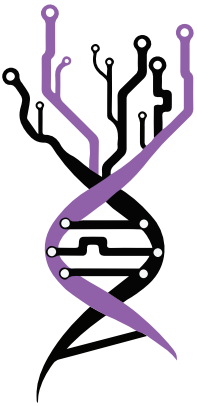
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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EDITORS
Dr. Ivana Morić
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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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TABLE OF CONTENT

KEYNOTE LECTURES

INVITED LECTURES

ORAL PRESENTATION

POSTER PRESENTATION

In Silico analysis and prediction of novel pharmacogenomic markers of pediatric ALL treatment

Vladimir Gašić*[1], Nikola Kotur[1], Biljana Stanković[1], Đorđe Pavlović[1], Marina Jelovac[1], Jelena Perić[1], Bojan Ristivojević[1], Sonja Pavlović[1], and Branka Zukić[1]

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Acute lymphoblastic leukemia (ALL) is the most common childhood neoplasm. Side effects of therapy occur in 75% of patients and 1-3% of patients have a lethal outcome due to treatment. More efficient treatment of pediatric ALL has been developed by avoiding drug adverse effects included in the treatment protocols. Therefore, implementation of pharmacogenomics is paramount in pediatric ALL treatment. Next generation sequencing (NGS) contributed to discovery of novel genetic markers, potential candidates for targeted therapy and predictors of efficacy and toxicity of drugs.
We aimed to discover novel potential pharmacogenomic markers in pediatric ALL.
DNA samples from bone marrow of 17 pediatric ALL patients were analyzed using the platform TruSeq Amplicon – Cancer Panel (Illumina) for somatic mutations in 48 oncogenes. DNA samples from blood of 100 individuals, using the platform TruSightOne (Illumina), were analyzed for germinative mutations. An in-house virtual panel for GC response markers was designed. Predicting the effects of novel variants was performed using the SIFT, PolyPhen-2 and PROVEAN software tools. For protein structure stability and modeling we used STRUM method and i-TASSER server.
In the NGS study of somatic mutations in pediatric ALL, 9 novel variants have been identified. Bioinformatic analysis has shown that *STK11* c.1023G>T and *ERBB2* c.2341C>T possess potential as pharmacogenomic markers, therefore, they are candidates for molecular targeted therapy. In the exome sequencing study, according to the prediction algorithms, 3 new potential markers in pharmacogenes related to GC response have been identified, *ABCB1* c.947A>G, *NCOA3* rs138733364 and *TBX21* rs14059812.
Using NGS analysis and prediction algorithms, we have detected 2 novel somatic mutations, candidates for targeted molecular therapy, as well as 3 novel germinative variants, potential pharmacogenomic markers of GC response in pediatric ALL. Pharmacogenomic profiling of each pediatric ALL patient is indispensable for new therapy approaches and it could lead to better outcomes.

Keywords: Acute lymphoblastic leukemia, Pediatric, Pharmacogenomics

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