VII Polski Kongres Genetyki
Wrocław, 21-24 września 2026 r.

SESJE PLENARNE

Poniedziałek, 21 września 2026 r.

12.00-14:00 Walny Zjazd Członków PTG (120')

14.00-15:00 Obiad

14.00-15:00 Spotkanie zarządu PTGC (60')

15.00-15:20 Otwarcie Kongresu (20')

15.20-17:00 Sesja Plenarna I

Wykład plenarny I (50')
Tosso Leeb

Wykład plenarny II (50')
Leszek Lisowski

17.00-18:00 Sesja honorowa PTGC (60')

18.00-20:00 Sesja Plakatowa I - Genetyka Człowieka (120')

Wtorek, 22 września 2026 r.

8:30-10:30 Sesja Plenarna II

Wykład plenarny I (30')
Grzegorz Grabe

Wykład plenarny II (30')
Cedric Notredame

Wykład plenarny III
Dziedziczne zaniki nerwów wzrokowych – nowe perspektywy
Hereditary optic nerve atrophies – the new perspectives (30')
Maciej Krawczyński

Wykład sponsorowany (15')

Wykład sponsorowany (15')

Środa, 23 września 2026 r.

8:30-10:30 Sesja Plenarna III

Wykład Plenarny I
Tracing age and lifestyle through epigenetics: new frontiers in forensic genetics and public health (30')
Ewelina Pośpiech

Wykład Plenarny I (30')
Ilona Kryczek

Wykład Plenarny II
Carrot transposable elements (30')
Dariusz Grzebelus

Od Exela do sprawnej analizy danych NGS - doświadczenia laboratoriów diagnostycznych z wykorzystaniem oprogramowania BroVar od Genomed S.A.BroVar jako autorskie oprogramowanie do analizy danych NGS w praktyce laboratoriów diagnostycznych (20') logo: Genomed

Nowoczesne rozwiązania NGS - od próbki do analizy (15') logo: 3gene
Jakub Wudarski

18:15-20:00 Sesja plakatowa - Bioinformatyka, Genetyka zwierząt, Genetyka Roslin, Genetyka Sądowa, Genetyka Mikroorganizmów (105')

Czwartek, 24 września 2026 r.

11:00-13:00 Dyskusja panelowa (w języku polskim) – Genetyka przyszłości między nadzieją a odpowiedzialnością

WARSZTATY SPONSOROWANE

Poniedziałek, 21 września 2026 r.

10:00-13:00 Wstęp do analizy danych DRAGEN - część teoretyczna i praktyczna (180')

Środa, 23 września 2026 r.

11:00-13:00 Wstęp do analizy danych DRAGEN - część teoretyczna (120')

GENETYKA CZŁOWIEKA

Wtorek, 22 września 2026 r.

10.30-11.00 Przerwa kawowa

11.00-13.15

Sesja C1 - Genetyka Człowieka
Zmiany germinalne w nowotworach narządowych człowieka
Prowadzący: Jan Lubiński, Joanna Trubicka

Summary of Research Findings on Polyposis Syndromes in Poland (10')
Andrzej Pławski

Beyond NF1: The Diagnostic Value of Reanalysis and Expanded Panels in Neurofibromatosis Type 1 Testing (10')
Katarzyna Smolińska-Król

Prevalence of Cancer-Predisposing Germline Variants in Children Undergoing Phenotype-Driven Genetic Testing: Results from the Nationwide ONKOPRED Study (10')
Agata Pastorczak

Diagnostic efficiency of whole-exome sequencing (WES) in identifying hereditary cancer predisposition: an analysis of 370 patients (10')
Katarzyna Reszka

Exploring Novel Cancer Predisposition Genes in Children with Secondary Malignancies Using Whole-Genome Sequencing (10')
Kamila Wypyszczak

Germline therapeutic compass – how genetic predispositions modify clinical decisions in pediatric oncology (10')
Joanna Trubicka

Significance of germline variants as predictive biomarkers in precision oncology (10')
Tomasz Stokłosa

An international cohort stuy of breast cancer survival in young women (10')
Jacek Gronwald

Dietary patterns in women attending a genetic counseling clinic according to high-risk breast cancer mutation status (10')
Ewa Grzybowska

Low selenium status and cancer risk in BRCA1 pathogenic variant carriers: a prospective study (10')
Jan Lubiński

