5th LIFE SCIENCES CONGRESS

Acıbadem University
Kerem Aydınlar Campus
Conference Hall

April 18th - 19th 2026

09.00 - 19.00

ACIBADEM
ÜNİVERSİTESİ

Değerli Katılımcılar,

ACUGEN 5. Yaşam Bilimleri Kongresi'ne hoş geldiniz.

18–19 Nisan 2026 tarihlerinde Acıbadem Üniversitesi'nde düzenlenen bu kongre, ulusal ve uluslararası düzeyde genç araştırmacıları, akademisyenleri ve bilim insanlarını bir araya getirerek bilimsel fikir alışverişi ve disiplinler arası etkileşim için güçlü bir platform sunmaktadır.

Bu yıl kongremiz, yaşam bilimlerinin geleceğini yapay zekâ teknolojileri ve uzay biyolojisinin kesişiminde ele alan yenilikçi bir tema etrafında şekillenmiştir. Yapay zekâ destekli biyolojik analizler ve ekstrem koşullarda yaşam araştırmaları, bilimsel keşfin yeni ufuklarını ortaya koymaktadır.

Kongre kapsamında moleküler biyoloji, biyoinformatik, nörobilim, biyoteknoloji, immünoloji ve rejeneratif tıp gibi birçok alanda düzenlenen oturumlar, workshoplar ve poster sunumları ile katılımcılara zengin bir bilimsel içerik sunulmaktadır.

Genç araştırmacıların çalışmalarını sunabilecekleri ve alanında uzman bilim insanları ile etkileşim kurabilecekleri bu ortamı oluşturabilmekten büyük mutluluk duyuyoruz.

Katkı sağlayan tüm konuşmacılara, katılımcılara ve organizasyon ekibine teşekkür eder, verimli ve ilham verici bir kongre geçirmenizi dileriz.

Saygılarımızla,
ACUGEN Organizasyon Ekibi

Dear Participants,
On behalf of the organizing committee, we are delighted to welcome you to the ACUGEN 5th Life Sciences Congress, held on April 18–19, 2026 at Acıbadem University.

This congress brings together young researchers, academics, and professionals from both national and international platforms, providing a dynamic environment for the exchange of scientific ideas and interdisciplinary collaboration.

This year, our congress is centered around a forward-looking theme that explores the future of life sciences at the intersection of artificial intelligence and space biology. By combining AI-driven approaches with research on life in extreme environments, we aim to highlight innovative perspectives shaping the next generation of scientific discovery.

Our scientific program covers a broad spectrum of disciplines including molecular biology, bioinformatics, neuroscience, biotechnology, immunology, and regenerative medicine. Through keynote talks, scientific sessions, workshops, and poster presentations, we strive to create a platform where knowledge is shared, ideas are challenged, and collaborations are born.
We are especially proud to support young researchers by providing opportunities to present their work and engage with leading scientists in their fields.

We sincerely thank all participants, speakers, and contributors for being part of this inspiring scientific journey.
We wish you a productive and enjoyable congress.

Sincerely,
ACUGEN Organizing Committee

KONGRE HAKKINDA GENEL BİLGİLENDİRME

GENERAL INFORMATION ABOUT CONGRESS

The ACUGEN 5th Life Sciences Congress is an international scientific event organized by Acıbadem University Molecular Biology and Genetics Club ACUGEN, bringing together young researchers, academics, and professionals from diverse fields of life sciences.
The congress is centered around a forward-looking theme that explores the future of life sciences at the intersection of artificial intelligence technologies and space biology. It highlights the growing role of AI-driven approaches in biological data analysis, as well as the impact of extreme space environments on living systems, encouraging innovative perspectives that emerge from the convergence of these rapidly evolving fields.
In addition to this interdisciplinary framework, the congress encompasses a wide range of core and applied disciplines, including molecular biology, bioinformatics, neuroscience, biotechnology, immunology, and stem cell biology. Particular emphasis is placed on precision immunology, targeted therapies, and immune engineering approaches, alongside stem cell-based therapeutic strategies, regenerative medicine, and tissue engineering applications, reflecting the expanding role of life sciences in advancing personalized and translational medicine.
Through keynote lectures, thematic scientific sessions, workshops, and oral and poster presentations, the congress aims to foster interdisciplinary collaboration, support young researchers, and provide a platform for sharing cutting-edge scientific research.

About the Congress

The ACUGEN 5th Life Sciences Congress is an international scientific meeting that aims to bring together young researchers and scientists working across diverse fields of life sciences.
The congress focuses on fostering interdisciplinary collaboration and promoting innovative research at the intersection of biology, artificial intelligence, and space sciences.
The program includes keynote lectures, thematic scientific sessions, workshops, and oral and poster presentations, offering participants the opportunity to share their research and engage in meaningful discussions.

ACUGEN TANITIMI
PRESENTATION OF ACUGEN

2015 yılında kurulan Acıbadem Üniversitesi Moleküler Biyoloji ve Genetik Kulübü (ACUGEN), biyoloji ve genetik alanlarında bilimsel farkındalık yaratmak, öğrencilerin araştırma kültürünü geliştirmek ve multidisipliner düşünme becerilerini desteklemek amacıyla kurulmuş bir öğrenci topluluğudur.
Kurulduğu günden bu yana ACUGEN, her yıl düzenlediği seminerler, workshoplar, film gösterimleri, bilimsel kongreler ve sosyal farkındalık etkinlikleriyle öğrencileri bilimle daha yakın bir ilişki kurmaya teşvik eden aktif bir öğrenci topluluğu olmuştur. Geçmiş yıllarda düzenlenen çeşitli akademik ve uygulamalı etkinliklerle, üyelerimizin hem laboratuvar deneyimi hem de bilimsel iletişim becerileri güçlendirilmiştir.
2025–2026 döneminde kulübümüz; bilimsel tartışma oturumları, dergi çalışmaları, workshoplar ve sosyal buluşmalar aracılığıyla öğrencilere çok yönlü bir öğrenme ortamı sunmayı sürdürmektedir.
Ayrıca, Nisan 2026'da düzenlenecek olan 5. Yaşam Bilimleri Kongresi ile ulusal ve uluslararası düzeyde genç araştırmacıları bir araya getirmeyi hedeflemekteyiz. ACUGEN olarak amacımız; bilimsel merakı, yenilikçi düşünceyi ve toplumsal sorumluluk bilincini bir araya getirerek, geleceğin bilim insanlarına ilham veren bir topluluk olmaktır.

Acibadem University Molecular Biology and Genetics Club (ACUGEN) was founded in 2015 and is a student organization established with the aim of raising scientific awareness in the fields of molecular biology and genetics, fostering a strong research culture among students, and supporting the development of multidisciplinary thinking skills.
Since its establishment, ACUGEN has been an active student community that encourages students to build a closer connection with science through seminars, workshops, film screenings, scientific congresses, and social awareness events organized annually. Through various academic and hands-on activities held in previous years, our members have strengthened both their laboratory experience and scientific communication skills.
In the 2025–2026 academic year, our club will continue to provide students with an effective learning environment through scientific discussion sessions, journal clubs, workshops, and social gatherings. Particularly, with the 5th Life Sciences Congress, planned to be held in April 18-19 2026, ACUGEN aims to bring together young and hardworking students at both national and international levels.
As ACUGEN, our mission is to inspire future scientists by combining scientific curiosity, innovative thinking, and a strong sense of social responsibility.

