional measurements of the intraocular pressure by rebound tonometer (IcareTonovet plus) provide us important information on the eye function and the health in the mice.

Imaging devices with high image quality and resolution are used to examine the anterior segment (Pentacam), retina (Optical coherent tomograph Heidelberg Engineering - OCT) and retinal vascular plexuses (OCT-A Heidelberg Engineering). All procedures are non-invasive, painless and allow long-term studies with repeated examination of eyes.

Pentacam scans the eye from 25-50 different angles and enables to measure many parameters of the cornea and the lens (e.g. surface, form, opacity, thickness and density) for each eye. The OCT scan quantifies reflections of a light beam from individual layers of the retina and composes virtual cross- sectional images of the retina. The OCT-A scan enables us to detect and analyze four retinal vascular plexuses (svc - superficial and dvc - deep vascular complex, choriocapillaris and choroid). Each cross-section is evaluated and a variety of parameters are measured, e.g. the thickness and the gross morphology of the retina (retinal layers), form and the position of the optic disc, structure and pattern of the superficial blood vessels and parameters of the blood plexuses, e.g. density, number of blood vessel junctions and endpoints per region. To prove any morphological changes in the retina at different time points of life in mice, the consecutive scans could be done. ERG measures electrical responses of different retinal cell types evoked by light stimulation. This examination enables us to compare/assess the physiological relevance of the morphological abnormalities in the retina for the vision and it is described in more detail in the Electrophysiological section.

Besides covering of the routine IMPC workflow, the unit also collaborated on many other research projects related to vision.

Fig. 1: OCT imaging device

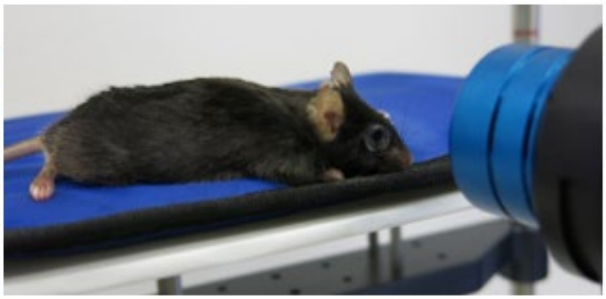

Fig. 2: Non-invasive measurement of retina by OCT

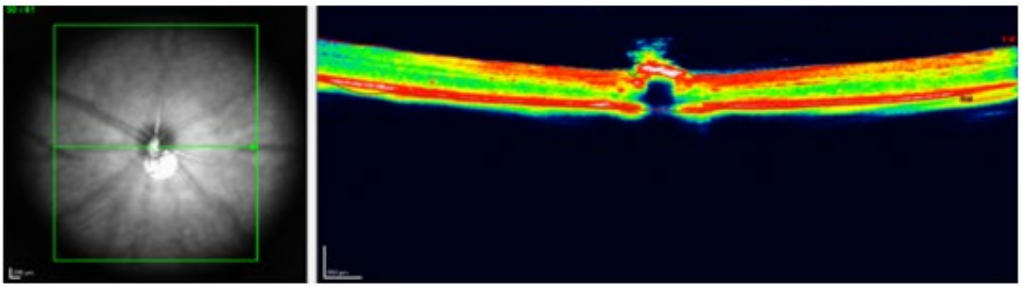

Fig. 3: Representative image of fundus and B-scan of the retina

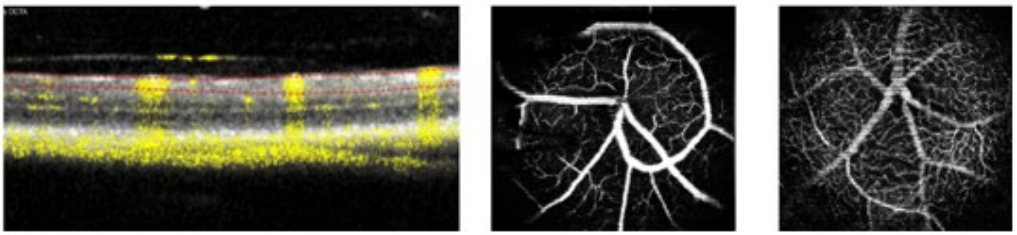

Fig. 4: 3D OCT imaging of retinal vasculature (blood flow corresponds to yellow dots)

