



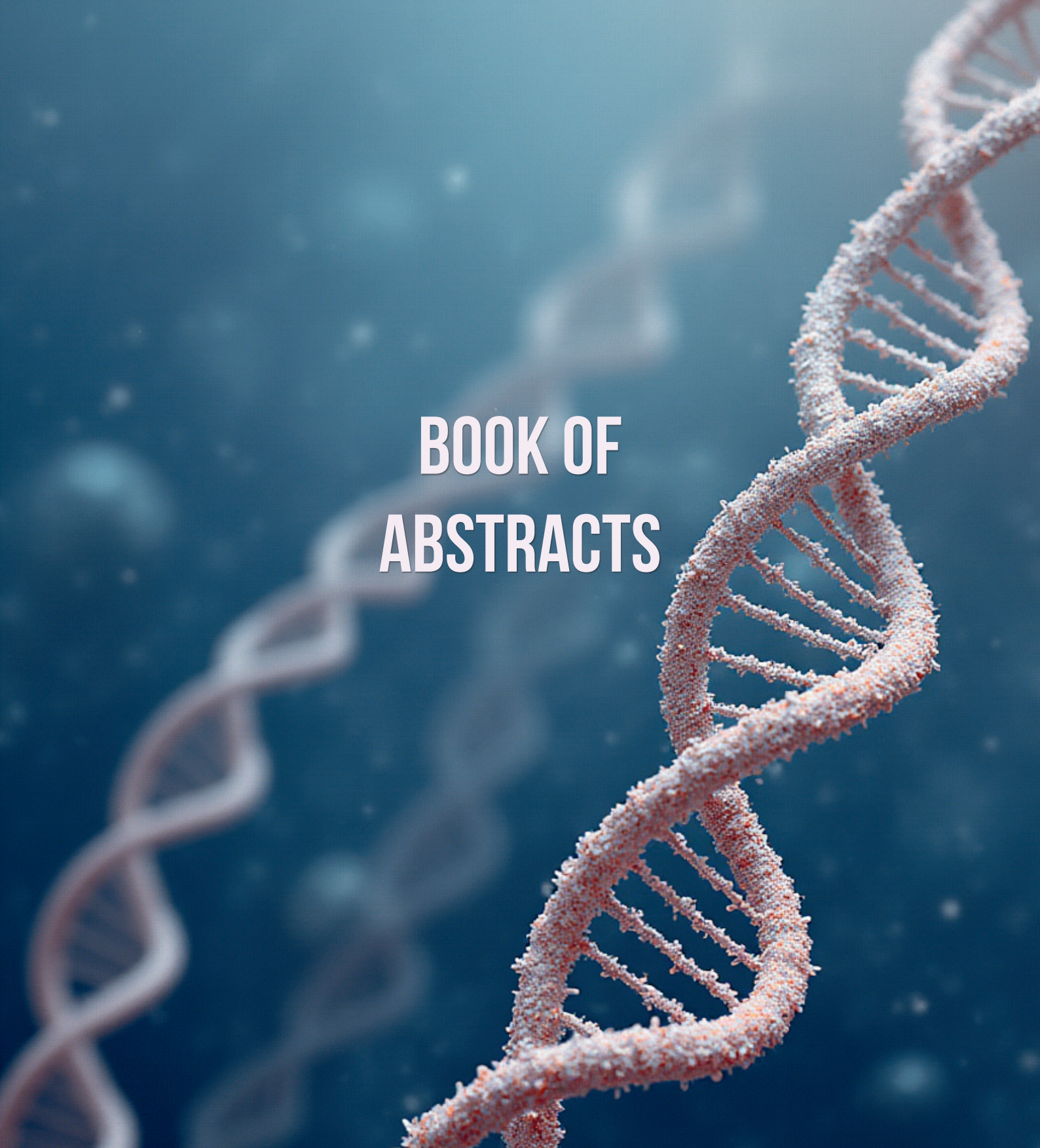
**EUCHEMBIJ 2025**

**II. International Conference  
on Chemistry and Biotechnology**

**05-07  
DECEMBER  
2025**

**ONLINE**  
based in  
Istanbul, Türkiye

**BOOK OF  
ABSTRACTS**





## II. International Conference on Chemistry and Biotechnology

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## WELCOME

We are pleased to invite you to participate in EUCHEM BIO J 2025: The II. International Conference on Chemistry and Biotechnology, which will be held online on 05-07 December 2025 (Istanbul, Türkiye).

The aim of EUCHEM BIO J 2025 is to investigate the rapidly developing topic of biotechnology and to bring together researchers in the field of Chemistry and Biotechnology. The topics discussed at the conference include application areas of biotechnology such as biomedical technology, biosensors, molecular biology, medicine, environment, agriculture, nanotechnology, and chemistry studies for application in the field of chemistry and biotechnology.

Leading experts from around the world will come together at the conference to share their studies, perspectives, and ideas on the latest developments in biotechnology.

This dynamic and multidisciplinary field will be fully explored at the conference, from cutting-edge technologies to creative applications, from fundamental concepts to theoretical frameworks. We look forward to your participation!

**Warm regards,  
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## SPEAKERS

### **Rabah Boukherroub**

Prof. Dr. Rabah Boukherroub graduated from the University of Paul Sabatier in Toulouse, France, with a Ph.D. in chemistry. He is currently a CNRS Research Director at the Institute of Electronics, Microelectronics, and Nanotechnology (IEMN), University of Lille, France. He is a Co-editor in Chief of AI & Materials and section editor of the European Chemistry and Biotechnology Journal. His areas of interest include surface chemistry, photophysics of semiconductor/metal nanostructures, and nanostructured functional materials, with a focus on energy-related applications, biosensors, nanomedicine, and electrocatalysis.

### **Chontisa Sukkasem**

Dr. Chontisa Sukkasem currently works at the Research Center in Energy and Environment / Food Science and Technology, Thaksin University. Dr. Sukkasem's research area is Biotechnology, Electrochemistry and Green Chemistry. She developed various configurations of microbial fuel cells for land field applications. She is one the editors of the European Chemistry and Biotechnology Journal.

### **Sebnem Essiz**

Assoc. Prof. Dr. Sebnem Essiz graduated from Koc University, Department of Chemistry in 2002, and from the University of Pittsburg, Biophysical Chemistry PhD program in 2009. She has been working as an academician at Kadir Has University, Department of Molecular Biology and Genetics since 2012. She worked as a researcher at Lawrence Livermore National Lab (CA USA) and as a postdoctoral researcher at the University of California at San Francisco, Department of Bioengineering between 2009-2010. Her research interests include computational structural biology and bioinformatics, NMDA and GABA neuronal receptors and membrane proteins, KRAS/RAF/MEK signaling pathway, accelerated molecular dynamics simulations, and protein homology modeling with genetic algorithms.

### **Sergey Varnavskiy**

Born and raised in Moscow, Russia, Sergey graduated with summa cum laude honors in Chemistry from the Moscow Institute of Steel and Alloys in 2003. He went on to earn a PhD in Chemistry in 2008, specializing in the synthesis of new compounds for various applications. Throughout his academic career, he participated in numerous studies across Poland, Finland, and the United States. Transitioning into high-tech industries, Sergey contributed to the aerospace and oil & gas sectors before moving into healthcare. His work in healthcare focused on developing medical equipment specifically for women's health. In 2021, he joined Elsevier, where he is responsible for life science solutions in the Middle East, Türkiye, and Eastern Europe.