ORGANİZASYON KOMİTESİ
ORGANIZATION COMMITEE

ORGANIZATION COMMITEE

Congress Advisor: Prof. Dr. Batu Erman

Club President: Maşallah Akiba

Club Vice President: Ferhat Keleş

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Team Member: Nehir Mert

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Team Member: Hilal Becerik

Team Member: Nur Sena Bakgör

Team Member: Zeynep Bilge

BİLİM KURULU

SCIENTIFIC COMMITEE

THE SCIENTIFIC COMMITEE

- Prof. Dr. Batu Erman, Acıbadem University
- Dr. Dilay Hazal Ayhan, Acıbadem University
- Dr. Nazan Saner, Acıbadem University
- Prof. Dr. Özden Hatırnaz NG, Acıbadem University
- Prof. Dr. Günseli Bayram Akçapınar NG, Acıbadem University
- Dr. Yiğit Kocagöz, Acıbadem University; and Bahçeşehir University

AKIŞ

SCIENTIFIC PROGRAM

5TH LIFE SCIENCES CONGRESS SCHEDULE

APRIL 18 OFFICIAL PROGRAM

08.00 - 09.00 : **Registration**

09.00 - 09.20 : **Opening Remarks**

PRECISION IMMUNOLOGY, TARGET-BASED THERAPIES AND IMMUNE ENGINEERING

09.20 - 10.20 : **Keynote - Prof. Dr. Béla Melegh, University of Pécs**

Rare diseases: Challenges and rewards in future research, diagnostics, and therapy

COFFEE BREAK

10.40 - 11.20 : **Invited Speaker - Prof. Dr. Mayda Gürsel, İzmir Biomedicine and Genome Center**

Vaccine development against bacterial and parasitic diseases

11.20 - 12.00 : **Invited Speaker - Prof. Dr. İhsan Gürsel, İzmir Biomedicine and Genome Center**

Immunomodulatory applications of Extracellular Vesicles

LUNCH BREAK & POSTER PRESENTATIONS

LIFE BEYOND EARTH: ASTROBIOLOGY AND ORIGINS OF LIFE

13.30 - 14.30 : **Keynote - Research Associate Daniela Bezdan, University of Tübingen**

Becoming Multi-Planetary: The Biology of Life Beyond Earth

14.30 - 15.05 : **Invited Speaker - Prof. Dr. Alexandre Rosado, King Abdullah University of Science and Technology**

Alien Life Starts on Earth:
Engineering Life for Earth and Beyond

COFFEE BREAK

15.20 - 16.00 : **Invited Speaker - Asst. Prof. Georgios Miliotis, University of Galway**

Insights from 30 Years of Microbial Tracking in Spacecraft, Orbital Stations, and Spacecraft Assembly Facilities

16.00 - *16.30 :* **Invited Speaker - Dr. Stefan Green, Rush University**

Effects of spaceflight on gut microbiome

COFFEE BREAK

16.45 - 18.30 : **WORKSHOPS**

ACIBADEM ÜNİVERSİTESİ

5TH LIFE SCIENCES CONGRESS SCHEDULE

APRIL 18 OFFICIAL PROGRAM

Poster Presentation Details:

Ece Öner - Yıldız Technical University

Modeling of biological networks and analysis of multi-omics data
Page 57

İlayda Döndürür - Marmara University

Antibacterial Activity of Hypogymnia tubulosa Lichen Extract Against
Page 58-59

İrem Ece Kadıoğlu - Çanakkale Onsekiz Mart University

Reprogramming of Alternative Splicing During Monilinia laxa Pathogenesis
Page 60-61

Kerem Çotuk - Acıbadem University

LAMA5 Variants Modulate Immune Cell Infiltration Across a 2D BBB Model in MS
Page 62-63

Musa Al Hassan Kromah & İbrahim Bah - Çukurova University

Machine Learning-Based Genomic Prediction and SHAP Interpretation of Meropenem Resistance in Klebsiella pneumoniae
Page 64-65

Seher Zeynep Sonkaya - Acıbadem University

Predicting Transcriptomic Responses to Genetic Perturbations via Similarity-Based Atlas Mapping
Page 66-67

Umut Kılınçkaya & Ariorad Moniri - Acıbadem University

CAPVIC: A Production-Grade MCP Server for Precision Oncology Variant Classification
Page 68-69

5TH LIFE SCIENCES CONGRESS SCHEDULE

APRIL 19 OFFICIAL PROGRAM

08.45 - 09.20 : **Registration**

COMPUTIONAL BIOLOGY, SYSTEMS MODELLING & AI DRIVEN BIOTECHNOLOGY

09.20 - 10.20 : **Keynote - Dr. Ahmet Süreyya Rifaioglu, Heidelberg University**

Engineering Machine Learning in the Era of Single-Cell and Spatial Data

COFFEE BREAK

10.40 - 11.20 : **Invited Speaker - Assoc. Prof. Ogün Adebali, Sabancı University**

Evolutionary representation at the molecular level provides insights into biology and health

11.20 - 12.00 : **Invited Speaker - Assoc. Prof. Mehmet Baysan, İstanbul Technical University**

Clinical NGS Analyses at the Intersection of Information and Genome Tech

LUNCHTIME

STEM CELLS, REGENERATIVE MEDICINE & TISSUE ENGINEERING

13.00 - 14.00 : **Keynote - Prof. Dr. Dilek Telci Temeltaş, Yeditepe University**

The Fate of a Cell: The Process of Carcinogenesis, the Dual Role of TG2, and Targeted Treatment Strategies

COFFEE BREAK

14.10 - 14.50 : **Invited Speaker - Assoc. Prof. Ahmet Acar, Middle East Technical University**

Establishing a Molecularly Characterised Living Biobank of Patient-Derived Organoids in Metastatic Colorectal Cancer

14.50 - 15.30 : **Invited Speaker - Asst. Prof. Ece Öztürk, Koç University**

Modeling cancer with tissue engineering

COFFEE BREAK

15.45 - 17.15 : Rising Stars: Young Researchers Oral Presentations

COFFEE BREAK

17.30 - 18.00 : Award Ceremony & Closing Remarks

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5TH LIFE SCIENCES CONGRESS SCHEDULE

APRIL 19 OFFICIAL PROGRAM

Rising Stars: Young Researchers Oral Presentations

***15.45 - 16.00 : Ferdi Oğuz* - Koç University**

Optimization of a GelMA-Based 3D Ex Vivo Model Using Amniotic Fluid and Chorionic Villus Cells for Fetoplacental Research

Page 46-47

16.00 - 16.15 : *Anmol Aggarwal* - UC Berkeley University

From Prediction to Generation: Decision Criteria for Selecting Traditional ML or Generative AI in Organizations

Page 48

16.15 - 16.30 : *Gulnoza Esenova* - Tashkent State Medical University

Genomic Analysis Of SARS-CoV-2 Variants Circulating In Uzbekistan

Page 49-50

16.30 - 16.45 : *Mehmet Alp Garipoğlu* - Konstantz University

Designing AAV Vector Delivery Systems with Nanobody Assisted Targeting

Page 51-52

16.45 - 17.00 : *Maftunakhon Sadikhova* - Research Institute of Plant Genetic Resources

Optimization Of CALLUS Induction From COTYLEDON Explants Of Tomato (SOLANUM LYCOPERSICUM L.) As A Platform For CRISPR/CAS9- Mediated Genome Editing

Page 53-54

OTURUM DETAYLARI

SESSION DETAILS

PRECISION IMMUNOLOGY, TARGET-BASED THERAPIES AND IMMUNE ENGINEERING

- *Rare diseases: Challenges and rewards in future research, diagnostics, and therapy*
- *Vaccine development against bacterial and parasitic diseases*
- *Immunomodulatory applications of Extracellular Vesicles*

LIFE BEYOND EARTH: ASTROBIOLOGY AND ORIGINS OF LIFE

- *Becoming Multi-Planetary: The Biology of Life Beyond Earth*
- *Alien Life Starts on Earth: Engineering Life for Earth and Beyond*
- *Insights from 30 Years of Microbial Tracking in Spacecraft, Orbital Stations, and Spacecraft Assembly Facilities*
- *Effects of spaceflight on gut microbiome*

WORKSHOPS

Laboratory & Data Analysis Skills

- *Quantifying Plant Pigments: A hands-on session using spectrophotometry to measure chlorophyll and anthocyanin levels in plants.*
- *WES Analysis (FASTQ to VCF): A step-by-step guide to processing whole exome sequencing data, moving from raw sequences to variant calling and prioritization.*
- *Primer Design: Covers the fundamental principles and practical use of tools like Primer3 for PCR and qPCR experiments.*
- *Excel 101 for Molecular Biology: Teaches students how to manage experimental data, create growth curves, and apply basic statistics using Excel.*

Research & Career Development

- *AI Tools in Academic Research: Explores how to integrate AI into your workflow for literature reviews, hypothesis generation, and scientific writing.*
- *CV and LinkedIn Workshop: Provides strategies for building strong, visible professional profiles to boost career opportunities.*

Ethics & Specialized Applications

- *CRISPR Ethics: A structured, scenario-based debate focusing on the complex ethical dilemmas surrounding gene editing and scientific responsibility.*
- *Perfume Making: An introductory workshop on the fundamentals of perfumery, where participants blend essential oils to create a custom fragrance.*

COMPUTIONAL BIOLOGY, SYSTEMS MODELLING & AI DRIVEN BIOTECHNOLOGY

- *Engineering Machine Learning in the Era of Single-Cell and Spatial Data*
- *Evolutionary representation at the molecular level provides insights into biology and health*
- *Clinical NGS Analyses at the Intersection of Information and Genome Tech*

STEM CELLS, REGENERATIVE MEDICINE & TISSUE ENGINEERING

- *The Fate of a Cell: The Process of Carcinogenesis, the Dual Role of TG2, and Targeted Treatment Strategies*
- *Establishing a Molecularly Characterised Living Biobank of Patient-Derived Organoids in Metastatic Colorectal Cancer*
- *Modeling cancer with tissue engineering*

RİSİNG STARS: YOUNG RESEARCHERS ORAL PRESENTATİONS

The "Rising Stars" session at the Acugen 5th Life Sciences Congress provides a dynamic platform for promising early-career researchers to showcase their innovative approaches and original research. Featuring poster and abstract presentations, the session highlights the latest scientific advancements across a broad spectrum of fields, from molecular biology and biotechnology to systems modeling and AI-driven analytics.