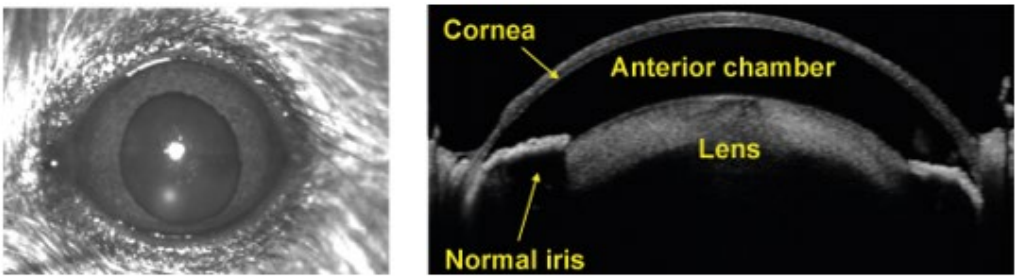


Fig. 5: OCT image of frontal eye segment – general view

## (PO–18) Bioimaging & Embryology Unit

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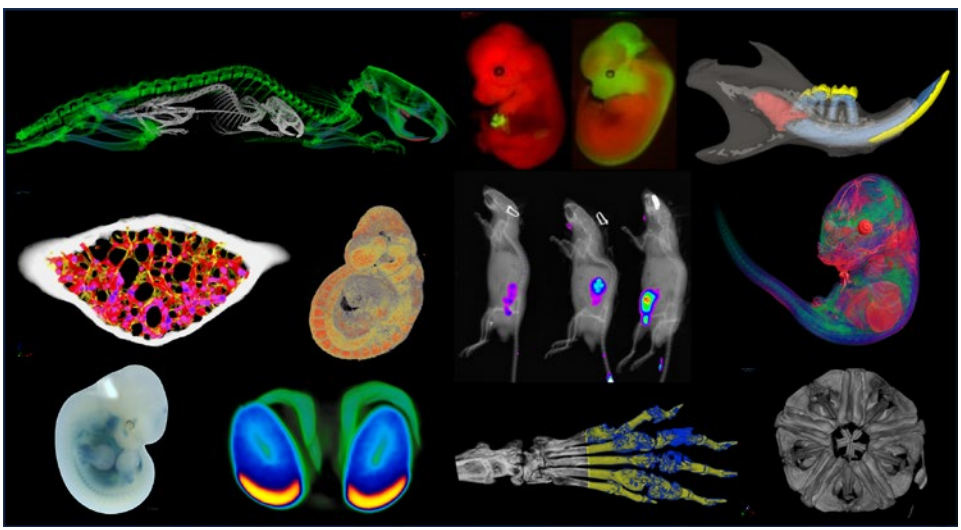
The Bioimaging and Embryology (BIE) unit is focused on functional morphology projects using state of art 3D imaging technologies of adult mice and rats as well as murine embryos, specific tissues as enamel etc. The unit also provides the knowledge base for conditional gene inactivation, embryonic tissue isolation and dissections for OMICs or establishment of primary cell cultures.

The key technological base of our work lies in 3D imaging with µCT which allows visualization not only of mineralized tissues but also of soft tissues with use of appropriate contrast with resolution from 100 down to 0.5 µm. The BIE unit also provides comprehensive data analysis platform. Besides the 3D imaging, the unit is equipped with whole body imaging system for imaging of fluorescence and bioluminescence reporters in mice and rats in vivo. This technology is very advantageous, especially for imaging of cancer models. Physiological processes like inflammation, kidney function or specific enzyme activity can be also non-invasively imaged and evaluated. The unit also provides functional assays on primary cells or their isolation for multiOMICs, offers harvesting and phenotypization of embryos or dissection of embryonic tissues followed by organ culture or primary cell line setup, alternatively including lineage immortalization. We can also visualize gene expression by different methods both in whole mount and on sections. These approaches help to substantially accelerate the research of genes whose mutations cause severe developmental, often embryonic lethal phenotypes.

**Examples of recent papers:**
Achondroplasia: aligning mouse model with human clinical studies shows crucial importance of immediate postnatal start of the therapy. Rico-Llanos et al., Journal of Bone and Mineral Research, 2024
Skeletal dysmorphology and mineralization defects in Fgf20 KO mice. Dlugosova (Cervenkova) et al. Front. Endocrinol., 2024



## (PO–19) Metabolism Unit

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Genetically modified mouse models are indispensable for elucidating the specific gene function, including those involved in the energy metabolism and glucose homeostasis. Our research initiates with foundational phenotyping, including intraperitoneal glucose tolerance tests, non-invasive body composition analysis, and indirect calorimetry. These tests establish a baseline for subsequent in-depth, hypothesis-driven studies.