### **Lakhveer Singh**

Prof. Lakhveer Singh is an Associate Professor cum Dean Research at the Department of Chemistry, Sardar Patel University, Mandi, H.P. India. His major areas of research expertise are energy production, bioelectrochemical systems, wastewater treatment, and nanomaterial synthesis for sustainable applications. Dr. Singh has 4 patents, has edited 30 books (ACS, Elsevier, CRC, and so on), and has authored over 130 scientific papers (>8000 citations; h-index 50). Dr. Singh has supervised 5 Ph.D. students and currently has 5 Ph.D students doing Ph.D under his supervision. He has completed over 10 research projects as a PI and Co-PI (Funding more than 2.0 crore). He has obtained a project from NMHS (1.20 crore funding) and DST (30 Lakhs) on sustainable chemicals and hydrogen production. He has delivered more than 20 keynotes and invited talks around the globe. He serves as an editorial board member for the Journal of Biomass Conversion and Biorefinery. He is listed in Stanford University's 2021, 2022, 2023, and 2024 lists of the world's top 2% of scientists in the field of Energy and Environment.



## SCIENTIFIC PROGRAMME

### EUCHEM BIO J 2025 - SCIENTIFIC PROGRAM

#### DECEMBER 5, 2025 - DAY 1

10.00-10.05	<b>Introduction</b> <b>Opening Speech:</b> Prof. Dr. Muhsin Konuk
<b>Session - 1</b>	
10.05-10.45	BioCircuit: A Low-Energy Breakthrough for Sustainable and Ecological Wastewater Treatment <b>Keynote Speaker:</b> Chontisa Sukkasem
10.45-11.20	Challenges and Opportunities in AI-Driven Chemistry: A CADD-Informed Perspective on Predictive Retrosynthesis, Impurity Prediction, and Forward Synthesis <b>Keynote Speaker:</b> Sergey Varnavskiy
11.20-11.40	Microbial Community Analysis in MFCs Treating Bilge Water <b>Dilan Akagündüz</b>
11.40-12.00	Antioxidant, Cytotoxic and Antimicrobial Activities of Porphyridium cruentum Microalgae Species <b>Emine Yiğiter</b>
12.00-13.00	Break
<b>Session - 2</b>	
<b>Moderator:</b> Asst. Prof. Çiğdem Sezer Zhmurov	
13.00-13.45	Bio-electrochemical System: Revolutionizing the future for sustainable Bio-hydrogen Production <b>Keynote Speaker:</b> Lakhveer Singh
13.45-14.25	Technological Advancements in Diabetes Management <b>Keynote Speaker:</b> Rabah Boukherroub
14.25-15.05	Multi-Scale Structural Dynamics of Proteins: From Single Point Mutations to Protein Complex Formation <b>Keynote Speaker:</b> Şebnem Eşsiz
15.05-15.20	Break



## SCIENTIFIC PROGRAMME

### Session - 3

**Moderator: Res. Assist. Irem Olgun**

15.20-15.40	Cytotoxic Effects of MFC Biofilm Byproducts and Antioxidants Response in Human Dermal Fibroblasts CCD-1064SK <b>Noon Abdelrazig</b>
15.40-16.00	Biosensing Antibiotic- Resistant Bacteria in Wastewater through Penicillin/Streptomycin Activity in Microbial Fuel Cells <b>Maryam Faiz</b>
16.00-16.20	Development of Process and Packaging Structure Compliant with Toxic NIAS Limits in Flexible Food Packaging <b>Hande Uçak Merdol</b>
16.20-16.40	Microbial Biomarker Discovery: Assessing the Impact of Non-Viable Microbial DNA on Community Profiling <b>Dilek Sever Kaya</b>
16.40-17.00	Imidazopyridine Family: Versatile and Promising Heterocyclic Skeletons for Different Applications <b>Giorgio Volpi</b>
17.00-17.20	Applications Genome Scale Metabolic Models for Different Domains of Life in Biotechnology <b>Pınar Kocabaş</b>
17.20-17.40	Machine Learning Model Applications for Predicting the Most Potent AGE Precursors: A Glyoxal Case Study <b>Yankı Başaran</b>



## SCIENTIFIC PROGRAMME

### DECEMBER 6, 2025 - DAY 2

#### Session - 4

Moderator: Prof. Dr. Tunç Çatal

10.00-10.20	The Delaying Effect of Directly Applied Humic Acid on Senescence in Barley ( <i>Hordeum vulgare</i> L.) Leaf Segments <b>Özgenur Bülbül</b>
10.20-10.40	A Brief Study of 1-(4-hydroxyphenylthio)-8-chloroanthracene-9,10-dione: Fluorescent Nanoparticles as Enhancers of Chemiluminescence in Luminol-Based Assays <b>Alihan Kocabaş</b>
10.40-11.00	Dose-dependent Quercetin and Novel Curcumin Derivative Activity Against Sodium Arsenate Toxicity in vitro in ECV-304 Endothelial Cells <b>Aksana Kavaleuskaya</b>
11.00-11.20	Gene Engineering of the TP-84 Bacteriophage Portal Protein as a First Step in Creating Bionanoparticles <b>Jakub Mazur</b>

#### WORKSHOP

12.30	Introduction to in silico studies, ligand preparation, protein- ligand docking, molecular dynamics simulations
	Closing Remarks



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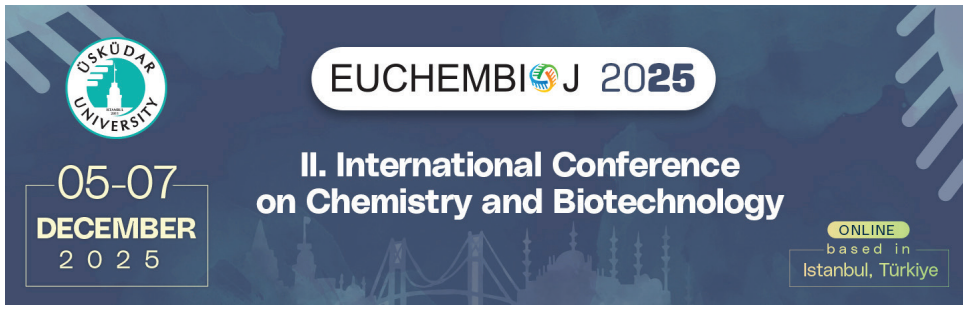
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# Keynotes



## **KE-01. BioCircuit: A Low-Energy Breakthrough for Sustainable and Ecological Wastewater Treatment**

**Chontisa Sukkasem**

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The global demand for sustainable wastewater management requires advanced technologies that reduce both environmental impacts and operational costs. The BioCircuit system represents a breakthrough bioelectrochemical-inspired platform designed to drastically reduce energy consumption while maintaining superior treatment performance.

Unlike conventional activated sludge systems, which typically consume 0.6–0.8 kWh/m<sup>3</sup> of treated wastewater, BioCircuit requires less than 0.05 kWh/m<sup>3</sup>, achieving over 90% reduction in energy demand. Pilot-scale demonstrations (5–100 m<sup>3</sup>/day) have consistently achieved >95% chemical oxygen demand (COD) removal, >90% biological oxygen demand (BOD<sub>5</sub>) removal, and 85–90% total suspended solids (TSS) reduction. A major advantage is the generation of negligible biomass sludge, eliminating up to 70–80% of sludge handling costs compared to conventional processes.

