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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& *Dr. Ivana Morić,*
On behalf of BelBi2023
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Poster presentation

***In silico* pre-selection of β -glucosidase gene for heterologous recombinant expression**

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Biofilms are ubiquitous in nature, and the food industry is vulnerable to the risks posed by biofilm formation. Not only do they interfere with the food production process, but they also pose a public health threat. However, complete elimination of biofilms on food and food contact surfaces cannot be achieved by conventional methods (cleaning and disinfection) alone. New biofilm control strategies must be developed to prevent its formation and/or persistence. Novel approaches may be based on enzymes that depolymerize components of the biofilm matrix, making bacterial cells accessible to antimicrobial agents.

Environmental microorganisms are an inexhaustible source of new enzymes. In *Salmonella Enteritidis* and *Escherichia coli*, known foodborne pathogens, cellulose is an important component of the biofilm matrix, so our isolates from untapped environments were tested for cellulolytic activity. Of the more than 70 isolates examined, isolate BG28 was selected as the most promising. Its genome was sequenced, annotated, and it was identified as Gram-positive *Microbacterium* sp. Genome mining revealed the presence of four complete genes for different β -glucosidases, one of three enzyme types of cellulase complexes. To select the best candidate for heterologous expression DeepTMHMM, ProtParam, and SoluProt were used to predict the presence/absence of signal peptide and transmembrane domains, instability index, aliphatic index, hydrophilicity, and soluble expression in *E. coli*. Based on the prediction results, the gene annotated as β -glucosidase B was selected for recombinant expression. In addition, I-TASSER was used to model the tertiary structure of the selected enzyme.

The β -glucosidase B was recombinantly expressed, purified, and tested for its anti-biofilm activity. It was active and showed a 50% inhibitory effect on *S. Enteritidis* and *E. coli* biofilm formation at a concentration of 100 μ g/ml. To further evaluate this *in silico* approach in the preselection of candidate enzymes for recombinant expression and purification, we will use it to identify other enzymes of the cellulase complex.

Keywords: β -glucosidase, bioinformatics tools, enzyme, biofilm

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