Selenium and arsenic status and cancer incidence in women with familial breast cancer predisposition (10')
Jan Lubiński

Germline testing practices across ERN GENTURIS member countries (10')
Milena Kiljańczyk

Overcoming NGS Coverage Bias with CMS Technology: Aplications in Clinical Research (15') logo: KAWA.SKA
Sun Lei

13.15-14.00 Obiad

14.00-16.00

Sesja C2 - Genetyka Człowieka
Badania wysokoprzepustowe - standaryzacja, jakość, VUS
Prowadzące: Izabela Łaczmańska, Marzena Wojtaszewska, Monika Gos

RUO Under Scrutiny: Validation of Molecular Laboratory Testing Methods in Light of IVDR (EU) 2017/746 and ISO 15189:2023 (15')
Izabela Łaczmańska

Niepewność pomiaru w metodach ilościowych na przykładzie oznaczenia ilości kopii BCR::ABL1 (15')
Marzena Wojtaszewska

From DNA to reliable WGS results: optimizing wet-lab parameters and quality control during NGS platform implementation (15')
Martyna Rosa

Dyskusja (10')

Next-Generation Sequencing in regulated Clinical Diagnostics environment (15') logo: Altium International
Bartosz Wojciechowicz

Should every variant of uncertain clinical significance (VUS) be reported in postnatal diagnostics using aCGH? (15')
Ewelina Łazarczyk

Raportowanie wariantów o niepewnym znaczeniu klinicznym (VUS) zgodnie z ACMG (15')
Monika Gos

Dyskusja (20')

16.00-16.15 Przerwa kawowa

16.15-18.00

Sesja C3 - Genetyka Człowieka
Badania prekoncepcyjne, prenatalne i postnatalne
Prowadzący: **Beata Nowakowska, Robert Śmigiel, Hanna Moczulska**

The genetic, chromosomal, and epigenomic landscape of male infertility (15')
Marta Olszewska

Implementation of a Quick and Coordinated Genetic Diagnostic Program for Newborns and Infants with developmental delay and congenital defects: Results and Conclusions from Three Years of Experience (15')
Robert Śmigiel

Nine months of pilot population-based newborn screening for spinal muscular atrophy and severe combined immunodeficiency using a combined assay in Poland (15')
Paulina Kubiszyn

PURA-related neurodevelopmental disorder: clinical delineation and genotype-phenotype study in further seven individuals (15')

Agnieszka Madej-Pilarczyk

Phenotypic characteristics of Polish patients with AGO1 and AGO2 mutations (10')
Michał Zawadka

Clinical evolution and quality of life in Kabuki Syndrome: a 2-year observational study of 45 genetically confirmed Polish patients (15')
Snir Boniel

Exome sequencing for the genetic evaluation of fetuses with craniofacial abnormalities (10')
Agata Kucińska

Dyskusja (10')

16.15-18.00

Sesja C8 - Genetyka Człowieka
Zmiany somatyczne w guzach litych człowieka
Prowadzący: Małgorzata Oczko-Wojciechowska, Magdalena Koczkowska, Artur Kowalik

Application of molecular methods in the differentiation and characterization of bone tumors in children – our own experience (15')
Monika Lejman

Breast cancer in males report on 48 cases (15')
Małgorzata Lisik

Retrospektywna ocena niestabilności mikrosatelitarnej (MSI) jako narzędzie wspierające tworzenie złożonych zbiorów próbek biologicznych (15') logo: Thermo Fisher Scientific

From Validation to Clinical Application: Duplex Sequencing for Detection of Low-Level Mosaicism (15')
Monika Horbacz

The Essential Role of DNA/RNA Next-Generation Sequencing, Rather than Immunohistochemistry, in the Molecular Subtyping of Intrahepatic Cholangiocarcinoma (15')
Małgorzata Chłopek

Epigenetyka w diagnostyce nowotworów ośrodkowego układu nerwowego i mięsaków - game changer w klasyfikacji nowotworów (15')
Joanna Trubicka

Dyskusja (15')

18.00-18.15 Przerwa kawowa

Walne Zebranie Członków PTGC (105')

Środa, 23 września 2026 r.

