

#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE 2023

EDITORS

Dr. Ivana Morić

Dr. Valentina Đorđević

ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title	4 th Belgrade Bioinformatics Conference BOOK OF ABSTRACTS
Publisher	Institute of Molecular Genetics and Genetic Engineering, University of Belgrade Vojvode Stepe 444a, Belgrade, Serbia https://www.imgge.bg.ac.rs/
Editors	dr. Ivana Morić dr. Valentina Đorđević
Technical editor	Dušan Radojević
ISBN	978-86-82679-14-1
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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

Determinants of CRISPR array non-canonical adaptation mechanism

Marko Tumbas^{1*} and Marko Đorđević¹

¹Quantitative Biology Group, Faculty of Biology, University of Belgrade,
Studentski trg 16, 11000 Belgrade, Serbia

marko.tumbas@bio.bg.ac.rs

CRISPR-cas systems are incredibly diverse and currently are classified in six major types and over 30 subtypes. Apart from their role in adaptive immunity it has been shown that some of the CRISPR-cas subtypes are also involved in host gene regulation and even in collateral damage leading to bacteriostatic or lethal outcomes for the host. CRISPR array spacers direct and influence canonical and non-canonical functions of the CRISPR-cas system together with subtype Cas proteins. Better understanding of spacer adaptation mechanisms is crucial for uncovering intricacies of evolutionary arms race between prokaryotes and phages.

Here we present large-scale analysis of CRISPR array spacers originating from 31845 complete bacterial genomes. All bacterial and 16388 viral genomes were retrieved using NCBI datasets API. CRISPRidentify and CRISPRcasIdentifier tools were used for CRISPR array, Cas genes detection and subtyping. Viral genomes were mapped to their hosts using the latest version of the Virus-Host DB. Mapping was performed on the genus level of the hosts phylogenetic tree. Gumbel extreme value distribution was used to determine statistical significance of each spacer Smith-Waterman alignment score.

Differences in melting energy and GC content between identified spacers, origin bacterial genomes and infecting bacteriophages were explored for different CRISPR-cas subtypes and for different bacterial genera. Spacers from the extremes of the GC content distribution were aligned to the origin bacterial and infecting phage genomes in order to determine their origin.

GC content of the spacers was lesser than the GC content of the source bacterial genome but greater than infecting viral genome. This observation aligns with the hypothesis that the majority of CRISPR spacers were adapted from the bacteriophage genomes and serve canonical function. Alignments of the spacers from GC rich distribution tail have shown their preferential targeting of host genomes which further supports the hypothesis that GC rich spacers originated from the bacterial genome and have non-canonical function.

Keywords: CRISPR-cas, melting energy, extreme value distribution



ISBN: 978-86-82679-14-1