As presenters share their key findings, methodologies, and the potential clinical and scientific implications of their work, they will have the invaluable opportunity to engage directly with established experts. Designed to strengthen interdisciplinary collaboration and foster scientific productivity, the "Rising Stars" session empowers young scientists to gain visibility and expand their academic networks, ultimately creating an inspiring, interactive, and insightful experience for all attendees.

KONUŞMACI PROFİLLERİ

SPEAKER PROFILES

Precision Immunology, Target-Based Therapies and Immune Engineering



Prof. Dr. Béla Melegh

University of Pécs, Hungary

Prof. Dr. Béla Melegh, MD, PhD, DSc, is Professor of Medical Genetics and Pediatrics at the University of Pécs, Hungary, where he graduated in 1978. His long-standing scientific interest focuses on the genetic and genomic basis of rare and undiagnosed diseases.

Dr. Melegh is actively involved in the undergraduate and postgraduate education of medical doctors and biologists and previously served as Vice-Dean of the Faculty of Medicine at the University of Pécs (2003–2007).

Throughout his career, he has held several leading professional roles, including President of the Hungarian Society of Human Genetics (2010–2018), Board Member of the European Society of Human Genetics (2010–2015), President of the Medical Genetics and Genomics Branch of the European Board of Human Genetics (2014–2019), and President of the Clinical Genetics Section of the UEMS (2014–2018).

He has participated in 23 national and EU-funded research projects and has co-authored more than 400 peer-reviewed scientific publications.

Precision Immunology, Target-Based Therapies and Immune Engineering



Prof. Dr. İhsan Gürsel

Izmir Biomedicine and Genom Center

Prof. Dr. İhsan Gürsel is the former Director of Izmir Biomedicine and Genome Center (IBG) and currently leads the ThorLab Adjuvant Innovation and Nanobiotechnology Research Laboratory.

With over 30 years of experience in research and governmental institutions, his work focuses on immunology, vaccinology, nanomedicine, and biomaterials.

His research explores the immunomodulatory effects of DNA on the mammalian immune system and aims to develop innovative therapies for cancer, autoimmune, autoinflammatory, and infectious diseases through an interdisciplinary approach.

He has supervised more than 50 graduate theses and published over 100 peer-reviewed articles and book chapters, along with multiple patent applications.

His lab co-pioneered the development of a Virus-Like Particle (VLP) COVID-19 vaccine, the only candidate containing all four structural protein antigens to reach first-in-human clinical trials during the pandemic.

With more than 15,500 citations (H-index: 51), he is a full member of the Turkish Academy of Sciences and a former president of the Turkish Society of Immunology.

Precision Immunology, Target-Based Therapies and Immune Engineering



Prof. Dr. Mayda Gürsel

Izmir Biomedicine and Genom Center

Prof. Dr. Mayda Gursel received her PhD from the University of London, The School of Pharmacy, in 1995. Her research focuses on pattern recognition receptor ligands and their therapeutic applications as immune modulators and vaccine adjuvants.

Between 1998 and 2006, Dr. Gursel worked at the U.S. Food and Drug Administration (FDA), Center for Biologics Evaluation and Research (CBER) at the NIH campus, first as a postdoctoral fellow and later as a senior scientist, where she was involved in the regulation of viral vaccine products.

Following her position at Middle East Technical University (METU), Prof. Gursel joined the Izmir Biomedicine and Genome Center (IBG). Her research at IBG focuses on deciphering the mechanisms and immunotherapeutic applications of innate immune system sensors. Another important line of her research investigates the immunomodulatory effects of microbial-derived extracellular vesicles, as well as the design of effective adjuvants and vaccines against infectious diseases.

Her research group also pioneered the development of a Virus-Like Particle (VLP) vaccine during the COVID-19 pandemic. Currently, she is heavily investing her efforts in understanding the immunological manifestations of primary immune deficiencies and the mechanisms underlying immune dysregulation.

Prof. Gursel has published over 100 peer-reviewed articles and book chapters, which have received more than 14,000 citations (H-index: 44), and she is listed as co-inventor on more than 10 international patents.

Computational Biology, Systems Modelling and AI Driven Biotechnology



Assoc. Prof. Mehmet Baysan

Istanbul Technical University

Assoc. Prof. Mehmet Baysan is currently a faculty member in the Department of Computer Engineering at Istanbul Technical University. He is also the founder and head of BaysanLab, an interdisciplinary research group bringing together experts from Computer Engineering, Genetics, Biotechnology, and Medicine.

Dr. Baysan graduated from the Department of Computer Engineering at Bilkent University in 2003. He then completed his M.S. and Ph.D. degrees in Computer Science at The University of Texas at Dallas in 2005 and 2008, respectively.

In 2010, Dr. Baysan shifted his research focus to computational biology as a postdoctoral researcher at the Neuro-Oncology Branch of the National Cancer Institute (NCI), part of the National Institutes of Health (NIH) in the United States. He later continued his bioinformatics research as a full-time researcher at the NYU Cancer Institute in 2013 and at Weill Cornell Medical College in 2015.

His research mainly focuses on transforming health, particularly genetic, data into efficient diagnostic and therapeutic information through computational methods, and developing practical tools that can advance biotechnology and medicine.

Computational Biology, Systems Modelling and AI Driven Biotechnology



Assoc. Prof. Ogün Adebali

Sabancı University

Dr. Ogün Adebali received his undergraduate degree from the Department of Molecular Biology and Genetics at Middle East Technical University. He began his doctoral studies in the United States at the University of Tennessee, where he transitioned from experimental biology to computational biology and completed his PhD on the molecular evolution of proteins.

He continued his research as a postdoctoral fellow at Oak Ridge National Laboratory, and later at the University of North Carolina, focusing on genome-scale analyses of DNA damage and repair.

Since 2018, Dr. Adebali has been leading his own research group at Sabancı University, where he conducts research on DNA damage responses, mutational mechanisms, and evolutionary genetics.

Dr. Adebali has received several prestigious awards, including the 2018 EMBO Installation Grant, the 2019 TÜBİTAK International Fellowship for Outstanding Researchers, the 2019 BAGEP Award, the 2021 TÜBA-GEBİP Award, the 2022 METU Mustafa Parlar Foundation Research Incentive Award, and the 2024 TÜBİTAK Incentive Award.



Dr. Ahmet Süreyya Rifaioğlu

Heidelberg University, Germany

Dr. Ahmet Süreya Rifaioğlu is a researcher at the Institute for Computational Biomedicine, Heidelberg University, Germany. He received his PhD from the Department of Computer Engineering at Middle East Technical University, where his doctoral research focused on applying machine learning and deep learning approaches to computational drug discovery.

During his PhD, he also spent one year as a predoctoral visiting researcher at the European Bioinformatics Institute (EMBL-EBI) in Cambridge, UK.

Following the completion of his PhD, Dr. Rifaioğlu joined the Saez Lab at Heidelberg University as a postdoctoral researcher in the Deep Learning for Single Cell in Cancer (DEEP-SC2) project, funded by Germany's Federal Ministry of Education and Research (BMBF). In 2023, he was awarded the Medical Data Scientist Fellowship by Heidelberg University.