10.35-11.00 Przerwa kawowa

11.00-13.00

Sesja C4 - Genetyka Człowieka
Hematologia w erze genomiki – od aberracji chromosomowych do wariantów molekularnych.
Prowadzące: Magdalena Zawada, Monika Lejman, Agata Filip, Beata Grygalewicz

Czy genom krąży we krwi? Nowa era diagnostyki molekularnej chłoniaków (15')
Magdalena Zawada

Kiedy kariotyp to za mało. Rola aCGH w hematoonkologii dziecięcej (15')
Monika Lejman

Gdy problemem nie jest sekwencja, tylko liczba. Dziedziczna alfa-tryptazemia (HαT) patomechanizm, diagnostyka, znaczenie kliniczne (15')
Dorota Link-Lenczowska

Regulation of mTOR pathway components by miR-199b-5p, a candidate tumor suppressor in T-ALL (10')
Natalia Maćkowska-Maślak

ETV6-Related Hereditary Thrombocytopenia with Cancer Predisposition in Pediatric Acute Lymphoblastic Leukemia: Insights from a Nationwide Cohort of 1811 Patients (10')
Ewa Juścińska

Genomic landscape and clinical correlates of copy number alterations and loss of heterozygosity in pediatric B-cell acute lymphoblastic leukemia with ETV6::RUNX1 rearrangement (10')
Borys Styka

Clinical and molecular characteristics of inherited bone marrow failures in the Polish population (10')
Katarzyna Bąbol-Pokora

Neurofibromatosis type I vel Fanconi anemia – diagnostic odyssey of two patients with biallelic variants in FANCI and FANCL genes (10')
Anna Repczyńska

Innovative anticancer therapy: from CAR-T to gene therapy (10')
Łukasz Łaczmański

Dyskusja (15')

13.00-14.00 Obiad

14.00-16.00

Sesja C5- Genetyka Człowieka
Genetyka wieku dorosłego - tranzycja, etyka, komunikacja
Prowadzące: Maria Libura, Jolanta Wierzba, Olga Haus

A model of collaboration between clinicians and a patient foundation in the development of translational research on the ultra-rare PACS2 syndrome (15')
Sylwia Czarnecka

How a patient-led initiative accelerates drug development in ultra-rare MAP2K2-related RASopathy (15')
Aleksandra Świeca

Adult phenotype of Cornelia de Lange syndrome: clinical characteristics of a Polish patient cohort (15')
Karolina Śledzińska

Assessment of circulating microRNA profiles in patients with Ehlers-Danlos Syndrome (EDS) (15')
Anna Junkiert-Czarnecka

A critical role of physiotherapy in adults with Ehlers-Danlos syndrome (15')
Marta Jokiel

The Genetic Landscape of Lennox–Gastaut Syndrome in adults (15')
Dorota Hoffman-Zacharska

Personalized therapy in lower extremity artery disease: biomarkers and pharmacogenetics in the COLSTENT study (15')
Ewa Strauss

Dyskusja (15')

16.00-16.15 Przerwa kawowa

16.15-18.15

Sesja C6 - Genetyka Człowieka
Genetyka przyszłości, możliwości terapii
Prowadzący: Grzegorz Węgrzyn, Agata Filip, Jacek Majewski

The Genetics of Epigenetics - dissecting the crosstalks between DNA, RNA, and chromatin (25')
Jacek Majewski

Autophagy Modulation in Huntington's Disease: Insights into Pathogenesis and Therapeutic Potential (20')
Aneta Szulc

Genistein-mediated modulation of mitochondrial and lysosomal pathways in CRISPR/Cas9-engineered cellular models of Huntington's disease (15')
Lidia Gaffke

Development and pilot validation of a targeted NGS panel for analysis of clinically relevant deep intronic and regulatory variants in rare genetic diseases (15')
Katarzyna Wertheim-Tysarowska

WES i co dalej? (15')
Beata Nowakowska

Dyskusja (15')

16.15-18.15

Sesja C9 - Genetyka Człowieka
Neurogenetyka
Prowadzące: Dorota Hoffman-Zacharska, Maria Jędrzejowska, Magdalena Badura-Stronka

Prevalence of genetic variants with therapeutic potential in a Polish Amyotrophic Lateral Sclerosis Cohort: a Single-Center Experience (20')
Monika Jurkowska

Genetic heterogeneity of neurotransmitter-related disorders in undiagnosed Polish children with suspected monoamine defects (20')
Klaudia Ślusarczyk

DYRK1A Syndrome in a Polish Cohort: Phenotypic Characteristics and Parental Quality of Life (20')
Agnieszka Pawelak

Molecular background of Emery-Dreifuss muscular dystrophy – insights into progenitor muscle cells dysfunction (20')
Katarzyna Piekarowicz

ReNU Syndrome in a Polish Cohort: Phenotypic Characteristics, Diagnostic Challenges, and Clinical Implications (20')
Agnieszka Pawelak

Dyskusja (20')

18.00 -18.15 Przerwa kawowa

Czwartek, 24 września 2026 r.