Environmental chambers equipped with adjustable light:dark cycles, humidity, and temperature settings facilitate the performance of cold challenges, thermoneutral studies, and alterations in light-dark patterns. We collect indirect calorimetric data from mice or rats undergoing these environmental challenges. Additionally, we can evaluate the impact of specialized diets, such as high-fat diets, on overall metabolism.

To investigate glucose metabolism in detail, we employ several tests: basal and maximal blood insulin concentrations are measured during glucose tolerance tests, while insulin sensitivity is assessed using insulin tolerance tests. These complementary methodologies aid in explaining potential defects in glucose metabolism resulting from genetic modification or specific treatments.

Our team has integrated telemetry of physiological parameters, including body temperature at two body locations and real-time blood sugar measurements. These parameters can be monitored in home-caged mice or in conjunction with indirect calorimetry.

We utilize non-invasive body composition analysis based on TD-NMR technology, which offers a swift and accurate approach to determining lean and fat mass, as well as free fluids in mice and rats. The non-invasive nature and rapid analysis allow for repeated measurements of body composition over time.

Like all units at CCP, our metabolism services benefit from integration with other units of the centre, enabling the systemic and comprehensive characterization of experimental rodent models.

**Instrumentation & technologies**
Indirect Calorimetry including activity, food and water monitoring intake (PhenoMaster TSE Systems).
Stellar Telemetry antenna & wireless monitoring dual temperature transmitters (TSE Systems) and glucose blood concentration (DSI).
Body composition analyzer by Time-domain Nuclear Magnetic Resonance (TD-NMR) using (Minispec LF90II, Bruker)
Projects in Selected Publications:

**Comprehensive Transcriptional Profiling and Mouse Phenotyping Reveals Dispensable Role for Adipose Tissue Selective Long Noncoding RNA Gm15551.**
Engelhard CA, Huang C, Khani S, **Kasparek P, Prochazka J, Rozman J, Reguera DP, Sedlacek R**, Kornfeld JW. Noncoding RNA. 2022 May 6;8(3):32. doi: 10.3390/ncrna8030032

**Mitochondrially targeted tamoxifen alleviates markers of obesity and type 2 diabetes mellitus in mice.**
Vacurova E, Trnovska J, Svoboda P, Skop V, **Novosadova V, Reguera DP, Petrezselyová S, Piavaux B**, Endaya B, **Spoutil F, Zudova D**, Stursa J, Melcova M, Bielcikova Z, Werner L, **Prochazka J, Sedlacek R**, Huttl M, Hubackova SS, Haluzik M, Neuzil J. Nat Commun. 2022 Apr 6;13(1):1866. Doi: 10.1038/s41467-022-29486-z.

**A previously uncharacterized Factor Associated with Metabolism and Energy (FAME/C14orf105/CCDC198/1700011H14Rik) is related to evolutionary adaptation, energy balance, and kidney physiology.**
Julian Petersen, Lukas Englmaier, ArtemV. Artemov, Irina Poverennaya, Ruba Mahmoud, Thibault Bouderlique, Marketa Tesarova, Ruslan Deviatiiarov, Anett Szilvásy-Szabó, Evgeny E. Akkuratov, **David Pajuelo Reguera, Jan Rozman, Petr Kasparek, Jan Prochazka, Radislav Sedlacek**, et al. Nat Commun. 2023 May 29; 14:3092. Doi: https://doi.org/10.1038/s41467-023-38663-7

## (PO–20) PDX and Cancer Models Unit

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The PDX and Cancer Models Unit is dedicated to creating innovative oncology research models and committed to providing tools that propel effective treatments for cancer. We offer customizable study designs, access to a comprehensive collection of PDX mouse models, cancer cell line xenografted models, and immuno-oncology models to test the effectiveness of novel or existing immunotherapeutic compounds. Moreover, to complement our offerings, our in-house multidomain analysis spans an array of disciplines, including histopathology, hematology, biochemistry, immunology, bioimaging, and metabolomics. These cutting-edge approaches have the transformative potential to elevate any project to unparalleled heights of success. These sophisticated models and applications combine creativity, solid reliability, and a relentless commitment to customer satisfaction, ensuring access to clinically relevant mouse models and precision services.

## (PO–21) Biosafety Level 3 facility for Preclinical Testing and Efficacy Studies of antivirals against infectious pathogens

**Arbon D [1]**, Cechova B [1], Gambini F [1], Dufkova L [1], Prochazka J [1], Sedlacek R [1]
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The Unit of Models of Infectious Diseases at the Czech Centre for Phenogenomics (CCP) presents an Animal Biosafety Level 3 (ABSL-3) facility, dedicated to advanced research and preclinical testing in infectious diseases. As one of the largest ABSL-3 infrastructures in the Czech Republic, the unit supports both in vivo and in vitro experimentation, enabling research on a broad spectrum of human and animal pathogens, such as viruses (including SARS-CoV-2, hepatitis B, or monkeypox), bacteria (Acinetobacter baumannii), yeasts, or protozoa. Equipped to study both acute and chronic phases of infection, the facility specializes in animal physiology and pathology, integrating advanced technology for pathogen infection research, therapeutic screening, and vaccine evaluation.