His research focuses on developing problem-driven algorithms for computational scientific discovery to advance our understanding of disease mechanisms. Currently, he is designing methods to identify clinically relevant spatial regions and cellular interactions in cancer, with a particular focus on brain tumours, using large-scale spatial and single-cell data.



Asst. Prof. Dr. Georgios Miliotis

University of Galway, Ireland

Dr. Georgios Miliotis is an Assistant Professor at the School of Medicine, University of Galway, working at the intersection of microbial ecology, infectious diseases, and space microbiology/planetary protection.

He leads a hybrid wet-lab and computational research group that integrates cultivation, multi-omics, and comparative genomics to investigate how microorganisms persist, adapt, and evolve across extreme and engineered environments, including spacecraft cleanrooms, the International Space Station, and terrestrial clinical and environmental systems relevant to One Health.

His research focuses on translating ecological and evolutionary insights into practical risk frameworks by linking genotype to phenotype, analyzing mobile genetic elements, and identifying virulence and fitness determinants that affect microbial survival, transmission, and treatment outcomes.

His team also develops predictive models for microbial survivability under mission-relevant conditions, including simulated microgravity and resource-limited environments, using quantum and quantum-inspired optimization methods.

Dr. Miliotis is a member of the Scientific Committee of the European One Health Association (EOHA) and is affiliated with the Ryan Institute at the University of Galway and the Centre for Personalised Medicine at Ulster University.



Danlela Bezdan

University of Tübingen

Dr. Daniela Bezdan is a genomics scientist and serial biotech entrepreneur working at the intersection of astronaut health, astrobiology, and AI-driven precision medicine.
She has contributed to major astronaut omics research initiatives, including the NASA Twin Study, and has led pathogen surveillance studies on the International Space Station, generating important datasets on biological adaptation in microgravity.
She serves as Chair of the NASA GeneLab Microbes Analysis Working Group and Co-Chair of ISSOP, where she contributes to the standardization and large-scale integration of space omics data.
Her research on extremophiles also addresses fundamental questions about the origin and limits of life.
Dr. Bezdan is the CEO of dxOmics GmbH, a company developing AI-driven genomic diagnostics that aim to reduce clinical timelines from weeks to nearly one hour. She is also the founder of Hairy Therapeutics, which is building a non-invasive platform for patient-specific stem cells and organoids for precision medicine and space-enabled drug discovery.
Her work brings together space biology, genomics, and clinical translation to advance healthcare both on Earth and beyond.



Prof. Dr. Alexandre Rosado

King Abdullah University of Science and Technology

Prof. Alexandre S. Rosado is a Professor of Bioscience at King Abdullah University of Science and Technology (KAUST). He is a Fellow of the American Academy of Microbiology, an International Fellow of The Explorers Club, and serves as a Global Ambassador for Applied Microbiology International (AMI).

He is a microbial ecologist whose research explores the hidden potential of microbes to address global challenges, ranging from climate resilience to biotechnology and space exploration. His work focuses on extremophiles, microbiomes, and microbial innovation, investigating how life adapts to extreme environments, from deserts and deep-sea ecosystems to simulated extraterrestrial conditions.

Prof. Rosado's research combines classical microbiology, including microbial isolation and physiology, with advanced omics and analytical approaches to study the evolution of metabolisms, novel biochemical pathways, and their biotechnological applications.

Before joining KAUST, he served as a Full Professor at the Federal University of Rio de Janeiro (UFRJ), a Visiting Professor at UC Davis, and Director of the Institute of Microbiology.

At the congress, Prof. Rosado will contribute to the session with his talk:
"Alien Life Starts on Earth: Engineering Life for Earth and Beyond"



Dr. Stefan Green

Rush University

Dr. Stefan Green is a Professor in the Department of Internal Medicine, Division of Infectious Diseases, at Rush University. He also serves as the faculty advisor for the Genomics and Microbiome Core Facility (GMCF), Director of Core Lab Services in the Office of Research Affairs, and Institutional Official at Rush University.

With over 15 years of leadership experience in academic core facilities at UIC and Rush University, Dr. Green has built a distinguished career at the intersection of microbial ecology, molecular biology, and translational research.

Scientifically, he is a microbial ecologist and molecular biologist whose work focuses on investigating biological systems through cultivation-independent molecular analyses of DNA and RNA. Over the years, he has studied microbial communities in hypersaline environments, plant roots, and contaminated groundwater.

His current research primarily explores the interactions between complex microbial communities and eukaryotic hosts across a variety of experimental and disease settings. A major focus of his recent work is the effect of spaceflight on host-associated microbial communities, particularly the gut microbiome.

Dr. Green has contributed to the analysis of fecal microbiome data in several major spaceflight studies, including RR-1, RR-6, RR-7, MHU-8, and the NASA Twins Study. With more than 30 years of research experience, he has authored over 275 peer-reviewed publications.



Prof. Dr. Dilek Telci Temeltaş

Yeditepe University

Prof. Dr. Dilek Telci Temeltaş is a Professor of Molecular Cell Biology in the Department of Genetics and Bioengineering at Yeditepe University. She received her BSc in Biology, MSc in Medical Genetics and Immunology, and PhD in Molecular Cell Biology from Middle East Technical University, Brunel University London, and Nottingham Trent University, respectively.

Following her postdoctoral and research associate fellowships at Sabancı University and Aston University, she joined the Department of Genetics and Bioengineering at Yeditepe University

The primary focus of Prof. Dr. Telci Temeltaş's research is on cell adhesion, migration, and signalling mechanisms that regulate extracellular matrix remodeling in fibrosis, cancer metastasis, and therapy resistance.

Her research has been supported by both national and international grants, including projects funded by the European Union, TÜBİTAK, and TÜSEB.

More recently, her work has expanded into translational studies on the role of tissue transglutaminase (TG2) in cancer progression and metastasis, biomarker discovery in endometriosis, and the molecular mechanisms underlying repeated implantation failure (RIF) in assisted reproduction. She also works on the development of targeted therapeutic strategies for breast and prostate cancer.



Assoc. Prof. Ahmet Acar

Middle East Technical University

Assoc. Prof. Dr. Ahmet Acar received his undergraduate degree from Middle East Technical University (METU) in Ankara, Türkiye. He completed his PhD at the Cancer Research UK Manchester Institute in 2012.

Following his doctoral studies, he carried out postdoctoral research in cellular and cancer biology at the University of Manchester and the Institute of Cancer Research in London.

In early 2020, Dr. Acar returned to Türkiye to establish his own research group at METU with the support of the TÜBİTAK International Fellowship for Outstanding Researchers Program. His laboratory focuses on understanding the mechanisms of drug resistance through evolutionary principles.

Dr. Acar is also the founder and CEO of HistoCan, a startup developing AI-driven digital pathology solutions.

Throughout his career, he has been recognized with several awards for young scientists and research excellence, including honors from TÜSEB, TÜBA, BAGEP, MOKAD, the Aydın Doğan Foundation, the Parlar Foundation, and TÜBİTAK.



Asst. Prof. Dr. Ece Öztürk

Koç University

Dr. Ece Öztürk is an Assistant Professor at the Department of Medical Biology, School of Medicine, and the Research Center for Translational Medicine (KUTTAM) at Koç University. She received her bachelor's degree in Chemical and Biological Engineering from Koç University, and completed her master's and doctoral studies in Biomedical Engineering at ETH Zurich.

During her PhD, Dr. Öztürk focused on cartilage tissue engineering and the development of biomimetic materials for chondrocyte implantation and cartilage regeneration. She later received the Swiss National Science Foundation Fellowship to pursue her postdoctoral research at the Department of Biomedical Engineering at Columbia University.

At Columbia University, she worked on lung tissue engineering and on modeling the organotropism of breast cancer metastasis using integrated multi-tissue platforms, for which she received the NSF Innovation Corps Award.

In 2020, Dr. Öztürk established her independent laboratory at KUTTAM. Her current research focuses on tumor tissue engineering, engineered patient-derived tumor organoid models, and modeling tumor progression and metastasis.

She has received several prestigious grants and awards, including the TÜBİTAK International Fellowship for Outstanding Researchers and National Young Leaders Programs, the Marie Skłodowska-Curie Fellowship, the L'Oréal-UNESCO For Women in Science Award, and the TÜBA-GEBİP Award.