BioCircuit can be flexibly applied as pretreatment for high-strength wastewater (>8,000 mg/L COD) and as a secondary polishing step for effluents <2,000 mg/L COD. Its biofilm-driven configuration allows stable degradation of complex pollutants while specifically targeting sulfur and nitrogen inorganic salts. These compounds are critical because they act as substrates for the generation of toxic hydrogen sulfide (H<sub>2</sub>S) gas and promote cyanobacterial blooms after discharge, both of which severely harm aquatic ecosystems. By eliminating these pollutants, BioCircuit directly reduces ecological risks beyond conventional organic load removal.

The modular and scalable design of BioCircuit enables deployment for decentralized applications (500–5,000 population equivalents) and industrial plants up to 100 m<sup>3</sup>/day pilot scale, with a clear pathway toward full-scale implementation. Economic assessments indicate a payback period of less than 5 years, driven primarily by energy savings and the elimination of sludge management requirements.

The integration of BioCircuit into existing wastewater treatment infrastructures provides a transformative pathway toward circular economy objectives by reducing energy dependency, lowering operational expenditure, and ensuring compliance with stringent discharge regulations. In doing so, BioCircuit directly supports United Nations Sustainable Development Goals (SDGs) 6 and 12.

**Keywords:** wastewater treatment, low-energy process, negligible sludge, sulfur and nitrogen removal, bioelectrochemical system, sustainability



## KE-02. Challenges and Opportunities in AI-Driven Chemistry: A CADD-Informed Perspective on Predictive Retrosynthesis, Impurity Prediction, and Forward Synthesis

Sergey Varnavskiy

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In the dynamic landscape of drug discovery and chemical science, Computer-Aided Drug Design (CADD) remains the strongest convergence of biology, chemistry, and computation. CADD spans structure-based (SBDD) and ligand-based (LBDD) approaches, leveraging molecular modelling, docking, QSAR, pharmacophore modelling, and increasingly powerful AI/ML tools to predict target engagement, pharmacokinetics, metabolism, and safety. Realizing the full potential of AI-driven chemistry hinges on data quality, coverage, provenance, interoperability, and robust uncertainty quantification. Data-rich sources enable reliable predictions, reproducibility, and generalization across chemical space. Among data sources, Reaxys provides best-in-class raw data, extracted from millions of publications, offering broad coverage of reactions, structures, properties, and bioactivities that strengthen model training, validation, and deployment. When paired with FAIR data practices and transparent data provenance, such data ecosystems mitigate biases and support trustworthy AI. A data-centric, human-in-the-loop strategy is proposed to bridge computational predictions with real-world outcomes. Key components include FAIR data ecosystems, model cards, uncertainty estimates, explanations, and rigorous experimental validation (in vitro and in vivo). The synthesis-relevant knowledge from CADD emphasizes Lipinski-like drug-likeness constraints, reliable protein structure predictions (e.g., AlphaFold-family tools), and the integration of MD simulations and docking with ML-based predictions to improve accuracy and generalizability. Multi-omics integration (genomics, transcriptomics, proteomics, metabolomics) alongside comprehensive literature and patent data can enable more holistic, personalized drug design, albeit requiring careful governance and reproducibility standards.

We identify three near-term, high-impact developments to anchor this trajectory:

- Predictive retrosynthesis: literature-anchored, interpretable route proposals with traceability to precedents, enabling human validation and extension.
- Impurity prediction: mechanism-informed forecasting of impurities, including genotoxic concerns, across multi-step syntheses to enable safer design and regulatory readiness.
- Forward synthesis: data-driven reaction optimization and automated synthesis planning, leveraging model-based experimentation and digital twins to optimize conditions, yields, and sustainability, while closing the loop with high-throughput experimentation.

To operationalize these goals, we advocate: (i) integrated data ecosystems that fuse literature, patents, and experimental/clinical data; (ii) standardized schemas and ontologies for seamless interoperability; (iii) robust uncertainty quantification and explainability to build trust; (iv) governance frameworks aligned with regulatory and ethical standards; and (v) scalable automation, digital twins, and lab-instrument integration to accelerate iteration from prediction to experiment. This data- and human-centered approach, grounded in CADD practice and AI-enabled chemistry, powered by high-quality sources like Reaxys, promises safer, faster, and greener drug discovery and more reproducible chemical research.

**Keywords:** Artificial intelligence in chemistry, Computer-Aided Drug Design (CADD), Data Interoperability, Data Quality, Forward Synthesis, Impurity Prediction, Open Science and Reproducibility, Predictive Retrosynthesis.



### **KE-03. Bio-electrochemical System: Revolutionizing the Future for Sustainable Bio-hydrogen Production**

**Pankaj Kumar, Lakhveer Singh\***

*Department of Chemistry, Sardar Patel University Mandi, Himachal Pradesh 175001*

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Bio-electrochemical hydrogen production using microbial electrolysis cells (MECs) is a viable technology for long-term energy production and decarbonization of energy system. MEC have the potential to recover chemical energy from home and industrial wastes as hydrogen gas. However, the electrochemical performance, scalability, and high cost of pricey materials limit the application of MECs. In an attempt to scale up, a distinctive 10L up-flow MEC reactor has been designed, achieving a cathode surface area-to-reactor volume ratio of up to 40 m<sup>2</sup>/m<sup>3</sup>, and is assessed to maximize current density and H<sub>2</sub> recovery without the use of a separator. A high volumetric H<sub>2</sub> production rate of 6.1 L/L/d was attained at a volumetric current density of 985 A/m<sup>3</sup>. Furthermore, the reported current densities of the large reactor were properly anticipated using the internal resistance analysis of small-scale MECs, proving the scalability of the single chamber MEC design.

**Keywords:** Biohydrogen, Bio-Electrochemical System, Energy, Wastewater Treatment



## KE-04. Technological Advancements in Diabetes Management

**Rabah Boukherroub**

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Diabetes is defined as a chronic elevation of glycemia. Due to acute and chronic complications, the disease poses a major economic, social, and medical burden on society worldwide. Diabetes is characterized by insufficient insulin plasma level to meet the organism demand. In type 1 diabetes, absolute deficiency of insulin production results from massive auto-immune destruction of pancreatic beta cells. For this reason, the main therapy consists in delivering exogenous insulin. The treatment methods require numerous daily injections of insulin administered by subcutaneous needle injection, insulin pen and catheters connected to insulin pumps. These methods are however both painful and inconvenient as the invasive multiple injections of precisely calculated amounts of insulin present a significant deterioration of the life quality of the diabetic patients. The discomfort associated with this type of administration has led diabetic patients to neglect or even give up the therapy. There is thus an increasing demand for the design of new insulin administration systems and this has led to the investigations of oral, nasal, buccal, pulmonary, rectal, ocular and transdermal routes. Buccal insulin (Oral-lyn™) and pulmonary insulin (Exubera®) were launched on the market although with small positive feedback by consumers. Oral administration of insulin is encountered with major problems such as hydrolysis in the low pH of gastric medium, splitting by proteinases in the stomach and weak penetration through the membrane of epithelial cells of the intestine.