8.30-11.00

Sesja C7 - Genetyka Człowieka
Genetyka narządów zmysłów
Prowadzący: Monika Ołdak, Maciej Krawczyński, Olga Haus

Wykład sponsorowany (15')

Genetic landscape of Usher syndrome in a Polish cohort: high diagnostic yield and functional validation of splice-altering variants (20')
Natalia Bałdyga

Contribution of functional studies to variant interpretation in isolated and syndromic hearing loss (20')
Dominika Oziębło

From Targeted Panels to Whole-Genome Sequencing: Genomic Diagnostics of Hereditary Hearing Loss in a Cohort of 1022 Patients (15')
Dominika Oziębło

Mniej znaczy więcej: kliniczne znaczenie nowej generacji badań NIPT (15')

First transcriptomic analysis of retinal samples from living patients with high myopia (20')

Joanna Świerkowska-Janc

Genetically determined causes of nystagmus in children with pervasive developmental disorders using whole exome sequencing (WES) and RNA sequencing (IMiD research project No. 510-18-50 for the years 2026-2027) (15')
Dorota Barchanowska

Molecular Characterization of Oculocutaneous Albinism in a Single-Center Pediatric Cohort Using Next-Generation Sequencing (15')
Beata Chałupczyńska

CeGaT Exome Xtra - większa skuteczność diagnostyczna (15')
Jacek Łukasik

GENETYKA ZWIERZĄT

Wtorek, 22 września 2026 r.

11.00-13.15

Sesja Z1 - Choroby Genetyczne i Cytogenetyka:

Variants in the 5'UTR region of BRCA1 gene in dogs with mammary gland tumours (30')
Jagoda Radoń

Assessment of chromosomal abnormalities in bull sperm using molecular cytogenetic methods (20')
Wiktoria Kowal-Mierzwa

Reproductive aging and increased sex chromosome aneuploidy in purebred Arabian stallion sperm: a longitudinal sperm-FISH study (20')
Kornelia Gała

Heteroplasmy in the mitochondrial genome observed in dogs with malignant mammary gland tumours (20')
Krzysztof Kowal

Reproductive aging in stallions assessed by sperm RNA profiling: preliminary insights (15')
Kornelia Gała

Dyskusja (30')

13.15-14.00 Obiad

14.00-16.00

Sesja Z2 - Genomika i Epigenomika cz. 1:

Omentin-1 remodels the transcriptome of GT1-7 GnRH neurons and identifies calcium, MAPK and GnRH secretion pathways as targets of metabolic regulation (30')
Natalia Respekta-Długosz

The impact of aflatoxin B1 on the mitochondrial MT-ATP6 gene in the domestic pig (20')
Adrianna Styk

Tissue-specific microRNA expression following in ovo administration of galactooligosaccharides and sodium butyrate in broiler chickens (20')
Sebastian Knaga

Scaling up bovine muscle satellite cell culture towards cultivated meat production: from flasks to bioreactors - preliminary studies (15')
Karolina Zygmunt

Effects of dietary Lepidium meyenii supplementation on molecular and metabolic traits in pigs (15')
Joanna Nowacka-Woszuk

Dyskusja (20')

16.00-16.15 Przerwa kawowa

16.15-18.00

Sesja Z3 - Genomika i Epigenomika cz. 2:

Evaluating the Hepatoprotective Effects of Medicinal Herbs Against Aflatoxin B1 Anatomic and Molecular Toxicity: An In Vivo Pig Model (30')
Chandra Shekhar Pareek

Analysis of mutations in the mitochondrial MT-ND1 gene in dogs with mastocytoma (20')
Oktawia Wojtaszek

A candidate piRNA drives DNA methylation changes in equine sarcoid cells (15')
Ewelina Semik-Gurgul

Deciphering the Hepatic MicroRNA Response to Silybum marianum Herbal Supplementation in a Porcine Model (15')
Sharmin Sultana

Transcriptome analysis revealed differential gene expression in mammary gland lymph nodes of sheep with opposite SRLV infection status and different TMEM154 E35K genotypes (20')
Ewa Grochowska

Dyskusja (5')

Środa, 23 września 2026 r.