The research services incorporate complex animal models, including genetically modified and infection-sensitized mice, organ-specific infection models, and models with medical alterations, such as obesity or cancer. The CCP team provides a full spectrum of analyses, from molecular profiling (ELISA, PCR, RT-qPCR, Western Blot) to advanced immunological, metabolic, and physiological evaluations. The capabilities include preclinical pharmacokinetics, toxicity studies, cardiovascular and pulmonary function, behavioral analysis, histopathological examinations or whole-body bioimaging and can be supported by wide range of other specializations. Supporting translational research, the unit offers project design, custom assay development, and legal support for the introduction of new infectious agents or genetically modified organisms, ensuring compliance with national and international regulations. The integrative approach includes comprehensive bioinformatics, statistical evaluation, and detailed reporting which enables customizable studies and provides high-quality, reproducible results.


Viral and bacterial infection models
Hepatitis B
SARS-CoV-2
ESKAPEE bacteria
Monkeypox
Czech Centre for Phenogenomics
BSL-3
Our services
In vivo analyses
Ex vivo procedures
lung function measurement
tracking weight changes
health monitoring
blood collection and hemo analysis
cardiac activity monitoring
behavioral testing
Organ collection
Terminal blood collection
ELISA
RNA isolation
DNA isolation
Histopatological evaluation
Flow cytometry
Flow cytometry
Side light scatter (SSC)
Forward light scatter (FSC)
qPCR
Genotyping

## (PO–22) Neurobiology & Behaviour Unit

**Pysanenko K [1]**, Sabotova A [1], Jina P [1], Lindovsky J [1], Prochazka J [1], Sedlacek R [1]
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Genetic engineering opens an avenue of research opportunities to probe molecular bases of a variety of human diseases. Neurobehavioural tests using transgenic animal models make it possible to understand genetic mechanisms underlying neurological and psychiatric disorders including, but not limited to, anxiety, schizophrenia, mood disorders, and Parkinson's disease.

The Neurobiology and Behaviour Unit employs a number of tests to examine motor abilities, cognitive functions, emotion, sensory processing as well as neurological, and gait impairments in transgenic mice. We offer standardized primary and secondary phenotype screens based on IMPC (International Mouse Phenotyping Consortium) protocols (https://www.mousephenotype.org/impress). Primary/mandatory screens include modified SHIRPA and dysmorphology evaluation, Open Field, Grip Strength, Acoustic Startle and PPI, Light/Dark Box, and Fear Conditioning. The Unit also offers more specific secondary/optional screens that comprise tests evaluating animal emotionality and affect (Elevated Plus Maze, Forced Swim Test, Tail Suspension Test), cognitive function (Cued and Contextual Conditioning, Context Discrimination, Y-Maze Spontaneous Alternation, Barnes Maze, Novel Object Recognition), neuromotor abilities (RotaRod, Gait Analysis), pain sensitivity (Hot/Cold Plate, Tail Flick, Plethysmometer, von Frey Test), social preference, and last but not least evaluation of animal cognitive function and circadian activity in more natural conditions in IntelliCages. Social group housing in a large enclosure, free from human handling stress, equipped with multiple gadgets in IntelliCage provides environmental enrichment beyond typically employed protocols.

## (PO–23) Preclinical testing at the Czech Centre for Phenogenomics

**Koubkova G [1]**, Suchanova S [1], Bukova I [1], Novosadova V [1], Labaj J [1], Stefancova E [1], Gluščenko M [1], Arbon D [1], Prochazka J [1], Sedlacek R [1]