Transdermal delivery of insulin, a simple and painless method, represents a viable alternative for the controlled release of insulin over time together with high patient compliance. Insulin delivery through the skin has several advantages, including avoidance of the first-pass metabolism, avoidance of gastrointestinal side effects, possibility of extended therapy, therapy at demand, painless and friendly application. However, transdermal delivery is limited by the low permeability of the stratum corneum, the skin outermost layer, allowing only small (<500 Da) hydrophobic molecules to be delivered. In this presentation, I will discuss our original contribution on insulin transdermal delivery upon photothermal or electrothermal activation.

**Keywords:** diabetes, insulin delivery, transdermal



## **KE-05. Multi-Scale Structural Dynamics of Proteins: From Single Point Mutations to Protein Complex Formation**

**Şebnem Eşsiz**

*Kadir Has University, İstanbul, Türkiye*

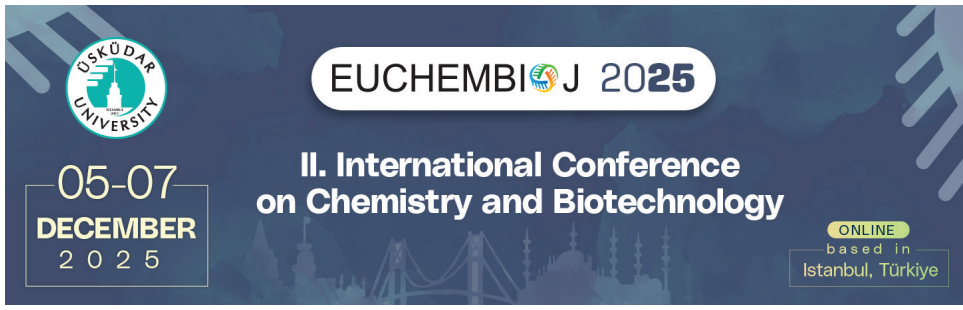
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With the computational power we have today, the techniques to bridge the gap between experimentally available protein structures and the dynamic picture of their functional states are improving daily.

In this seminar, I will explain the application of molecular dynamics (MD) studies with enhanced sampling techniques to explore functional transitions in various biological systems, addressing different scales of molecular representation. At the most localized scale of interactions, I will present results from an MD study investigating the effects of point mutations on the formate dehydrogenase enzyme, focusing on enhancing reverse reaction dynamics for effective CO<sub>2</sub> capture process. Following that, I will delve into the reactivation of the acetylcholine esterase enzyme with oximes, analyzing it from both quantum and atomistic perspectives. This enzyme has an unusually deep binding pocket, making reactivation of the enzyme particularly challenging due to its strong covalent interactions with substrates.

Finally, I will share results from the study of the KRAS-BRAF-MEK signaling pathway complex, emphasizing protein-protein interactions. This example will demonstrate a different level of biomolecular representation, integrating experimental approaches with protein structural modeling techniques, as well as intermediate conformation generation through a novel multiscale machine-learned modeling Infrastructure in the simulation.

**Keywords:** Molecular Modelling, Site-directed mutagenesis, Enzyme Dynamics, Conformational Changes of Proteins



## Oral Presentations



## OP-01. Microbial Community Analysis in MFCs Treating Bilge Water

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Microbial fuel cells (MFCs) represent an emerging and sustainable technology for the treatment of industrial and marine wastewaters, while simultaneously producing bioelectricity. This study investigates the shifts in microbial community (MC) structure during sequential treatment of bilge water using a single-chamber MFC system. Unlike traditional physicochemical methods, biological treatment in MFCs relies on electrogenic microorganisms that play dual roles in biodegradation and electron transfer. To characterize this microbial shift, 16S rRNA gene sequencing was performed on biofilm samples collected before and after MFC operation. The untreated sample reflected the initial adaptation phase after inoculation, while the treated sample represented the community structure following exposure to synthetic, processed, and raw bilge waters. At the phylum level, Proteobacteria was the most dominant group in both untreated (63.93%) and treated (64.56%) samples, highlighting its vital role in electron transfer and system stability. Notably, Campylobacterota showed a marked decrease (from 20.90% to 15.35%), while Firmicutes (from 0.87% to 3.54%) and Actinobacteriota (from 2.16% to 3.77%) increased in the treated condition, indicating microbial adaptation to complex pollutants. At the genus level, the untreated biofilm was primarily composed of Pseudarcobacter (20.31%) and Rhodospirillaceae (19.81%), both associated with nitrogen cycling and fermentative pathways. In contrast, the treated sample was dominated by Rhodocyclaceae (31.92%), a genus well-known for denitrification and pollutant removal. The relative abundance of Proteiniphilum (5.35%) and Pseudomonas (3.96%) also increased after treatment, suggesting enhanced acetate degradation and electroactivity. These genera are strongly associated with syntrophic acetate oxidation and heavy metal tolerance, crucial for bilge water bioremediation. This shift in community composition demonstrates that prolonged bilge water exposure acts as a selective pressure that enriches taxa with enhanced bioremediation and electrochemical capabilities. Eur. Chem. Biotechnol. J. X(X): eXXXX (20XX) The results underline the potential of microbial community engineering in optimizing MFCs for simultaneous pollutant removal and electricity generation.

**Keywords:** 16S rRNA gene sequencing, bilge water, microbial community, microbial fuel cell, Proteobacteria



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## **OP-02. Cytotoxic Effects of MFC Biofilm Byproducts and Antioxidants Response in Human Dermal Fibroblasts CCD-1064SK**

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Microbial fuel cells (MFCs) are widely regarded as sustainable and eco-friendly systems for bioenergy production. However, their electroactive bacterial biofilms release redox-active metabolites, and until now, their potential impact on mammalian cells has been largely overlooked. This study investigates whether these metabolites cause oxidative stress in human dermal fibroblasts and explores the post-exposure recovery potential of natural antioxidants.

Our hypothesis proposed that MFC-derived byproducts could induce oxidative injury in fibroblasts and that Ascorbic Acid (AA), Quercetin (QUE), or their combination might support cellular recovery. Experimental results confirmed the hypothesis: biofilm byproducts significantly reduced fibroblast viability and disrupted cell structure, suggesting a previously undocumented cytotoxic mechanism.

While moderate doses of AA and QUE individually led to partial morphological recovery, Quercetin at 5  $\mu$ M was the only treatment to restore both cell structure and viability. In contrast, combinations of AA and QUE, surprisingly, resulted in lower cell viability despite visibly improved morphology. This result directly contrasts previous findings using rutin (a glycosylated form of quercetin) combined with AA, which enhanced fibroblast recovery in UV-induced oxidative models. To our knowledge, the AA + QUE combination had not been tested before, and our findings suggest an unexpected inhibitory interaction at the cellular level.

These results highlight the need for deeper investigation into the cellular effects of MFC byproducts and further investigation is also warranted to understand whether the observed antagonism between AA and Quercetin is dose-dependent, cell-type specific, or influenced by redox state. These next steps will be critical in assessing the biomedical safety of MFC systems and optimizing antioxidant-based interventions.