10.35-11.00 Przerwa kawowa

11.00-13.00

Sesja Z4 - Genomika i Epigenomika cz. 3:

Transcriptomic Landscape of Coding and Non-Coding RNAs in Normal and Abnormal Canine Gonads (30')
Świtoński Marek

Beyond morphological equivalence: heterogeneity of mtDNA, lipid, and transcript profiles in sister blastomeres of 2-cell parthenogenetic porcine embryos (20')
Marta Janczyn

Hepatic microRNA Profiling Reveals Novel Regulatory Transcripts in Pigs Exposed to Silymarin or Aflatoxin B1 (15')
Varunkumar Asediya

Transcriptomic evidence for tumor suppressor-like activity of eca-miR-200b in equine sarcoid cells (15')
Klaudia Pawlina-Tyszko

Hepatic microRNA Profiling in Pigs Identify a Novel DE Transcripts Associated with DMSO Administration (15')
Athul P. Kurian

Dyskusja (25')

13.00-14.00 Obiad

14.00-16.00

Sesja Z5 - Genetyka populacji i cech ilościowych, nutrigenomika

Native chicken breeds, characteristics of genomes and genetic distances (30')
Marek Sztuka

Changes in the genetic characteristics of rainbow trout in the Rutki Fish Farm in 2011–2025 and their potential importance in aquaculture and conservation of salmonid fish (20')
Dariusz Kaczmarczyk

Associations Between Rumen Microbiome, Production Traits, and Host Genomic Variation in Holstein Cows (10')
Daniel Motyka

Selective hippocampal transcriptional adaptation to chronic cannabidiol exposure in mice (10')
Artur Gurgul

Human-Mediated Dispersal and Environmental heterogenity shape genetic variation of Mytilus spp. in South American Coastal Hybrid Zones (10')
Anita Poćwierz-Kotus

Assessment of Genetic Variability in the Polish Hunting Spaniel Population (10')
Paulina Jundziłł-Bogusiewicz

Parentage testing, genetic diversity and population structure of Huacaya Alpacas (10')
Angelika Mąsior

Dyskusja (20')

16.00-16.15 Przerwa kawowa

GENETYKA ROŚLIN

Wtorek, 22 września 2026 r.

10.30-11.00 Przerwa kawowa

11.00-13.15

Sesja R1 - Genome Organization, Genetic Diversity and Trait Mapping

Prowadzący: Dariusz Grzebelus, Anna Kulma

Hidden diversity within the Medicago truncatula HapMap collection: new chromosome-scale genomes reveal extensive genomic variation and question species boundaries (30')
Agnieszka Żmieńko

Evolutionary Conservation of Pericentromeric Crossover Hotspots in Arabidopsis thaliana (20')
Maja Szymanska-Lejman

Identification of QTLs for yield, thousand-seed weight, and seed coat proportion using a newly developed genetic map of narrow-leaved lupin (20')
Maciej Jakobina

From Genome-Wide Association Analysis to Plant Breeding Practice: Development and Validation of PCR Markers for Marker-Assisted Selection of Blackleg Resistance in Rapeseed (20')
Janetta Niemann

Development and characterization of interspecific hybrids between autotetraploid bilberry (Vaccinium myrtillus L.) and highbush blueberry (Vaccinium corymbosum L.), and identification of genes associated with phenolic compound accumulation in bilberry fruits using NGS (20')
Monika Markiewicz

Dyskusja (25')

13.15-14.00 Obiad

14.00-16.00

Sesja R2 - Epigenetics, RNA Biology and Gene Regulation
Prowadzący: Magdalena Simlat, Agnieszka Żmienko

Molecular Echoes of Time: Non-coding RNA Signatures of Seed Ageing (30')
Maja Boczkowska

Weighted gene co-expression network analysis (WGCNA) reveals candidate genes related to phosphorus-deficiency tolerance in rye (Secale cereale L.) (20')
David Chan-Rodriguez

Histone acetyltransferase expression dynamics during wheat microspore embryogenesis reveal genotype-dependent and homeolog-specific regulatory patterns (20')
Dorota Weigt

