

#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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# FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge,

two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5<sup>th</sup> Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević*  
& *Dr. Ivana Morić,*  
On behalf of BelBi2023  
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**Groundwater and soil as a reservoir for polyurethane-degrading bacteria**Milica Ciric<sup>1\*</sup>, Brana Pantelic<sup>1</sup>, Vladimir Šaraba<sup>1</sup>, and Jasmina Nikodinovic-Runic<sup>1</sup>

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Plastic waste is a global environmental burden. Polyurethanes (PU), toxic and ubiquitous synthetic polymers, do not biodegrade quickly, leading to their rapid accumulation in the soil and water environments. Highly efficient PU-degrading microorganisms are rare in nature and are of fundamental importance for achieving circular plastic economy. Bacterial isolates from groundwater, originating from magmatogenic massif and Tertiary basin within metamorphic area, as well as soil isolates collected from various pristine (PS) and contaminated sites (CS), were screened using PU model compound Impranil® DLN-SD (IMP) as sole C source to identify PU-degrading isolates. Phylogenetic analysis of 16S rRNA gene sequences from IMP-degrading isolates was performed using the neighbor-joining method to observe their clustering. Thirty one of 96 isolates (32.3 %) from groundwater and 18 of 220 isolates (8.2%) from soil produced prominent IMP-clearing zones. Thirteen IMP-degrading isolates from each type of environment, belonging to 8 genera (*Pseudomonas*, *Proteus*, *Enterobacter*, *Flavobacterium*, *Serratia*, *Pantoea*, *Acinetobacter* and *Stenotrophomonas*) for groundwater and to 6 genera (*Streptomyces*, *Pseudomonas*, *Rhodococcus*, *Achromobacter*, *Bacillus* and *Paenibacillus*) for soil environment, were included in phylogenetic analysis. No clear grouping of groundwater and soil isolates was observed, indicating that isolates are too distinct. Stronger clustering was observed for groundwater compared to soil isolates. For groundwater, strongest clustering was observed for 2 isolates belonging to *Proteus* genus, 2 belonging to *Flavobacterium* and 2 to *Pseudomonas*. For soil samples, strongest clustering was observed for 3 isolates belonging to genus *Streptomyces*. There was no clear grouping within isolates from CS and PS. In the future, wider range of environmental niches should be included in screening efforts for development of biocatalytic processes for management of plastic waste. Subterranean ecosystems, which are not readily accessible for sampling and represent largely unexplored reservoir of biotechnologically relevant enzymatic activities, should also be more represented in such screenings.

**Keywords:** groundwater, soil, polyurethane-degrading bacteria, 16S phylogeny

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