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The development of new drugs is an interdisciplinary, time-consuming, and costly process and critically depends on the selection of appropriate and predictive preclinical models. Developing safe and efficacious drugs requires thorough preclinical testing using in vitro, in vivo, and increasingly also in silico approaches. Based on the experiences from high throughput phenotyping of mouse models, the Czech Centre for Phenogenomics (CCP) offers a broad portfolio of highly standardized, state-of-the-art test assays (some in GLP mode) that can be applied in non-clinical studies in experimental rodent models reproducing certain features of human disease. Established preclinical tests comprise toxicity studies, hematological, and biochemical testing of samples taken from animals during toxicity studies, determination of active substances, and metabolites in plasma or other biological matrices, histopathology, ECG and echocardiography for effects on cardiovascular functions, body composition analysis, monitoring of energy fluxes, substrate utilization, feeding and drinking behavior, and locomotor activity, as well as various imaging modalities. The CCP has also implemented neurobehavioral testing and established model systems in the field of asthma and lung fibrosis, liver fibrosis, and induced colitis models. Furthermore, we offer efficacy testing in established CDX/PDX models and we can also provide new cancer model development starting with in vivo growth kinetics of the required cell line. Our CDX/PDX modality is strongly supported by the Bioimaging unit including services for in vitro experiments.We can offer genomic modification of provided cell line (e.g. to get luminescent cells or more sophisticated tasks). We can provide therapy testing also on several models for rare diseases using genetically modified animals (e.g. models of Prader-Willi and Angelman syndromes, Netherton syndrome) and also for some human infections – even when the wildtype mice are resistant (e.g. Covid-19 – using various GM mouse models). Further preclinical models are under development.

## (PO–24) Hearing & Electrophysiology Unit

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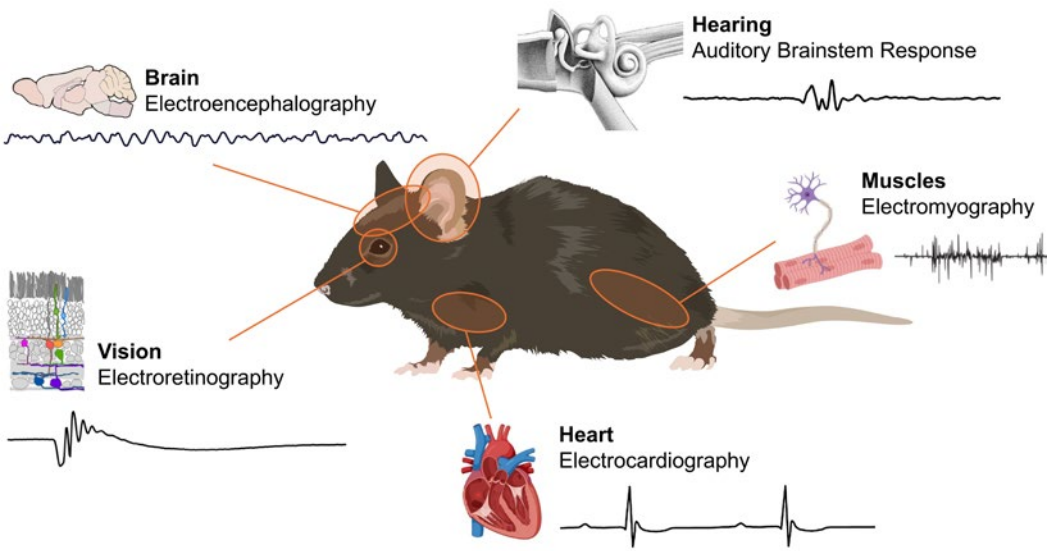
The unit provides electrophysiological methods for functional testing of hearing and vision in laboratory rodents, while also supporting broader applications in neural and systemic bioelectric signal acquisition.

In principal, techniques used are based on recording of electric potentials of sensory pathways evoked by relevant stimuli. Presence or absence and size or form of the evoked potentials is then interpreted as a correlate of activity and functional status of individual structures of the nervous system.

Hearing is mainly tested using the Auditory Brainstem Response (ABR), which is a sound-triggered electrical signal recorded by small needle electrodes placed under the skin on top of the animal's head. This signal reflects the combined activity of nerve cells involved in hearing, starting from the auditory nerve and continuing through the cochlear nucleus, superior olivary complex, and the inferior colliculus. Vision is assessed using Electroretinography (ERG) and Visual Evoked Potentials (VEP). ERG records the retina's electrical response to light. Signals are collected by a golden wire electrode from the surface of the eye under different lighting conditions, stimulus strengths, and timing setups, allowing to evaluate the function of specific retinal cell types. VEP is recorded from the back of the animal's head and shows activity in the final part of the visual pathway, the visual cortex.

We also provide techniques for delivering drugs, viral vectors, or cell-based therapies directly into brain tissue via a stereotaxic surgery. This approach bypasses the highly selective blood-brain barrier and can be done either as a single injection or through repeated dosing using a permanently implanted cannula.