**Keywords:** antioxidants, biofilms, cytotoxicity, fibroblasts, microbial fuel cells, oxidative stress



## OP-03. Biosensing Antibiotic- Resistant Bacteria in Wastewater Through Penicillin/Streptomycin Activity in Microbial Fuel Cells

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Bacterial antimicrobial resistance (AMR) is a major health threat worldwide, with wastewater playing a significant role as a major reservoir for disposed antibiotics, antibiotic-resistant bacteria (ARB), and antibiotic-resistant genes (ARG) (Antimicrobial Resistance Collaborators, 2022). Microbial fuel cells (MFC) can serve as a convenient tool to prevent rising AMR by detecting specific pathogens at early stages of the infection cycle through wastewater surveillance (WWS) (Cui et al., 2019; Tiwari et al., 2022). This research aimed to develop an MFC-based biosensor to detect ARB from wastewater enriched with electroactive biofilm by introducing selective pressure through antibiotic application. Two single-chamber air cathode MFCs were inoculated with mixed culture bacteria. Once a stable voltage was established, compound mixture of penicillin and streptomycin was added to the channels in the concentrations 100 ngmL<sup>-1</sup> and 500 ngmL<sup>-1</sup>. Four batches were run at each concentration to record the voltage fluctuation trend. Higher concentration induced a slight drop in voltage in both channels before increasing, implying selective pressure on bacterial species competing against the electroactive resistant bacterial species. Maximum voltage was produced at lower antibiotic concentration in both channels, correlating to rapid growth of electroactive resistant bacteria due to adaptation in the absence of competition from non-electroactive non-resistant bacteria (Mathieu et al., 2016). The findings of the research confirm MFCs can efficaciously be utilized as whole-cell electrochemical biosensors since it successfully detected the shift in bacterial metabolic activity after antibiotic addition. MFCs have the potential to serve as economically feasible biosensors to efficiently detect ARB through real-time monitoring.

**Keywords:** antibiotic resistant bacteria, bioremediation, biosensor, microbial fuel cell.



## **OP-04. Development of Process and Packaging Structure Compliant with Toxic NIAS Limits in Flexible Food Packaging**

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Flexible packaging plays a critical role in maintaining food safety and shelf life. Laminated multilayer structures composed of materials such as polyethylene (PE), polyethylene terephthalate (PET), aluminum foil, and paper are commonly used for food packaging due to their barrier and mechanical properties. The adhesives used in these laminates, often polyurethane or polyester-based systems, can be sources of Non-Intentionally Added Substances (NIAS). NIAS are chemical compounds not intentionally included in the formulation but formed as by-products of reactions, degradation, or contamination during manufacturing, storage, or use.

This project, conducted by Bak Ambalaj R&D Center, focuses on identifying the origin and controlling the migration of NIAS in food contact adhesives. Particular attention is given to cyclic oligomers and orthophthalic acid, which are frequently encountered NIAS in polyester and polyurethane adhesive systems. Cyclic oligomers are ring-structured low-molecular-weight compounds formed during incomplete polymerization reactions, while orthophthalic acid is a degradation product of phthalic anhydride-derived resins. Both can migrate into food under certain conditions, posing potential toxicological risks, including endocrine disruption.

Advanced analytical methods such as Gas Chromatography-Mass Spectrometry (GC-MS), Liquid Chromatography-Mass Spectrometry (LC-MS), and High-Performance Liquid Chromatography (HPLC) were employed to detect and quantify NIAS components. Adhesive formulations were evaluated based on their compliance with the Specific Migration Limits (SML) and Overall Migration Limit (OML) as defined in EU Regulation No 10/2011. The study also incorporated risk-based assessment strategies, using SML thresholds categorized by target consumer groups (infants, children, adolescents, and adults).

Experimental work included formulation and testing of alternative adhesives, modification of crosslinker components, and lamination of mono-polyolefin films under optimized process conditions. Prototypes were subjected to migration testing and toxicological evaluation. Adjustments to processing parameters such as curing temperature and machine speed were made to minimize solvent residues and NIAS formation. Supplier audits and raw material certificates were used to pre-screen adhesive inputs for NIAS risk.

Results demonstrated that cyclic oligomer formation can be reduced by using high-purity polymers and optimizing polymerization conditions. Orthophthalic acid migration was mitigated by adopting isophthalic or phthalate-free polyester alternatives. In several formulations, NIAS levels were maintained below OML thresholds, confirming regulatory compliance and suitability for food contact applications.



This study establishes a practical framework for NIAS monitoring and reduction in flexible packaging adhesives. The integration of analytical testing, regulatory compliance, and process optimization ensures safer packaging systems. The findings are directly applicable to industrial production and contribute to the development of sustainable, low-risk packaging technologies. The results also support corporate compliance with EU and FDA food regulations while addressing growing consumer and regulatory concerns about chemical safety in packaging.

**Keywords:** Adhesives, Food Packaging, Lamination of Flexible Films, NIAS

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## **OP-05. Imidazopyridine Family: Versatile and Promising Heterocyclic Skeletons for Different Applications**

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In recent years, there has been increasing attention focused on various products belonging to the imidazopyridine family; this class of heterocyclic compounds shows unique chemical structure, versatile optical properties, and diverse biological attributes. The broad family of imidazopyridines encompasses different heterocycles, each with its own specific properties and distinct characteristics, making all of them promising for various application fields. In general, this useful category of aromatic heterocycles holds significant promise across various research domains, spanning from material science to pharmaceuticals. The various cores belonging to the imidazopyridine family exhibit unique properties, such as serving as emitters in imaging, ligands for transition metals, showing reversible electrochemical properties, and demonstrating biological activity. (Sanapalli et al., 2022; Chaudhran & Sharma, 2022; Priyanga et al., 2019; Kumar Bagdi et al., 2015; Vanda et al., 2019) Recently, numerous noteworthy advancements have emerged in different technological fields, including optoelectronic devices, sensors, energy conversion, medical applications, and shining emitters for imaging and microscopy. (Volpi et al., 2025; Volpi, 2022; Ramana Reddy et al., 2022) This presentation intends to provide a state-of-the-art overview of this framework from 1955 to the present day, unveiling different aspects of various applications. This extensive literature survey may guide chemists and researchers in the quest for novel imidazopyridine compounds with enhanced properties and efficiency in different uses.

**Keywords:** imidazopyridine, luminescence, heterocycle



## OP-06. Applications Genome Scale Metabolic Models for Different Domains of Life in Biotechnology

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Genome-scale metabolic models (GEMs) have become indispensable tools in biotechnology, offering a systems-level understanding of metabolism across different domains of life — Bacteria, Archaea, and Eukarya (Gu et al., 2019). In bacteria, GEMs are widely used to optimize strains for industrial production of biofuels, amino acids, and pharmaceuticals. *Escherichia coli*, for example, has been modeled extensively to guide metabolic engineering strategies that enhance production of bioethanol, succinate, and recombinant proteins (McCloskey et al., 2013). Similarly, *Bacillus subtilis* GEMs have been applied to improve enzyme secretion and biopolymer synthesis, demonstrating how bacterial models can serve as robust platforms for cell factory design and metabolic optimization.

In the archaeal domain, GEMs have facilitated exploration of extremophiles as potential biotechnological workhorses. Models of methanogenic archaea such as *Methanosarcina acetivorans* have been instrumental in studying methane metabolism and engineering archaeal systems for bioenergy applications (Nazem-Bokae et al., 2016). These models reveal unique pathways and metabolic robustness under extreme conditions, providing valuable insights for designing processes involving high temperature, salinity, or pH. The integration of GEMs with omics data has further advanced understanding of archaeal adaptation and expanded their potential use in bioremediation and sustainable energy generation.