WORKSHOPLAR

WORKSHOPS

5th LIFE SCIENCES CONGRESS WORKSHOP



RESEARCH ASSISTANT
ELİF PULAT,
PHD CANDIDATE

QUANTIFYING PLANT PIGMENTS: FROM SPECTROPHOTOMETRY TO ADVANCED MOLECULAR ANALYSIS

In this workshop, the quantitative determination of major plant pigments -chlorophylls and anthocyanins- will be performed through hands-on spectrophotometric analysis. Following simple extraction protocols, participants will learn how to calculate total pigment content from absorbance measurements. The limitations of spectrophotometric analyses will be discussed, and advanced molecular and analytical approaches for the identification and quantification of specific metabolites will be introduced theoretically. The workshop aims to provide a framework for understanding the importance of metabolite analysis in plants, highlighting how molecular-level characterization of essential metabolites contributes to molecular biology research.

ACU GEN

5th LIFE SCIENCES CONGRESS WORKSHOP



RESEARCH ASSİSTANT
UTKU ERTETİK, PHD CANDİDATE

PRIMER DESIGN WORKSHOP: FROM BASIC PRINCIPLES TO PRACTICAL APPLICATIONS IN PCR AND QPCR

In this workshop, participants will learn the fundamental principles of primer design, including specificity, melting temperature (Tm), GC content, and amplicon size.
Participants will gain hands-on experience using tools such as Primer3 and NCBI Primer-BLAST to design primers for target sequences. Common issues such as primer-dimer formation and non-specific binding will be addressed. The session will also cover basic strategies for primer validation and optimization in PCR and qPCR experiments.



5th LIFE SCIENCES CONGRESS WORKSHOP



ALPER BÜLBÜL, PHD CANDIDATE IN BIOINFORMATICS

FROM FASTQ TO VCF: PRACTICAL APPLICATİONS IN WHOLE EXOME SEQUENCING (WES) ANALYSIS

Join our workshop to explore the journey of genomic data from raw sequences to biological insights!
Participants will first be introduced to essential concepts and data formats such as
FASTQ, BAM, and VCF.

Following this, we will conduct a step-by-step hands-on analysis on a sample dataset, covering the entire pipeline: quality control, alignment, variant calling, annotation, and variant prioritization.

ACU GEN

ACIBADEM ÜNİVERSİTESİ

5th LIFE SCIENCES CONGRESS WORKSHOP



YASİN POLAT, FOUNDER & CEO AT SOLVİEN

EFFECTIVE USE OF AI TOOLS IN ACADEMIC RESEARCH

Join our workshop to discover how AI can support academic research from idea development to publication! Participants will first be introduced to the practical use of AI tools in key stages of the research process, including literature review, data analysis, hypothesis generation, and scientific writing.

Following this, we will explore real-world examples and guided workflows to demonstrate how AI can be effectively integrated into research practice, helping improve productivity, accuracy, and decision-making throughout the academic journey.



ACIBADEM ÜNİVERSİTESİ

5th LIFE SCIENCES CONGRESS WORKSHOP



NURULLAH KARACAKAYA,
HR MANAGER AT ACIBADEM HEALTHCARE GROUP

EXCEL 101 FOR MOLECULAR BIOLOGY AND GENETICS STUDENTS

Learn how to effectively manage and analyze experimental data using Excel. In this workshop, participants will explore essential Excel functions, data organization techniques, and basic analysis methods tailored for molecular biology. The session includes creating graphs such as growth curves and applying key concepts like mean, standard deviation, and data normalization. Through hands-on exercises, participants will gain practical skills to handle laboratory data efficiently and improve their analytical workflow.

XLS

5th LIFE SCIENCES CONGRESS WORKSHOP



CEREN GÜLSER İLİKAN RASİMOĞLU, ASSISTANT PROFFESOR AT ACIBADEM UNIVERSITY

EXAMINE THE ETHICAL CHALLENGES OF CRISPR RESEARCH THROUGH STRUCTURED DEBATE

In this workshop, participants will engage in a guided, scenario-based discussion focused on a complex ethical dilemma in gene editing. The session follows a structured debate model, encouraging participants to explore multiple perspectives and critically assess the implications of CRISPR research.

Through interactive group work, participants will address issues such as scientific responsibility, risk and uncertainty, human enhancement, and governance, while developing skills in ethical reasoning and argumentation.

ACU GEN

5th LIFE SCIENCES CONGRESS WORKSHOP



ASST. PROF. YASEMİN YAĞAN UZUNER

PERFUME MAKING WORKSHOP: CREATE YOUR OWN FRAGRANCE

In this workshop, participants will be introduced to the fundamentals of perfumery, including fragrance families and the roles of top, middle, and base notes. Participants will explore a variety of essential oils and aroma compounds, learning how to combine them to create balanced and harmonious scents. Basic blending techniques and scent composition principles will be covered. By the end of the session, participants will design and create their own personalized perfume.



5th LIFE SCIENCES CONGRESS WORKSHOP





TUBA YAĞCI KAYA & KÜBRA GÜLENÇ,
HR AND RECRUİTMENT MANAGERS AT ACIBADEM HEALTHCARE GROUP

CV AND LINKEDIN WORKSHOP: BUILDING A STRONG PROFESSIONAL PROFILE

In this workshop, participants will learn how to prepare an effective CV and create a strong LinkedIn profile.

Key elements of a well-structured CV, including formatting, content, and highlighting skills and experiences, will be discussed. Participants will also learn how to optimize their LinkedIn profiles for visibility and networking.

By the end of the workshop, participants will have improved their CVs and LinkedIn profiles for career opportunities.

BİLDİRİ ÖZETLERİ

ABSTRACT BOOK

ABSTRACT BOOK

Optimization of a GelMA-Based 3D Ex Vivo Model Using Amniotic Fluid and Chorionic Villus Cells for Fetoplacental Research

Ferdi Oguz (Koç University)
Duygu Aydemir (Istanbul University)
Emel Sokullu (Koç University)
Birsen Karaman (Istanbul University)
Tuğba Kalaycı (Istanbul University)
Tuğba Saraç Sivrikoz (Istanbul University)

Amniotic fluid (AF) and chorionic villus sampling (CVS)–derived cells are valuable cellular sources that reflect fetal and fetoplacental biology and can be expanded ex vivo. After routine prenatal diagnostic procedures are completed, the use of cells that will be disposed of according to laboratory guidelines offers a significant opportunity to investigate the molecular mechanisms of fetal development without the need for additional invasive interventions. Despite this potential, most studies involving AF- and CVS-derived cells have relied on conventional two-dimensional (2D) culture systems, which do not adequately reproduce the structural and functional complexity of the fetoplacental microenvironment. Furthermore, gelatin methacrylate (GelMA)-based three-dimensional (3D) ex vivo culture systems have not yet been applied to AF or CVS-derived cells.

ABSTRACT BOOK

In this study, we aimed to develop and optimize a GelMA-based 3D ex vivo model that could serve as a physiologically relevant platform for maternal–fetoplacental studies. To determine the optimal conditions for hydrogel formation and cell compatibility, different GelMA concentrations (3.5–10%), Irgacure photoinitiator concentrations (0.1–1%), hyaluronic acid (HA) (0.2), and UV exposure times (15–60 seconds) were systematically evaluated based on the viability of AF- and CVS-derived cells. According to the optimization analyses, the most suitable parameters for both cell types were identified as 10% GelMA, 0.2% HA, 0.2% Irgacure, and 15 seconds of UV exposure.

Following the optimization process, the established 3D culture conditions were further characterized through analyses of cell morphology, oxidative stress, and cell proliferation to confirm the biological compatibility and stability of the model. This study reports the first optimization of a GelMA-based 3D ex vivo culture system for AF and CVS-derived cells, providing a novel reference model for fetoplacental research.

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ABSTRACT BOOK

From Prediction to Generation: Decision Criteria for Selecting Traditional ML or Generative AI in Organizations

Anmol Aggarwal (UC Berkeley)

Product organizations have increasingly faced a consequential choice between predictive machine learning (ML) systems and generative artificial intelligence (GenAI) systems. While both are often grouped under "AI," they vary fundamentally in output structure, evaluability, reliability controls, operational costs, and compliance overhead they carry. This paper proposes a managerial decision framework to guide product leaders in choosing among predictive ML (including deep learning), GenAI, hybrid architectures, or deliberate non-automation.