## (PO–25) Cardiovascular Unit

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The cardiovascular system is essential for maintaining homeostasis and supporting the body's physiological processes. At CCP, IMG's Cardiovascular Unit provides diverse services designed to investigate cardiovascular traits in rodent models such as mice and rats.
We employ various non-invasive techniques, such as echocardiography, to utilize ultrasound for detailed exploration of heart and vascular structures. This approach allows us to analyze blood flow patterns, chamber efficiency, and more. Our Cardiovascular Unit performs examinations on fetuses, pups, and adults, offering 4D visualization and strain analysis for a thorough cardiac evaluation. Electrocardiography enables us to monitor electrical activity of the heart in both conscious and anesthetized rodents. Additionally, we measure blood pressure to enhance our understanding of cardiovascular health.

Our sonography services extend to gravidity checks, blood flow evaluations across various anatomical structures, and quantification of tumor size and vascularization. The imaging expertise therefore extends across multiple organ systems. A notable feature of our services is the Image-Guided Injection technique, which uses ultrasound for precise delivery of small volumes of substances, such as viruses or drugs, into specific organ regions at all developmental stages.

An additional innovative method available in our unit is photoacoustic imaging with the VEVO system. This hybrid technique combines the high spatial resolution of ultrasound with the molecular sensitivity of laser-induced photoacoustics, allowing for real-time, non-invasive assessment of tissue oxygenation, perfusion, and vascularization.

We also address cardiovascular challenges by applying controlled physiological stress tests, such as treadmill-based exercise protocols or pharmacological stimulation to mimic pathological conditions. Complementing these in vivo approaches, we study individual cardiomyocytes using the Langendorff isolation technique and the xCELLigence Cardio ECR system, enabling real-time analysis of the cardiomyocytes contraction and electrical activity.

Our work aims to reveal gene functionality and understand disease mechanisms, contributing to the refinement of therapeutic strategies and the potential enhancement of human health.

## (PO–26) Bioinformatics Unit

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The Bioinformatics Unit of CCP provides computational, statistical, and analytical support both to other CCP Units and to external customers. Our services cover a broad spectrum of activities, including data analysis, biostatistics, tool and application development, and assistance with the automation of routine laboratory processes. We also contribute to education by organizing training workshops in biostatistics and programming.

A central part of our work is the management of phenotyping data, where we ensure quality control, perform statistical analyses, and make the results available through public repositories. To support these efforts, we develop and maintain dedicated tools such as Phenolyze (https://ccp-tools.img.cas.cz/apps/phenolyze-2/), which enables comprehensive analysis of all mutant strains processed through the primary phenotyping pipeline. We also make use of 3D images generated in the primary pipeline and are developing a tool for automatic 3D analysis of mouse skulls, allowing the detection of subtle abnormalities in shape and size.

Beyond standard phenotyping data analysis, we focus on large and complex datasets. This includes neurobehavioral data analysis, with particular emphasis on datasets generated from IntelliCages and other platforms, as well as the evaluation of metabolism data from calorimetry measurements. Furthermore, we provide statistical support in GLP-compliant studies, where we take responsibility for the experimental design, integrity and reproducibility of data analyses. Our expertise also extends to next-generation sequencing (NGS), covering both mRNA and DNA. These activities are complemented by our involvement in large-scale integrative bioinformatics projects, where we apply advanced methods, including deep learning, to our projects.

Through this combination of services, tool development, and collaborative research, the Bioinformatics Unit plays a key role in enabling high-quality, reproducible, and innovative phenotyping research.