In eukaryotic systems, GEMs of yeasts, plants, and microalgae are transforming metabolic engineering by enabling prediction of cellular behavior under genetic or environmental perturbations. For instance, *Saccharomyces cerevisiae* GEMs are extensively used for production of bioethanol, organic acids, and pharmaceuticals, while plant and algal GEMs — such as those of *Chlamydomonas reinhardtii* — guide engineering for enhanced lipid and pigment synthesis for biofuel production (Arend et al., 2023; Yao et al., 2023). These models integrate compartmentalized metabolism and complex regulatory networks, bridging fundamental biology and applied biotechnology. Collectively, GEMs across all domains of life empower rational design of organisms, facilitating sustainable bioprocess development and contributing to the broader goals of synthetic biology and industrial biotechnology.

**Keywords:** genome scale metabolic models



## OP-07. Machine Learning Model Applications for Predicting the Most Potent AGE Precursors: A Glyoxal Case Study

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Advanced Glycation End Products (AGEs) are harmful compounds that form through non-enzymatic reactions between reducing sugars and proteins or lipids. Glyoxal, a highly reactive dicarbonyl compound, plays a central role as a precursor in AGEs formation. This study investigates the use of various machine learning regression models to predict glyoxal concentrations in processed packaged foods based on multiple nutritional components, including saturated fat, fiber, salt, total fat, fructose, sugar, glucose, sucrose, carbohydrates, and lipids.

Model performance was evaluated using key metrics such as  $R^2$  score, RMSE, MAE, RRSE, RAE, and processing time. Among the models tested, advanced ensemble algorithms especially CatBoost demonstrated superior predictive accuracy. CatBoost achieved the lowest RMSE (78.52) and MAE (43.75), making it the most effective model. LightGBM and XGBoost also performed well, though to a slightly lesser extent. In contrast, simpler models like Linear Regression ( $R^2 = -37.49$ ) and tree-based methods such as Decision Tree and Random Forest yielded poor results, indicating their inability to adequately model the underlying relationships, particularly the strong impact of certain nutrients like fructose.

Notably, feature analysis revealed that fiber had minimal impact, while fructose emerged as a highly influential predictor of glyoxal content. This suggests that focusing on certain sugar types may be more relevant in AGE-related risk assessments. Additionally, while neural networks provided relatively accurate predictions, their high computational cost limits practical usability.

Overall, this study underscores the advantage of using modern ensemble learning approaches, particularly CatBoost, for accurately modeling complex biochemical predictors like glyoxal in food systems. These findings may support future strategies for assessing and reducing AGE precursors in food products.

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**Keywords:** Machine Learning, Glycation, Food , AGEs



## OP-08. The Delaying Effect of Directly Applied Humic Acid on Senescence in Barley (*Hordeum vulgare* L.) Leaf Segments

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Humic acids are widely used in agriculture to improve soil structure and promote plant growth; however, only a limited number of studies have focused on their overall impact on plant metabolism, and their stimulatory or delaying effects remain controversial. Studies investigating the effects of humic acid when directly applied to the leaf surface, such as tissue improvement or delay of senescence, are also very limited. This study aimed to evaluate the short-term effects of direct application of humic acid to leaf segments rather than to the soil. Barley (*Hordeum vulgare* L.) seedlings were grown for 15 days. Segments of 3 cm in length were cut from the first leaves, and four segments obtained from four different plants were placed in each Petri dish. A total of 6 ml of solution was added to each Petri dish. Distilled water (D.W.) was used as the control, while humic acid (HA) solutions of 0.025 ml L<sup>-1</sup> and 0.25 ml L<sup>-1</sup> were used as the experimental groups. Incubation conditions in the Petri dishes were kept constant, and the segments were incubated for 2 days. Symptoms of senescence, indicated by changes in leaf coloration, were observed. To examine tissue-level changes, fresh weight, chlorophyll and carotenoid contents, cell integrity, and antioxidant enzyme activities were analyzed. In both humic acid concentrations, senescence was delayed in leaf segments compared to the control group, and healthier tissue development was observed. A more pronounced improvement was particularly evident at the higher concentration (0.25 ml L<sup>-1</sup>). This preliminary study demonstrates that humic acid can exert a direct protective effect on leaf tissues when applied to the leaf surface and may delay the senescence process. The findings suggest that humic acid may be beneficial not only in soil applications but also in the context of exogenous applications. It is recommended that future studies employ quantitative physiological and biochemical analyses to elucidate the underlying mechanisms.

**Keywords:** barley, humic acid, leaf segments, petri incubation, senescence



## OP-09. A Brief Study of 1-(4-hydroxyphenylthio)-8-chloroanthracene-9,10-dione: Fluorescent Nanoparticles as Enhancers of Chemiluminescence in Luminol-Based Assays

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Chemiluminescence (CL) reactions are effective chemical reactions used for the determination of many analytes (Huang and Ren, 2012). Some of the molecules used for this purpose, which exert their effects through this reaction mechanism, are structures that act as enhancers for fluorescence-active molecules, whose activity can be enhanced by chemiluminescence resonance energy transfer (CRET) (Cinquanta et al., 2017; Yan et al., 2020). The CRET mechanism can be defined as the non-radiative energy transfer from the chemiluminescence (CL) reagent to the energy acceptor during the CL reaction. Because the reaction process does not require excitation from an external source, CRET-based assays have low background and high sensitivity. Acceptor molecules that can effectively increase CL intensity have high quenching efficiencies, thus expanding the application area of CRET from biosensors and biological imaging to biomedicine and therapy (Karabchevsky et al., 2016; Bedouhène et al., 2017; Wang et al., 2021). In this study, the characterization of the 1-(4-hydroxyphenylthio)-8-chloroanthracene-9,10-dione molecule synthesized by the nucleophilic substitution was performed, and its use in combination with luminol, which has fluorescent activity, was discussed. Characterization of the chemical structure was achieved using UV-VIS, IR, and fluorescence spectroscopy. In the following steps, the CL mechanism was investigated using luminol, which can also be used as a marker in biological assays, through its fluorescence characteristics. It was observed that the CL effect was enhanced via the CRET mechanism when luminol was used as a complex with the 1-(4-hydroxyphenylthio)-8-chloroanthracene-9,10-dione sample. Experiments conducted on samples containing iron molecules, which are used in redox reactions that elicit luminescent activity during luminol applications, demonstrated that the 1-(4-hydroxyphenylthio)-8-chloroanthracene-9,10-dione sample could be used as a more effective complex for biomarking purposes.