Translational landscape of impaired photomorphogenesis in elo3-6 and urm11 urm12 mutants (20')
Magdalena Jarosz-Ostrówka

Wheat small interfering RNAs induced by inoculation with pathogenic and beneficial fungi (20')
Polina Havrysh

Dyskusja (10')

16.00-16.15 Przerwa kawowa

16.15-18.00

Sesja R3 - Functional genetics of plant development
Prowadzący: Małgorzata Podwaszyńska, Hanna Bolibok-Brągoszewska

The Conserved MiaA/MiaB Pathway Supports Chloroplast Translation and Cold Acclimation in Arabidopsis thaliana (30')
Piotr Gawroński

Comparative Analysis of Three-Dimensional Chromatin Organization in Carrot: Identification and Characterization of Topologically Associating Domains (20')
Monika Szewczyk

A mutation in the brassinosteroid biosynthesis gene CsCYP90B1 disrupts vegetative and reproductive development in cucumber (Cucumis sativus L.) (20')
Renata Słomnicka

Development and characteristics of intergeneric Brassica rapa L. subsp. pekinensis × Sinapis alba hybrids of early generations as a new germplasm for the breeding (20')
Piotr Kamiński

Dyskusja (15')

Środa, 23 września 2026 r.

11.00-13.00

Sesja R4 - Abiotic Stress, Adaptation and Plant Phenotyping
Prowadzący: Małgorzata Jędryczka, Agnieszka Kiełkowska

Multiple layers of rye's (Secale cereale L.) phosphorus deficiency response: genetics, epigenetics and beyond (30')
Hanna Bolibok-Brągoszewska

Studies of the effects of temperature and duration of vernalization on flowering time, frost tolerance and the development of the three lupins (Lupinus angustifolius L., Lupinus albus L., Lupinus luteus L.) (20')
Anna Surma

Hyperspectral Imaging as a Tool for Phenotypic Screening of Sugar Beet (Beta vulgaris L.) Genotypes Under Stress Conditions (20')
Michał Nowak

Expression changes of candidate genes for freezing tolerance in wheat under de-acclimated conditions (20')
Magdalena Wójcik-Jagła

Comparative proteome analysis of the response of two rye inbred lines (L9 and K3) to phosphate deficiency stress (20')
Brian Koboyi

Dyskusja (10')

13.00-14.00 Obiad

14.00-16.00

Sesja R5 - Plant Immunity, Plant–Microbe Interactions and Resistance Mechanisms
Prowadzący: Lidia Błaszczyk, Grzegorz Bartoszewski

Structural variation of the Receptor-Like Protein (RLP) Gene Family in the Arabidopsis thaliana genome revealed by Oxford Nanopore sequencing and de novo assemblies (30')
Anastasiia Satyr

Sequential chitosan-fungicide application improves early physiological response and chlorophyll fluorescence in Fusarium-infected barley (20')
Paweł Poznański

miR167c-3p-calmodulin-like (CML) module associated with the resistant flax response to Fusarium oxysporum (20')
Mateusz Chmielarz

Development of SNP marker for gene Pc39 determining oat resistance to Puccinia coronata (20')
Sylwia Sowa

Development of a CRISPR/Cas9-Based Genome Editing Strategy Targeting an ABA Hydrolase Gene in Flax (Linum usitatissimum L.) (20')
Marta Sobolewska

Dyskusja (10')

GENETYKA MIKROORGANIZMÓW

Wtorek, 22 września 2026 r.

10.30-11.00 Przerwa kawowa

11.00-13.15

Sesja M1 -Genetyka Mikroorganizmów

Targeting PNPase-Dependent RNA Homeostasis in Mycobacteria - Implications for Post-Transcriptional Gene Regulation (30')
Yaroslav Lavrynchuk

Bacterial Epigenetics as a Regulatory Layer in Development and Secondary Metabolism of Streptomyces coelicolor A3(2) (20')
Lizaveta Karpovich

Full-length 16S rRNA gene microbiome profiling in morbid obesity using the novel Oxford Nanopore Microbial Amplicon Barcoding Kit reveals associations with metabolic and inflammatory markers (20')
Wojciech Włoszek

Molecular and evolutionary insights into contact-dependent growth inhibition (CDI) systems associated with virulence plasmids of opportunistic bacteria of the genus Cronobacter (20')
Zofia Owczarzak