It starts by applying feasibility gates that cover safety and legal exposure, security and privacy limitations, and transactional correctness requirements for action-taking systems. It then evaluates value capture using unit economics, assurance scalability, and product-market fit. In practice, the criteria tend to resolve toward predictive ML when outputs are bounded and cost constraints are tight, toward GenAI where the interaction itself is what users are paying for, and toward hybrid designs when a product needs both, which, for most serious enterprise deployments, is more often than not.

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ABSTRACT BOOK

GENOMIC ANALYSIS OF SARS-CoV-2 VARIANTS CIRCULATING IN UZBEKISTAN

Esonova Gulnoza (Tashkent State Medical University)

Since the emergence of the COVID-19 pandemic in 2019, caused by the novel SARS-CoV-2 virus, it has had a significant global impact. Over time, SARS-CoV-2 has rapidly accumulated mutations, leading to increased genetic diversity and the emergence of new variants. Whole-genome sequencing has enabled the identification of circulating strains and their characteristic mutations, as well as assessment of their potential effects on viral transmissibility, virulence, and pathogenicity. Therefore, in this study, we aimed to identify SARS-CoV-2 variants and subvariants circulating in Uzbekistan and characterize variant-specific mutations using Sanger sequencing and next-generation sequencing (NGS).

Our findings revealed that Uzbekistan experienced four distinct waves during the COVID-19 pandemic. These waves were associated with the circulation of the Wuhan 20A strain, followed by the Alpha, Delta, and Omicron variants during the period 2020–2023. Whole-genome sequencing of samples collected across these waves identified significant mutations in multiple regions of the viral genome. These mutations have implications for viral transmissibility, virulence, and vaccine effectiveness.

ABSTRACT BOOK

Our comprehensive analysis demonstrated that the evolution of the COVID-19 pandemic in Uzbekistan paralleled the emergence of new variants, with a progressive increase in the number of mutations: 46 in Alpha, 146 in Delta, and 200 in Omicron. The highest number of amino acid substitutions was observed in the Spike protein, accounting for 115 changes.

This substantial accumulation of mutations in the Spike protein contributed to the emergence of new variants.Analysis of genomic mutations improves understanding of SARS-CoV-2 evolutionary trajectories and may aid in preparedness for future viral outbreaks. Furthermore, these findings may contribute to the development of vaccines targeting SARS-CoV-2 and its variants.

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ABSTRACT BOOK

Designing AAV Vector Delivery Systems with Nanobody Assisted Targeting

Mehmet Alp Garipoğlu
(University of Konstanz)

Gene therapy is a game-changing technology in the realm of medicine as it offers a revolutionary approach to treating hereditary diseases at their root cause as it targets the genome. By precise modifications on specific tissue of a patient, gene therapy can provide a big advantage which delivery systems play a vital role in. These delivery systems can be viral (e.g., adeno-associated virus, lentivirus) or non-viral (e.g., liposomes, nanoparticles). The ideal delivery system should allow targeted, precise, and effective treatments for a wide range of medical conditions.

An Adeno-associated virus (AAV) is a small, non-enveloped, single-stranded DNA virus that has earned significant attention in the field of gene therapy. AAV is considered a promising vector for gene delivery due to its safety profile, low immunogenicity, and ability to infect both dividing and non-dividing cells. AAV vectors are now commonly used to transport therapeutic genes into target cells for gene therapy applications. Their small size limits their capacity for exogenous genetic material, but their ability to integrate into the host cell genome ensures durable transgene expression.

ABSTRACT BOOK

AAV vectors can be pseudotyped with capsid proteins from different serotypes to target specific tissues, which makes them a valuable component in gene therapy.
Our objective was to develop an AAV targeting system based on a nanobody display approach. As a proof-of-principle, we utilized a GFP nanobody to create a recombinant AAV-capsid capable of specifically targeting cells with GFP displayed on their surface. The variable and surface exposed VR-4 and VR-8 regions of the AAV2 capsid protein were utilized to generate in-frame fusions with the GFP nanobody. We designed multiple linker sequences to ensure optimal positioning of the nanobody for effective antigen-binding paratope functionality. During this practical course, the AAV2 capsid was modified to allow seemless integration of the GFP nanobody. Furthermore, several linker-nanobody configurations were designed and explored for integration into the capsid sequence. Consistent with findings from other groups, the modification of the AAV capsid shows promise of high-specificity gene delivery tools for precise applications in research and healthcare.

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ABSTRACT BOOK

OPTIMIZATION OF CALLUS INDUCTION FROM COTYLEDON EXPLANTS OF TOMATO (SOLANUM LYCOPERSICUM L.) AS A PLATFORM FOR CRISPR/CAS9-MEDIATED GENOME EDITING

Maftunakhon Sodikova (Research Institute of Plant Genetic Resources)

Abiotic stresses, particularly drought and salinity, are primary constraints limiting tomato productivity worldwide. Developing climate-resilient varieties is essential for sustainable food security. This doctoral research focuses on utilizing CRISPR/Cas9 technology to precisely engineer the tomato genome by targeting specific negative regulators of stress response pathways.Based on comprehensive in silico analyses, three key target genes—SlAGL16, SlZIP38, and SlERA1—were identified for their potential roles in modulating environmental stress tolerance.

Currently, the research has progressed to the structural design of guide RNAs (gRNAs) and the cloning of these sequences into CRISPR/Cas9 expression vectors. This targeted approach aims to disrupt the function of these susceptibility genes to enhance the plant's natural resilience.Parallel to the molecular work, in vitro regeneration protocols for local tomato cultivars from Uzbekistan have been optimized to ensure efficient transformation.

ABSTRACT BOOK

This involved testing various plant growth regulator concentrations to determine the most effective shoot and root induction media. Current efforts are focused on performing Agrobacterium-mediated transformation and evaluating the transformation efficiency for these indigenous genotypes.

The preliminary findings from the in silico phase and the ongoing molecular cloning provide a strategic framework for developing stress-tolerant tomato lines.

By combining precise genome editing with optimized tissue culture techniques for local germplasm, this work contributes to the modernization of crop breeding and provides a foundation for future functional genomics studies in horticultural crops.Keywords: CRISPR/Cas9, Tomato, SlAGL16, SlZIP38, SlERA1, In silico analysis, gRNA design, Cloning, In vitro optimization, Abiotic stress.

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ABSTRACT BOOK

Tailoring Nanobody Properties by Random Mutagenesis and Site-directed Protein Fusion

Mehmet Alp Garipoğlu
(University of Konstanz)

Nanobodies (Nbs), single-domain high-affinity-and-specificity antigen-binding entities obtained mainly from camelids, are advantageous in many research approaches such as detection and manipulation of a variety of cellular processes due to their small size (around 15 kDA), robustness and ease of production. Similar to conventional antibodies they possess high affinity and specificity for their target and therefore also have the potential to replace antibodies in diagnostic and therapeutic procedures.

The study aimed to establish and validate a protocol that's goal is to increase affinity of nanobodies using in vivo error-prone mutagenesis driven by a mutated E. coli DNA polymerase I, developed by Professor Manel Camps' Lab. This approach introduces random point mutations in a certain length of the downstream of the plasmid with a mutation rate of ~0.9 mutations per 1,000 base pairs.

ABSTRACT BOOK

Combined with bacterial surface display and selection methods like Ni-NTA sorting and FACS, the protocol was tested using two model nanobodies: one targeting PPM1F, a human protein phosphatase, and another (GFP-trap nanobody) intended to bind the fluorescent protein mCerulean, as a showcase target.

Here we lay foundations of an in-vivo mutagenesis strategy to evolve and stringently select from nanobody mutant library. The potential of this strategy could open new avenues for the development of novel and more effective nanobodies with enhanced therapeutic and scientific potential.

These findings highlight key limitations in the current selection strategy and provide a foundation for further optimization toward the development of high-affinity nanobody reagents for research and therapeutic applications.