**Keywords:** Biological imaging, Chemiluminescence, Chemiluminescence resonance energy transfer



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## OP-10. Dose-dependent Quercetin and Novel Curcumin Derivative Activity Against Sodium Arsenate Toxicity *in vitro* in ECV-304 Endothelial Cells

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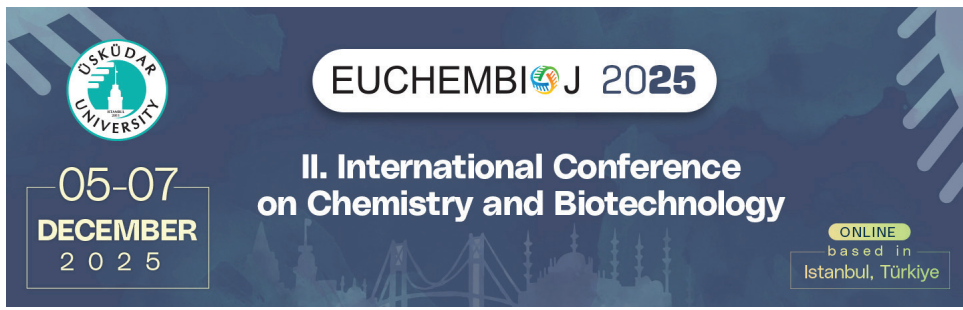
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In this study, the protective effects of quercetin and a curcumin derivative compound named (1*E*, 6*E*)-3,5-dioxohepta-1,6-dien-1,7-diyl) bis(2-methoxy-4,1-phenylene) dipropionate against arsenate toxicity induced *in vitro* in endothelial cells were investigated. ECV-304 cells were selected as a stable model for *in vitro* testing and comparison of antioxidants to examine the oxidative damage caused by sodium arsenate. This chemical may trigger oxidative stress, the damage of mitochondria, and an activation of apoptotic mechanisms. Modified MTT assay protocols were used to assess cell viability, and statistical analysis was conducted using one-way ANOVA. In the current research, 0 – 500  $\mu$ M sodium arsenate, a 10 – 500  $\mu$ g/mL quercetin and 0.04 – 100  $\mu$ g/mL of curcumin derivative were examined. According to results, it was determined that sodium arsenate at the concentration of 200  $\mu$ M killed 51% of endothelial cells in a 24-hour period. Cell viability decreased to approximately 40% when exposed to 300  $\mu$ M As, but treatment with 200  $\mu$ g/mL of quercetin increased viability to around 55% (\*\*\*\* $p < 0.0001$ ), suggesting a protective effect of the chemical. Treatment with the curcumin derivative (0.04 – 1.5  $\mu$ g/mL) notably improved cell viability, indicating a dose-dependent antioxidant protective effect against 300 – 400  $\mu$ M sodium arsenate-induced toxicity. However, increased cytotoxic activity was observed at higher concentrations of curcumin derivative ( $\geq 25$   $\mu$ g/mL). These findings highlight the significance of dose optimization when using antioxidant derivatives, as molecules with similar chemical structures may exhibit different biological effects at the same concentrations. In conclusion, results show that both quercetin and the new curcumin derivative exhibit protective effects against sodium arsenate-induced cytotoxicity in endothelial cells, supporting their potential application as antioxidant compounds in the mitigation of cellular damage associated with heavy metal exposure.

**Keywords:** antioxidant, arsenate, curcumin, quercetin, viability



## Poster Presentations



## PP-01. Antioxidant, Cytotoxic and Antimicrobial Activities of *Porphyridium Cruentum* Microalgae Species

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This study investigates the biochemical and bioactive properties of the red microalga *Porphyridium cruentum*, with a particular focus on its antioxidant and antibacterial activities. As the widespread demand for new, effective, and safe antimicrobial agents increases in the face of rising antibiotic resistance, microalgae have emerged as promising sources of natural compounds with therapeutic potential. *P. cruentum* stands out for its rich content of polysaccharides, polyunsaturated fatty acids, and phycobiliproteins, as well as its rapid growth and adaptability to diverse environmental conditions. In this research, *P. cruentum* was cultivated under controlled laboratory conditions, and sequential solvent extraction was performed to obtain bioactive fractions. The chemical composition of the extracts was characterized using gas chromatography–mass spectrometry (GC/MS), which identified palmitic acid methyl ester and stearic acid methyl ester as the dominant fatty acids, accounting for over 90% of the total identified volatiles. Antibacterial assays against *Staphylococcus aureus* revealed that the extracts exhibit dose-dependent inhibitory effects, with higher concentrations resulting in significant suppression of bacterial growth. These findings suggest the presence of potent antimicrobial compounds within the algal biomass. In addition to antimicrobial activity, the antioxidant potential of *P. cruentum* extracts was evaluated using the DPPH radical scavenging and  $\beta$ -carotene bleaching assays. The results demonstrated notable radical inhibition capacities at both tested concentrations (25 and 50 mg/mL), with inhibition rates of 47% and 40.2%, respectively. These effects were further supported by quantification of total phenolic content (TPC) and total flavonoid content (TFC), measured by standard spectrophotometric methods. The extracts displayed elevated TPC and TFC values compared to controls, highlighting their rich content of bioactive phytochemicals that contribute to the observed antioxidant effects. Overall, this comprehensive analysis affirms that *Porphyridium cruentum* possesses a complex biochemical profile, combining significant antimicrobial and antioxidant properties. The high levels of phenolic and flavonoid compounds, alongside fatty acid derivatives, underpin its bioactivity and suggest broad applicability in pharmaceutical, nutraceutical, and cosmetic industries. Furthermore, the study supports the potential of targeted cultivation and extraction of *P. cruentum* as a sustainable strategy for producing novel bioactive agents, with potential benefits for health, food safety, and environmental applications. In conclusion, *P. cruentum* represents a valuable resource for the development of next-generation antimicrobial and antioxidant agents, addressing the urgent need for alternative solutions to antibiotic resistance and oxidative stress-related diseases.

**Keywords:** antibacterial activity, antioxidant, bioactive compounds, microalgae, *Porphyridium cruentum*



## PP-02. Microbial Biomarker Discovery: Assessing the Impact of Non-Viable Microbial DNA on Community Profiling

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**Background:** The structure and function of microbial communities depend mainly on viable members. 16S rRNA amplicon sequencing is a widely used method for analyzing prokaryotic composition; however, it cannot distinguish between live and dead bacteria. In viability-based analyses, PMA<sub>xx</sub>, a photoreactive DNA-binding dye, is commonly used to selectively detect viable cells via PCR-based methods and is compatible with amplicon sequencing (Emerson et al., 2017).

**Objective:** This study aimed to investigate the impact of PMA treatment on the composition of healthy salivary microbiota to enhance specificity in identifying health-associated microbial taxa and potential biomarkers.

**Methods:** A saliva sample was collected from a healthy 50-year-old female participant using the spitting method (Fey et al., 2024) following written informed consent. The sample was divided into two aliquots: one treated with 50  $\mu$ M PMA<sub>xx</sub> (P) and the other left untreated (C). PMA<sub>xx</sub> (Biotium, USA) was photoactivated using a 500 W halogen lamp positioned 20 cm from the sample for 15 minutes. Microbial genomic DNA (gDNA) was extracted using the QIAamp PowerFecal Pro DNA Kit (Qiagen, Germany). The V3–V4 regions of the 16S rRNA gene were amplified and sequenced on the Element Aviti platform using paired-end technology. The raw sequence data were processed and analyzed with QIIME2.

**Results:** Firmicutes was the dominant phylum, decreasing in relative abundance from 55% in C to 43.4% in P. Other dominant phyla (>1%) also shifted in P, with increases in Bacteroidota, Proteobacteria, and Patescibacteria, and decreases in Actinobacteriota and Fusobacteriota. Streptococcus remained the most abundant genus. Among the ten most abundant genera, the greatest shifts were observed in Actinomyces (C: 5.7%, P: 2.7%), Rothia (C: 6%, P: 1.9%), Gemella (C: 4%, P: 0.6%), Porphyromonas (C: 4.3%, P: 9.9%), Prevotella\_7 (C: 7.3%, P: 11.1%), Neisseria (C: 4.7%, P: 10.7%), and Haemophilus (C: 0.7%, P: 2.8%). The majority of rare genera (<0.1%) increased after PMA treatment, with some exceeding 0.1% in relative abundance.