## (PO–27) Immunology Unit

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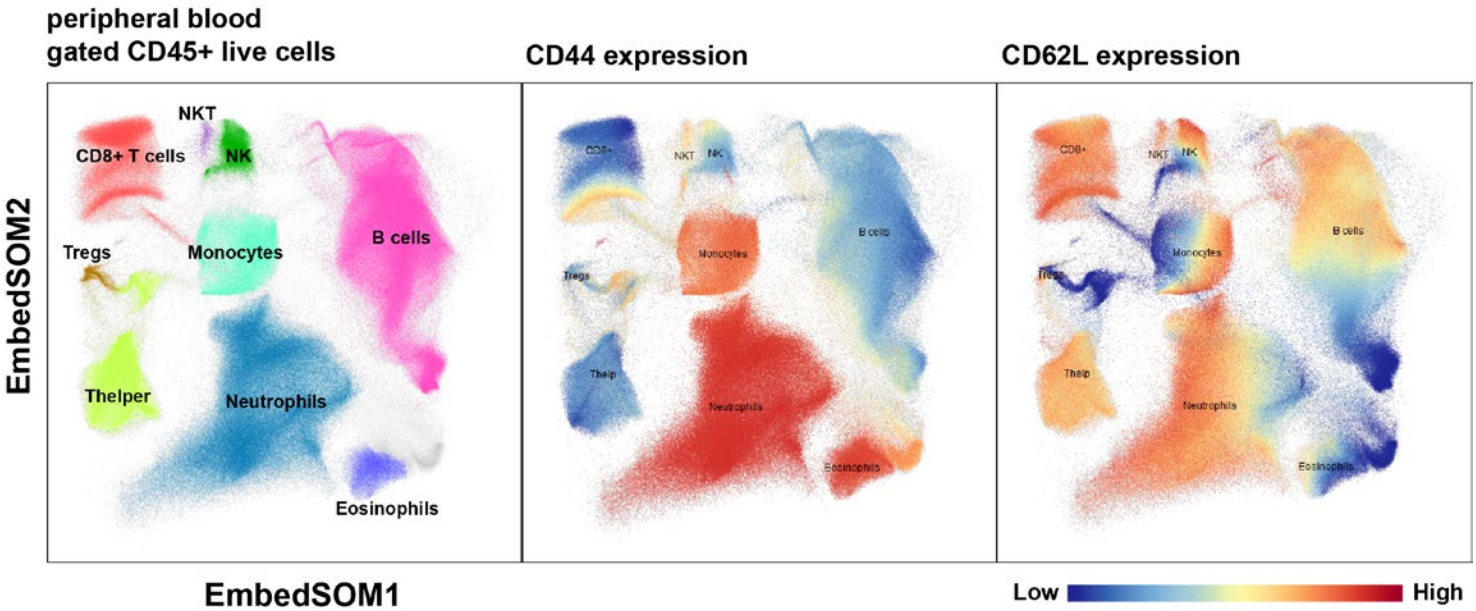
As an integral part of the terminal screen, immunophenotyping involves characterization of immune cell populations in terms of their cellularity and phenotype using multicolor flow cytometry (FCM). The procedures are based on standard protocols of the Adult and Embryonic Phenotype Pipeline that has been agreed by the research institutions involved: IMPReSS -International Mouse Phenotyping Resource of Standardised Screens and beyond. Accordingly, we have developed a comprehensive immune-phenotyping panel enabling discrimination of various populations of lymphoid and myeloid cells in the mouse spleen or other tissues (peripheral blood, lymph nodes, thymus, bone marrow, peritoneum,intestine) https://www.mousephenotype.org/impress/ProcedureInfo?action=list&procID=1463&pipelD=44. Additionally, we routinely use FCM assays to analyze cell populations in mouse blood, embryonic as well as adult hematopoiesis, thymus and tumor microenvironment under steady state or infection. To characterize the PDX models developed at CCP, we have optimized FCM panels to determine human leukocyte populations in humanized mouse strains. Moreover, we can design a suitable FCM panel to detect, characterize or purify cell populations of interest.

**Instrumentation & technologies**
The Unit is equipped with Cytek Aurora spectral flow cytometer. With 5 lasers (355, 405, 488, 532, 635nm), three scattering channels, 64 fluorescence channels and automated sample loader, the Aurora system is suitable to acquire high dimensional flow cytometry data in hightroughput. The FCM data is then analyzed in FlowJo or Omiq software and statistically evaluated. Furthermore, the Immunology Unit is equipped with gentleMACS tissue dissociator (Miltenyi Biotec), EasySep cell separation magnet for column-free cell separation (StemCell Technologies), bright field automated cell counter for counting of viable cells (Cellometer Auto T4, Nexcelom Bioscience) and a microplate spectrophotometer - ELISA reader (BioTek Epoch).