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ABSTRACT BOOK

Modeling of biological networks and analysis of multi-omics data

Ece Öner (Yıldız Technical University)

Due to the complexities of simulating bioenergetics, most Spiking Neural Network (SNN) models treat neurones as energetically unconstrained, omitting the metabolic costs of neural activity. We introduce a computational framework that employs thermodynamic variables to directly integrate metabolic regulation into network dynamics.
Using temperature-dependent Q10 scaling as a biophysical proxy for ATP availability, we developed a conductance-based leaky integrate-and-fire microcircuit (5,000 neurones) in Brian2 in which membrane leak conductance, and therefore the membrane time constant, emerges from temperature-dependent kinetics. This strategy translated metabolic state into intrinsic excitability across a physiologically relevant thermal sweep without requiring exhaustive biochemical pathways.The model simulated non-linear metabolic modulation of Hebbian plasticity, such as hypermetabolic fluctuations resulting in seizure-like avalanche dynamics and hypometabolic inhibition of LTP. The results of this study demonstrate that differential Q10 scaling provides a biologically valid and computationally efficient approach for incorporating metabolic variables into large-scale neuronal simulations.

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ABSTRACT BOOK

Antibacterial Activity of Hypogymnia tubulosa Lichen Extract Against

İlayda Döndürür - Barış Gökalsın
(Marmara University)

Food products carry the risk of contamination with various microorganisms. This situation can lead to serious problems in terms of food safety and public health. Every year worldwide, unsafe foods cause approximately 600 million foodborne illnesses and 420,000 deaths. Among foodborne pathogens, Listeria monocytogenes plays a significant role through listeriosis cases it causes. Despite its low incidence, listeriosis has one of the highest mortality rates among foodborne diseases. The present study aims to investigate the minimum inhibitory concentration (MIC) values, bacteriostatic effects, and bactericidal activity of acetone extracts of the lichen Hypogymnia tubulosa, collected from the Bolu Aladağlar region, against L. monocytogenes. For this purpose, L. monocytogenes isolated and identified from chicken food samples and L. monocytogenes ATCC 19111 strains were first observed on chromogenic Listeria agar and then inoculated into Tryptic Soy Agar and Tryptic Soy Broth media. The antibacterial activity was tested using the broth microdilution method in a 96-well microplate.

Different concentrations of the extracts were applied to the bacteria. The incubation process was carried out at 37 °C under continuous shaking, and absorbance measurements were taken at 600 nm after 21 hours. To determine bactericidal activity, spread plate inoculations were performed on TSA medium and the results were observed after 24 hours of incubation at 37 °C. Tetracycline antibiotic was used as the control group.

As a result of the experiments, it was determined that the H. tubulosa lichen extract had an MIC value of 200 µg/mL against L. monocytogenes isolates and provided approximately 90% growth inhibition at this concentration. The obtained findings indicate that lichens may be considered as potential natural antimicrobial agents against L. monocytogenes.

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ABSTRACT BOOK

Reprogramming of Alternative Splicing During Monilinia laxa Pathogenesis

İrem Ece Kadıoğlu (Çanakkale Onsekiz Mart University)
Hilal Özkılıç (Çanakkale Onsekiz Mart University)

Monilinia laxa is a necrotrophic fungal pathogen and one of the causal agents of brown rot disease, characterized by a relatively narrow host range. Although the molecular mechanisms underlying host–pathogen interactions in these pathosystems have been investigated from different perspectives, alternative splicing (AS) remains a major and underexplored aspect of these studies.

We hypothesized that AS plays a role in pathogen interactions with different hosts and therefore expected host-driven AS mechanisms. To test this hypothesis, we utilized long-read sequencing of the pathogen under in vitro conditions, as well as dual RNA-seq data obtained from pathogen interactions with peach and cherry hosts in our previous studies. These datasets were bioinformatically processed to identify and filter pathogen derived-mRNA isoforms across the conditions.

AS events were then characterized,
followed by differential transcript usage and isoform switching analyses. Preliminary analyses suggest that, upon infection, genes exhibiting alternative splicing tend to cluster into functional categories related to cellular signaling and metabolic/transport processes. Moreover, initial evidence suggests that isoforms underlying pathogenesis-related alternative splicing patterns are host-dependent.
Notably, intron retention and exon skipping were the dominant AS events,
showing differential inclusion levels between both hosts.

Overall, our results uncover extensive alternative splicing dynamics underlying M. laxa pathogenesis and host–pathogen interactions, representing an output of our ongoing alternative splicing–focused research in Monilinia pathosystems.

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ABSTRACT BOOK

LAMA5 Variants Modulate Immune Cell Infiltration Across a 2D BBB Model in MS

Kerem Cotuk[1], Umut Voyvoda[2], Hanbike Efe[2], Pamir Can Kaya[1], Sevim Naz Karisik[2], Meziyet Dilara Reda[2], Betul Cakici[2], Elif Celik[3], Ahmet Can Timucin[1], Umut Inci Onat[1],Ugur Uygunoglu[4], Melih Tutuncu[4], Aksel Siva[4], Eda Tahir Turanli[1,2,5]

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MS pathogenesis involves the compromise of the blood-brain barrier (BBB) integrity, allowing peripheral immune cells to breach the barrier and infiltrate the central nervous system, thereby initiating neuroinflammation and neurodegeneration in the brain and spinal cord. The primary objective of the study is to examine how variants of the LAMA5 gene, identified in MS families, influence immune cell infiltration across the BBB.

ABSTRACT BOOK

The LAMA5 p.Thr3126Ile missense mutation, present in MS families, was introduced into a human umbilical vein endothelial cell (HUVEC) line using cytosine base editing. Wild-type and mutant HUVEC cells were then co-cultured with peripheral blood mononuclear cells (PBMCs) in a Transwell co-culture system, and PBMC migration through the Transwell was optimized by stimulating the cells with TNFα and IFNγ. Additionally, the expression of ICAM1, VCAM-1, CLDN5, ITGB1, and ITGAL genes, known to be involved in lymphocyte migration across the BBB through interaction with LAMA5, was evaluated in both wild-type and mutant HUVEC cells using quantitative PCR.The results revealed that PBMC migration from the mutant HUVEC cells was 25% higher compared to the wild-type co-culture conditions. Furthermore, in comparison to the wild-type, the expression of ICAM-1, VCAM-1, and CLDN5 was significantly reduced in the mutant HUVEC cells, while the expression of ITGB1 and ITGAL was significantly increased.It has been observed that LAMA5 variants increase lymphocyte infiltration in the BBB 2D co-culture system. In subsequent investigations, the variants identified in MS families will be introduced into HUVEC cells using prime editing technology. To further explore immune cell infiltration, PBMCs will be analyzed by flow cytometry to identify distinct subtypes. Moreover, gene expression levels will be examined at the protein level through Western blot analysis. These forthcoming studies will provide valuable insights into the contribution of LAMA5 variants to the pathogenesis of MS.

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ABSTRACT BOOK

Machine Learning-Based Genomic Prediction and SHAP Interpretation of Meropenem Resistance in Klebsiella pneumoniae

Musa Al Hassan Kromah (Çukurova University, Graduate School of Natural and Applied Sciences, Department of Biotechnology)
Ibrahim Bah (Çukurova University, Graduate School of Health Sciences, Department of Translational Medicine)
Deren Aslan (Çukurova University, Graduate School of Natural and Applied Sciences, Biotechnology Research and Application Center)
Nursena Yıldız (Çukurova University, Graduate School of Natural and Applied Sciences, Department of Tissue Engineering)

Background: The rapid global spread of β-lactamase and carbapenemase genes in carbapenem-resistant Klebsiella pneumoniae (CRKP) strains represents a significant public health concern. The amalgamation of genetic data with interpretable machine learning is a viable method for precisely forecasting resistance traits and enhancing antimicrobial surveillance.

Methods: We developed an interpretable machine learning workflow to predict meropenem resistance in K. pneumoniae based on genomic antimicrobial resistance (AMR) profiles. A dataset of 1,195 clinical isolates was constructed by combining AMR genotypes and spatiotemporal metadata.

ABSTRACT BOOK

Binary resistance labels were created using important carbapenemase determinants (blaKPC, blaNDM, blaOXA, blaVIM, blaIMP). The genomic profiles were vectorized with CountVectorizer, and a Random Forest classifier was trained with five-fold stratified cross-validation. SHapley Additive Explanations (SHAP) were used to calculate the relevance of general features and make isolate-level predictions.

Geospatial analytical tools were employed to determine the geographic distribution of resistance.