Conclusions: Salivary microbiota has been extensively studied for its potential as a non-invasive diagnostic tool, with various disease-associated biomarkers identified (Shinde et al., 2024). In fact, one study reported an association between a specific biomarker genus in the salivary microbiota and a disease, based on its fold increase in abundance (Ganesan et al., 2023); another study developed a predictive formula using genera's relative abundances (Narita & Kodama., 2022). However, as also demonstrated in our study, the presence of dead cells may alter microbial composition and introduce bias in microbial biomarker analysis. Although a standardized protocol for PMA treatment has yet to be established, it remains one of the most effective methods currently available to distinguish viable microbiota in amplicon sequencing studies. Therefore, increasing the number of studies focused on standardizing the PMA method is essential. We believe that applying the PMA method in biomarker research will enhance specificity in identifying potential biomarkers and contribute to a more precise evaluation of the relationship between salivary microbiota, health, and disease.

**Keywords:** salivary microbiota, 16S rRNA, PMA, biomarker

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## PP-03. Gene Engineering of the TP-84 Bacteriophage Portal Protein as a First Step in Creating Bionanoparticles

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Bacteriophage applications in science can be broadened by the usage of the genetical engineering. Phage display is one such example. This technique allows to modify phage capsid protein so it will display desired peptide on the surface of the bacteriophage. This result can be obtained through gene engineering by modification of a specific gene region. Phage display is a popular technique used to test protein-protein interactions. [1]

Phage capsid proteins obtain ability to self-assembly, and thus are used to create non-infectious bionanoparticles. Those bionanoparticles lack phage genome and can be modified to act as a cargo vehicle, hence such structures are used in drug delivery systems. [2]

The goal of this research was to design and express two proteins: (i) Portal protein derived from thermophilic phage TP-84, fused with SpyTag motif, (ii) sfGFP fused with complementary SpyCatcher motif. SpyTag and SpyCatcher domains are created by splitting the CnaB2 domain of the FbaB protein from *Streptococcus pyogenes*. SpyTag/SpyCatcher system focuses on the spontaneous formation of an isopeptide bond between lysine and aspartic acid side chains. [3] By adding complementary Spy domains to the expressed proteins it can be possible for the two proteins to bind to each other.

This research is the first step in creating new generation bionanoparticles, based on TP-84 bacteriophage capsid proteins. Future research will involve replacing sfGFP reporter protein by a biologically active peptides or proteins, fused with SpyCatcher motif

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## Awards and Honorees

The Organizing Committee of EUCHEMBIOJ 2025 – The II. International Conference on Chemistry and Biotechnology, held online on 05–07 December 2025 (Istanbul, Türkiye), is honored to recognize exceptional scientific achievements that reflect innovation, excellence, and multidisciplinary impact.

In recognition of their outstanding contributions, the following awards were bestowed:

### **Industrial Innovation Award**

**Hande Uçak Merdol**

*Development of Process and Packaging Structure Compliant with Toxic NIAS Limits in Flexible Food Packaging*

### **Multidisciplinary Research Excellence Award**

**Giorgio Volpi**

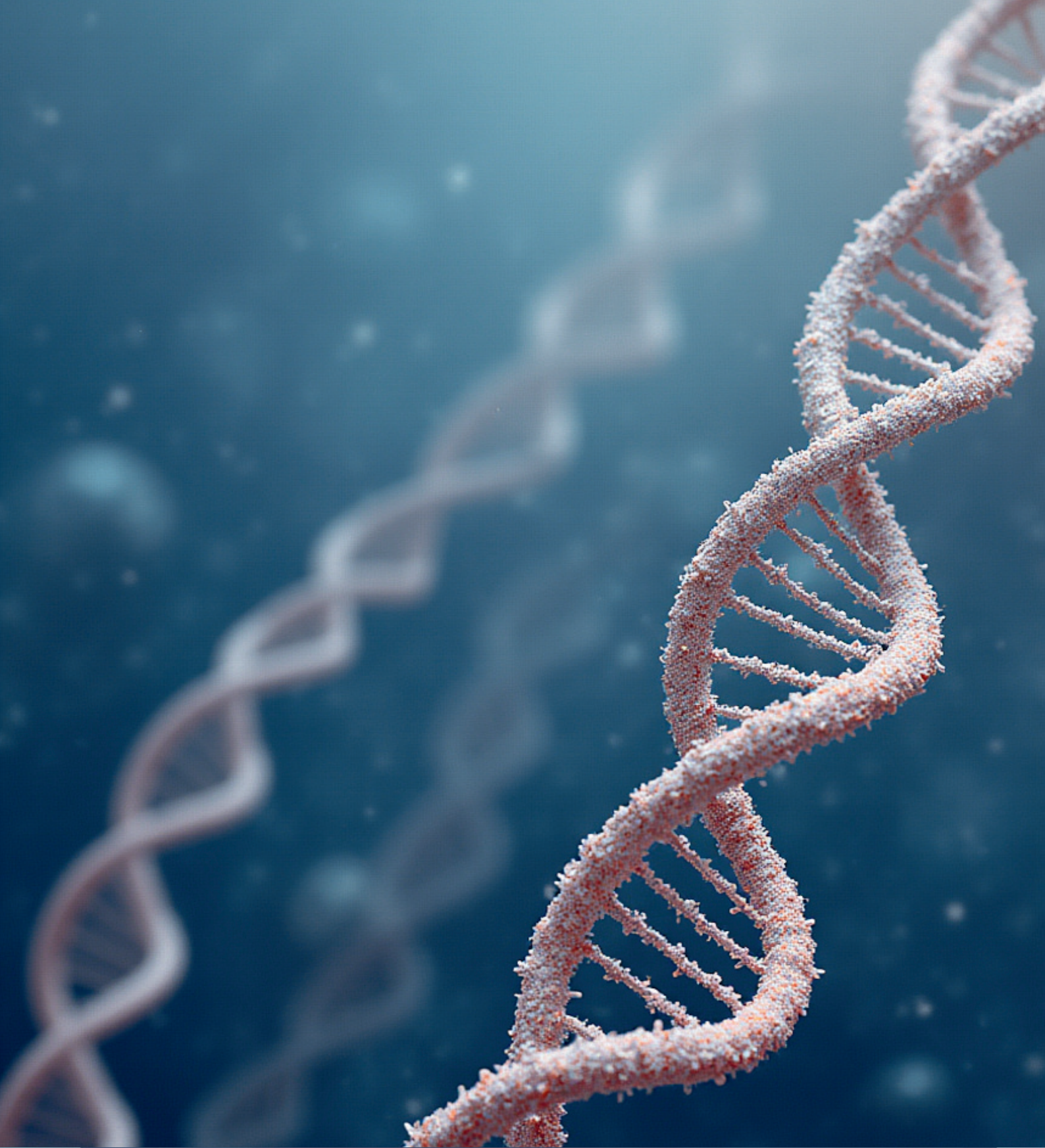
*Imidazopyridine Family: Versatile and Promising Heterocyclic Skeletons for Different Applications*

### **Young Investigator Award**

**Jakub Mazur**

*Gene Engineering of the TP-84 Bacteriophage Portal Protein as a First Step in Creating Bionanoparticles*

The Organizing Committee extends its sincere congratulations to the award recipients and expresses its appreciation for their significant contributions to the advancement of chemistry and biotechnology.



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