**Selected publications**

- New mouse model for inducible hACE2 expression enables to dissect SARS-CoV-2 pathology beyond the respiratory system. Gambini F, Arbon D, Nickl P, Zatecka V, Fedosieieva O, Labaj J, Novosadova V, Trylcova J, Weber J, Prochazka J, Balounova J, Sedlacek R. Mamm Genome. 2025 Feb 22.
- CUL4A exhibits tumor-suppressing role via regulation of HUWE1-mediated SMAD3 intracellular shuttling. Danek V, Tureckova J, Huebner K, Erlenbach-Wuensch K, Baranova P, Dobes J, Balounova J, Simova M, Novosadova V, Madureira Trufen CE, Prochazkova M, Talacko P, Harant K, Barinka C, Beck IM, Schneider-Stock R, Sedlacek R, Prochazka J. Cancer Lett. 2025 Mar 20:217663.
- Self-reactivity of CD8 T-cell clones determines their differentiation status rather than their responsiveness in infections. D Paprckova, V Niederlova, A Moudra, A Drobek, M Pribikova, S Janusova, K Schober, A Neuwirth, J Michalik, M Huranova, V Horkova, M Cesnekova, M Simova, J Prochazka, J Balounova, DH Busch, R Sedlacek, M Schwarzer, O Stepanek. Front Immunol. 2022 Oct 6;13:1009198. doi: 10.3389/fimmu.2022.1009198.
- Regulation of Inflammatory Response by Transmembrane Adaptor Protein LST1. M Fabisik, J Tureckova, N Pavliuchenko, J Kralova, J Balounova, K Vicikova, T Skopcova, F Spoutil, J Pokorna, P Angelisova, B Malissen, J Prochazka, R Sedlacek, T Brdicka. Front Immunol. 2021 Apr 27;12:618332. doi: 10.3389/fimmu.2021.618332
- SOM-based embedding improves efficiency of high-dimensional cytometry data analysis.
- M Kratochvil, A Koladiya, J Balounova, V Novosadova, R Sedlacek, K Fiser, J Vondrasek and K Drbal. bioRxiv (2019): 496869.



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## (PO–28) Metabolomics Unit

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The Metabolomics unit is expanding the method portfolio of the Metabolic and Clinical Biochemistry Units. The analysis of blood is part of our standard first-line phenotyping. Measuring only a limited number of biochemical markers, increases the risk of missing the physiological impact of a studied gene or a treatment, or the early onset of a disease. Therefore, we implemented metabolomics and lipidomics technology to analyze blood, serum or tissue homogenates that may even give a hint to the mechanistic basis of a diseaserelevant phenotype. Using reverse and hilic chromatography we are able to detect and quantify about 300 metabolites.

A specific MS/MS lipid library is designed for each lipidomics sample screen and usually consist of over 400 unique lipid species depending of sample type. Additionally, we can also track incorporation of labelled heavy carbon, delivered from 13C glucose, in cell culture samples. Our unit participates in preclinical screening in CCP by targeted detection of experimental compounds and provides stability and pharmacokinetics data. Besides analysis based on liquid chromatography we also provide the mass spectrometry analysis of tissue samples by MALDI imaging. Mass spectrometry imaging is mainly linked with histology and offer analysis of compounds in spatial context, which exceed the possibilities of classical histology. We are able to detect more than three hundreds of molecules on tissue slides. Our metabolomics unit has shown great potential in several biological applications. Discovery of diagnostic biomarkers, drug metabolization and their effects on whole metabolome, and progression of diseases are examples where studying metabolite profiles provided additional value also regarding translation to human disease. Using statistical methods allows to process and compare large data sets. Additional effort is put into the identification of unique metabolites and to map those to specific metabolic pathways which may be an important hint towards the molecular mechanism underlying the function of a gene.

## (PO–29) Phenolyze–2: Interactive Software for Statistical Analysis and Data Exploration of IMPC Pipeline Data at the Czech Centre for Phenogenomics

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Phenolyze 2 is a newly developed software platform designed to streamline statistical analysis and provide direct access to data generated by the International Mouse Phenotyping Consortium (IMPC) pipeline at the Czech Centre for Phenogenomics (CCP). Built in Python using the Dash framework, the application offers a fully interactive environment where researchers can efficiently explore and analyze complex datasets.

A key strength of Phenolyze 2 lies in its ability to analyze multiple genes simultaneously, making it especially valuable for comparative and integrative studies. Users can compare gene knockouts directly against each other, as well as against wild-type C57BL/6NCrl controls. This functionality accelerates the identification of meaningful biological patterns and enhances the potential for novel discoveries.

The platform supports a wide range of analysis types, including numeric data visualization with violin plots, categorical and correlation analysis, volcano plots, and time series numeric data using area-under-the-curve calculations. For multidimensional data, Phenolyze 2 incorporates Principal Component Analysis (PCA), enabling researchers to detect structure and variance across experimental groups. Statistical analyses are built-in, with options such as Tukey's test to provide robust comparisons across groups.

Another important feature is the integration of built-in visualization tools. Plots are automatically normalized for easier comparison with wild types, and centroids can be included for clarity in PCA results. Researchers benefit from simple export functionality, allowing them to quickly save plots, underlying data, and statistical results for reporting and further use.

By combining interactivity, versatility, and ease of use, Phenolyze 2 provides a powerful resource for researchers working with IMPC data. Its capacity to uncover relationships in large-scale phenotyping datasets supports not only hypothesis-driven research but also exploratory analyses, making it a valuable addition to the CCP's portfolio of tools for the international research community.

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