Result: The model performed quite well, with a 95.8% accuracy rate and an average F1 score of 0.955. SHAP studies found the blaKPC-2, blaOXA-1, aac(6′)-Ib-cr5, parC_S80I, and gyrA_S83I genes as key genomic predictors of meropenem resistance. SHAP visualizations addressed the "black box" character of classic machine learning models by quantifying gene-specific contributions. Geographic mapping highlighted regional disparities, identifying Tunisia, Brazil, and Pakistan as hotspots with large loads (accounting for more than 80% of anticipated resistance).

Conclusion: This study develops a highly accurate, scalable, and interpretable machine learning model for predicting meropenem resistance in K. pneumoniae using genomic features. This pipeline, which combines machine learning, SHAP interpretability, and spatial analytics, provides a powerful tool for genomic antimicrobial resistance (AMR) surveillance and precision antimicrobial management.

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ABSTRACT BOOK

Predicting Transcriptomic Responses to Genetic Perturbations via Similarity-Based Atlas Mapping

Seher Zeynep Sonkaya (Acıbadem University)
Osman Ugur Sezerman (Acıbadem University)

Predicting how cells respond to genetic perturbations is essential for understanding disease mechanisms and designing targeted therapies. Yet most of the human genome remains experimentally uncharacterized. We present a computational framework to predict cellular responses to unstudied gene knockdowns by leveraging the accumulated record of known perturbations.

Using a genome-wide CRISPRi dataset comprising ~10,000 gene knockdowns in K562 cells, we identified the most transcriptomically similar characterized perturbations for each query gene and used their known outcomes to predict the response of unstudied knockdowns. The principle is straightforward: genes with related biological roles produce similar cellular responses when silenced.

ABSTRACT BOOK

The framework achieves meaningful genome-wide prediction accuracy (median r=0.226, above chance across 99.6% of perturbations) and reveals clear biological structure. Genes in conserved protein complexes are enriched among top predictions (11 of 15 tested complexes, combined $p<10^{-50}$), achieving mean r=0.678. This demonstrates the model captures organized regulatory relationships rather than noise. Predictions generalize across cell lines without retraining (median r=0.508), and accuracy improves log-linearly with atlas size with no saturation observed.

Prediction reliability can be estimated before any experiment is run, enabling researchers to identify which knockdowns are confidently predictable and which require direct measurement. We are extending this approach to incorporate protein interaction networks, which may improve predictions for genes without close transcriptomic matches.

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ABSTRACT BOOK

CAPVIC: A Production-Grade MCP Server for Precision Oncology Variant Classification

Umut Kılınçkaya (Acıbadem University)
Ariorad Moniri (Acıbadem University)

Background: Clinical interpretation of somatic and germline variants requires molecular tumor boards (MTBs) to aggregate evidence from multiple knowledgebases and manually apply guidelines such as AMP/ASCO/CAP, ClinGen/CGC/VICC Oncogenicity SOP, and ACMG/AMP. This process is time-consuming and prone to inter-source discordance.
Objective: To develop an open-source Model Context Protocol (MCP) server that transforms LLM-based assistants (Claude, GPT, etc.) into virtual molecular tumor boards by integrating 10 clinical genomics data sources with deterministic, guideline-compliant classification logic.

Methods: CAPVIC was built in Python 3.11+ using FastMCP with asynchronous HTTP clients, rate limiting, and retry handling. Integrated sources include CIViC, ClinVar, OncoKB, VICC MetaKB, gnomAD (76,156 genomes / 807,162 exomes), UniProt, PubMed, LitVar2, MyVariant.info, and cancerhotspots.org. Twenty-nine tools support evidence aggregation,

ABSTRACT BOOK

HGVS normalization, population frequency lookup, protein domain mapping, in-silico predictions (SIFT, PolyPhen-2, REVEL, CADD, AlphaMissense), and a 7-signal driver/passenger assessment. Oncogenicity scoring implements the 18 evidence codes of the ClinGen/CGC/VICC SOP, while somatic classification applies the AMP/ASCO/CAP 4-tier system (Tier I–IV, evidence levels A–D). PP3/BP4 evidence strengths are calibrated using ClinGen SVI thresholds (Pejaver et al., 2022). Quality is ensured through 180+ unit tests, ruff linting, mypy type checking, and a GitHub Actions CI/CD pipeline on Python 3.11/3.12.

Results: CAPVIC performs evidence aggregation, variant classification, pathogenicity summarization, and cross-source concordance analysis from a single natural-language query. UniProt domain data (OM1), in-silico predictions (OP1/SBP1), and Cancer Hotspots recurrence (OS3) are automatically fed into the oncogenicity scorer when variant_classify is invoked, removing the need for manual tool chaining and producing reproducible, guideline-aligned outputs.

Conclusion: CAPVIC standardizes evidence gathering and variant classification workflows in precision oncology research, turning LLM assistants into guideline-compliant virtual MTBs. The tool is intended for research and educational use only; clinical decision-making requires validated laboratory procedures and qualified molecular pathologist review.

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CAMPUS LOCATION INFO

M8 Bostancı - Dudullu - Parseller Hattı:

En pratik yöntemlerden biridir. ***Küçükbakkalköy*** *durağında indiğinizde kampüs hemen karşınızda yer alır (yaklaşık 3 dakikalık yürüme mesafesinde).*

M4 Kadıköy - Sabiha Gökçen Havalimanı Hattı:

Kozyatağı *istasyonunda inip "Hal" çıkışını kullanabilirsiniz. Buradan Kayışdağı Caddesi istikametine yürüyerek kampüse ulaşabilir veya eğitim dönemlerinde hafta içi belirli saatlerde hizmet veren üniversitenin ücretsiz ring servislerini (Kozyatağı 4 numaralı çıkış yakınındaki Cafe Carino önünden kalkar) kullanabilirsiniz.*

Otobüs ile Ulaşım:

- *Kadıköy Rıhtım'dan: 19K, 19Y, 19V, 19S, 19T ve 14A numaralı hatları kullanabilirsiniz.*
- *Üsküdar'dan: 11T ve 320A numaralı hatları tercih edebilirsiniz. Bu otobüslerle "Acıbadem Üniversitesi" veya "Küçükbakkalköy" duraklarından birinde inerek kampüse kolayca ulaşabilirsiniz*

Arabayla Ulaşım:

- *Maltepe – Kadıköy yönünden (D100/E5): Hal-Ataşehir sapağından dönüp, yan yoldan Hal yolunu takip ederek Kayışdağı Caddesi'ne sağa döndüğünüzde yaklaşık 2 km sonra kampüse varabilirsiniz.*
- *Kadıköy – Maltepe yönünden (D100/E5): Ümraniye-Ataşehir-Hal sapağından dönün. Göztepe sapağını geçtikten sonra sağa Hal-Ataşehir yoluna dönün. Işıklardan sola Hal yoluna dönüp 400 metre sonra sağa Kayışdağı Caddesi'ne girdiğinizde kampüse ulaşabilirsiniz.*

M8 Bostancı - Dudullu - Parseller Line:

This is one of the most practical methods. When you get off at the ***Küçükbakkalköy*** *station, the campus will be right across from you (approximately a 3-minute walk).*

M4 Kadıköy - Sabiha Gökçen Airport Line:

You can get off at the ***Kozyatağı*** *station and use the "Hal" exit. From there, you can walk towards Kayışdağı Avenue to reach the campus, or you can use the university's free shuttle services, which operate at specific hours on weekdays during the academic terms (shuttles depart from in front of Cafe Carino, near Kozyatağı exit number 4).*

Transportation by Bus:

- *From Kadıköy Rıhtım (Pier): You can use bus lines 19K, 19Y, 19V, 19S, 19T, and 14A.*
- *From Üsküdar: You can use bus lines 11T and 320A. You can easily reach the campus by getting off at either the "Acıbadem Üniversitesi" or "Küçükbakkalköy" bus stops with these buses.*

Transportation by Car:

- *From the Maltepe – Kadıköy direction (D100/E5): Take the Hal-Ataşehir exit, follow the Hal road via the side road, and turn right onto Kayışdağı Avenue. You will arrive at the campus after approximately 2 km.*
- *From the Kadıköy – Maltepe direction (D100/E5): Take the Ümraniye-Ataşehir-Hal exit. After passing the Göztepe exit, turn right onto the Hal-Ataşehir road. At the traffic lights, turn left onto the Hal road. After 400 meters, turn right onto Kayışdağı Avenue to reach the campus.*

İLETİŞİM BİLGİLERİ

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