Oxford Nanopore-based metagenomic survey of bacterial community restructuring and functional predictions in the rhizosphere of invasive Impatiens parviflora (5')
Patryk Wiśniewski

The role of PstP phosphatease in the regulation of growth and coordination of the cell cycle in M. smegmatis (5')
Martyna Pisula

Transposone mutagenesis identifies genetic interactions between parA and genes involved in cell wall biosynthesis (5')
Justyna Ruszkowska

The Effect of Fusarium graminearum on the Expression of Debaryomyces hansenii Genes (5')
Urszula Wachowska

Novel Multifunctional Plasmid Toolkit for Gene Expression Studies in Enterococcus faecium (5')
Anna Barczak

Can we edit the genome of Wolbachia? Strategies for genetic modification of an intracellular bacterium (5')
Wiktor Jakubowski

Dyskusja (15')

13.15-14.00 Obiad

14.00-16.00

Sesja M2 - Mikroorganizmów

The influence of natural selection on the DNA gyrase genes of Mycobacterium tuberculosis (30')
Daria Zygała-Pytlos

PknB-dependent phosphorylation of CslA links beta-glucan synthesis to tip growth regulation in Streptomyces (20')
Bernhard Kepplinger

Structure-function characteristics of CemR regulators in Campylobacter jejuni and Arcobacter butzleri (20')
Łukasz Zambrowski

No room for two polyketides - coelimycin molecules suppress actinorhodin biosynthesis in Streptomyces coelicolor A3(2) (20’)
Bartosz Bednarz

Comparative genome characterisation of Mycobacterium bovis BCG PCM 2097 and PCM 2098 (5')
Katarzyna Bzowa

NanoRNases in Mycobacterium tuberculosis as Promising Molecular Targets for the Development of New Antituberculosis Therapies (5')
Justyna Zadylak

Influence of DNA extraction method on ITS2-based fungal identification (5')
Aleksandra Giza

Nutrient-dependent remodelling of the proteome and lysine acetylome in Rhizobium leguminosarum bv. trifolii TA1: a preliminary study (5')
Małgorzata Marczak

Novel M97 proteases from Bacteroidota phylum (5')
Danuta Mizgalska

Insight into the interactome and regulon of orphan histidine kinase CpkM in Streptomyces coelicolor A3(2) (5')
Mateusz Wenecki

16.00-16.15 Przerwa kawowa

16.15-18.00
Sesja M3 - Mikroorganizmów

The mycobacterial nucleoid-associated protein NapM exhibits stress-induced septal localization and modulates cell envelope gene expression (30’)
Kornel Milcarz

Bacteria resistant to β-lactam antibiotics isolated from horses (20’)
Aleksandra Anna Lepianka

Plasmidome diversity and plasmid-encoded effectors may contribute to pathogenic repertoire of the Legionella genus (20')
Piotr Koper

Sialic acid specificity of Erythrocyte Binding Antigen 140 orthologues in human- and ape infective Laverania species (5')
Patrycja Burzyńska

The Effect of Fusarium graminearum on the Expression of Debaryomyces hansenii Genes (5')
Urszula Wachowska

Autoregulation of the biosynthetic gene cluster by intracellular coelimycin precursors in Streptomyces coelicolor A3(2) (5')
Magdalena Kotowska

Insight into the interactome and regulon of orphan histidine kinase CpkM in Streptomyces coelicolor A3(2) (5')

Mateusz Wenecki

Interactions between the Hpn protein from Helicobacter pylori and amyloid-β in the context of Alzheimer's disease (5')
Oliwia Polańska

Molecular Basis of DivIVA-Driven Polar Growth in Streptomyces venezuelae (5')
Diana Valietova

Evolutionary dynamics of secondary metabolite gene clusters in Fusarium graminearum (5')
Katarzyna Bilska

BIOINFORMATYKA

Wtorek, 22 września 2026 r.

10.30-11.00 Przerwa kawowa

11.00-13.15
Sesja B1 - Bioinformatyka

From gut to brain: The impact of bacterial functional amyloids on neurodegeneration (30')
Małgorzata Kotulska

Evaluating Dimensionality Reduction Techniques and Neural Network Architectures for High-Dimensional, Small-Sample Microbiome Classification (20')
Marek Sztuka

Comparison of Hyperparameter Optimization Tools in Deep Learning Using Autoencoders in the context of Classification (20')
Joanna Szyda

Comparative evaluation of AVITI, MGI and Illumina NGS Platforms for Molecular Oncology Diagnostics (20')
Szczerba Ewelina

Attention-Based Imputation of Structural Variants: Genotype Prediction in Low- and High-LD Genomes (15')

Application of molecular dynamics for the analysis of selected peptide groups (15')
Paweł Mackiewicz

Dyskusja (15')

13.15-14.00 Obiad

14.00-16.00
Sesja B2 - Bioinformatyka

Changes in codon usage during evolution of SARS-CoV-2 genomes (30')
Pawel Blażej

SNP Analyser: a website tool for rapid bioinformatic interpretation of mitochondrial DNA variants (20')
Norbert Ozga

A Reproducible Bioinformatic Workflow for Nanopore-Based Bacterial Methylome Analysis (20')
Lizaveta Karpovich

Exploratory DNA methylation profiling uncovers subgroup heterogeneity in BCOR-altered central nervous system tumors (20')
Oktawia Korcz

Bioinformatic investigation of starch metabolism in ciliates (15')
Kacper Ludwig

PLegio: app for comparative visualisation of Legionella genus plasmidome (15')
Katarzyna Burda

16.00-16.15 Przerwa kawowa

16.15-18.00

Sesja B3 - Bioinformatyka

Alternative splicing in triple-negative breast cancer: from patient biopsies to patient-derived xenograft models (20')
Katarzyna Nowis

Omentin-induced transcriptomic remodeling of porcine granulosa cells: protein-coding and long non-coding RNA signatures of follicular microenvironment regulation (20')
Edyta Rytelewska

Variant-aware prediction and experimental validation of CRISPR-Cas9 nucleases and base editor off-target sites in HEK293T cells (15')
Maciej Powierża

Bioinformatic Identification of HMB-Responsive Genes and Pathways in a DMDmdx Rat Model (15')
Abdolvahab Ebrahimpour Gorji

Comparative Hepatic microRNA Profiling in Pigs Identifies Novel DE Transcripts Associated with Andrographis paniculata Hepatoprotection and Aflatoxin B1 Hepatotoxicity (15')
Prarthana Sharma

Synergetic Hepatic microRNA Profiling in Pigs Identifies Novel Differentially Expressed Transcripts Associated with DMSO and Aflatoxin B1 Hepatotoxicity (15')
Nihal Purohit

Dyskusja (5')

18.00-18.15 Przerwa kawowa

GENETYKA SĄDOWA

Środa, 23 września 2026 r.

10.35-11.00 Przerwa kawowa

11.00-13.00

Sesja S1 - Genetyka Sądowa

Investigative Genetic Genealogy: From Genome-wide SNP Data to Investigative Leads (30')
Marta Sobota

Validation of the FORCE Panel for Extended Kinship Analysis Using Massively Parallel Sequencing (20')
Maria Wróbel

Jak DNA prowadzi do wspólnego przodka? Molekularne, genealogiczne i algorytmiczne podstawy sądowej genealogii genetycznej (20')
Magdalena Spólnicka

FacePainter – a comprehensive tool for forensic DNA phenotyping (20')
Katarzyna Urbanelis

Assessment of the Kinfinder kit suitability for analyzing bone material for identification purposes (15')
Krzysztof Żak

From Turing models to neural networks: the genetic architecture of fingerprints in DNA phenotyping and forensic systems (15')
Natalia Rogalska-Niżnik

13.00-14.00 Obiad

14.00-16.00

Sesja S2- Genetyka Sądowa

Dilemmas in Predicting Biogeographical Ancestry from Mitochondrial DNA: The Case of the "Vampire" of Pień (30')
Tomasz Grzybowski

Comparison of EuroForMix and DNAStatistiX in likelihood ratio analysis of DNA mixtures (20')
Marcin Woźniak

Comparison of Likelihood Ratios for Real DNA Casework Mixtures Using DNAStatist X and LRmix Studio (20')
Magdalena Marcińska

Epigenetic age prediction in sperm cells for forensic applications using ForSpEC model (20')
Aleksandra Pisarek-Pacek

Automation makes the difference – manual vs automated DNA preferential lysis in sexual assault cases (15')
Agnieszka Parys-Proszek

Utilizing DNA Methylation Markers in Bone and Cartilage for Victim Identification (15')
Kamila Marszałek

16.00-16.15 Przerwa kawowa