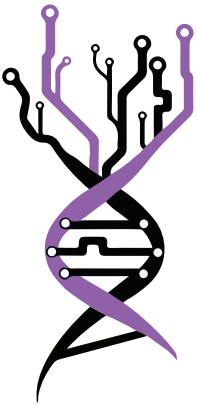
#BelBi2023 • Belgrade, Serbia

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 4th 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 Đorđevic

Technical editor Dušan Radojević

ISBN **978-86-82679-14-1**

BelBi2023 Committees

International Advisory Board

Alessandro Treves,
International School for Advanced Studies, Trieste, Italy

Guanglan Zhang,
Health Informatics Lab, Metropolitan College, Boston University, Boston, USA

Konstantin Severinov,
Waksman Institute for Microbiology, Rutgers University, Piscataway, USA

Lou Chitkushev,
Health Informatics Lab, Metropolitan College, Boston University, Boston, USA

Milena Stevanović,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia

Oxana Galzitskaya,
Institute of Protein Research, Russian Academy of Sciences, Moscow, Russia

Paul Sorba,
Laboratory of Theoretical Physics and CNRS, Annecy, France

Peter Tompa,
VIB Structural Biology Research Center, Flanders Institute for Biotechnology, Brussels, Belgium

Predrag Radivojac,
Khoury College of Computer Sciences, Northeastern University, Boston, SA

Sergey Volkov,
Bogolyubov Institute for Theoretical Physics, National Academy of Sciences, Kiev, Ukraine

Vladimir Brusić,
Li Dak Sum Chair Professor of Computer Science, University of Nottingham, Ningbo, China

Vladimir Uversky,
Department of Molecular Medicine, University of South Florida, Tampa, USA

Yuriy Orlov,
I.M. Sechenov First Moscow State Medical University, Moscow, Russia

Zoran Ognjanović,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia

International Program Committee

Alexandre de Brevern,
INSERM, Université Paris Cité, Université de la Réunion, Paris, France

Branislava Gemović,
VINCA Institute of Nuclear Sciences, University of Belgrade, Serbia

Branka Zukić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Branko Dragovich,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia

Dragan Matić,
Faculty of Sciences, Department of Mathematics and Informatics, University of Banja Luka, Bosnia and Herzegovina

George Patrinos,
Department of Pharmacy, University of Patras, Greece

Gordana Pavlović-Lazetić,
Faculty of Mathematics, University of Belgrade, Serbia

Hong-Yu OU,
Shanghai Jiao Tong University, The Microbial Bioinformatics Group, State Key Laboratory of Microbial Metabolism, Shanghai, China

Ivana Morić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Jelena Bojović,
Center for the Fourth Industrial Revolution, Belgrade, Serbia

Marko Đordević,
Faculty of Biology, University of Belgrade, Serbia

Mirjana Maljković,
Faculty of Mathematics,
University of Belgrade, Serbia

Nataša Kovacevic-Grujičić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Nataša Pržulj,
Catalan Institution for Research and Advanced Studies (ICREA), Spain;
Barcelona Supercomputing Center, Spain;
University College London, UK

Nenad Mitić,
Faculty of Mathematics,
University of Belgrade, Serbia

Nevena Veljković,
VINCA Institute of Nuclear Sciences,
University of Belgrade, Serbia

Predrag Radivojac,
Khoury College of Computer Sciences,
Northeastern University, Boston, USA

Saša Malkov,
Faculty of Mathematics,
University of Belgrade, Serbia

Sergei Kozyrev,
Department of Mathematical Physics,
Steklov Mathematical Institute RAS,
Moscow, Russia

Valentina Đorđević,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Vladimir Babenko,
Institute of Cytology and Genetics,
Novosibirsk, Russia

Local Organizing Committee

Anđela Rodić,
Faculty of Biology, University of Belgrade

Branislava Gemović,
VINCA Institute of Nuclear Sciences,
University of Belgrade

Branko Dragovich,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade

Gordana Pavlović-Lazetić,
Faculty of Mathematics,
University of Belgrade

Ivana Morić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

Jovana Kovačević,
Faculty of Mathematics,
University of Belgrade

Marko Đorđević,
Faculty of Biology, University of Belgrade

Marko Živanović,
Bioengineering Research and Development Center

Nenad Filipović,
Faculty of Engineering, University of Kragujevac

Nenad Mitić,
Faculty of Mathematics,
University of Belgrade

Radoslav Davidović,
VINCA Institute of Nuclear Sciences,
University of Belgrade

Saša Malkov,
Faculty of Mathematics,
University of Belgrade

Valentina Đorđević,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

Željko D. Popović,
Faculty of Sciences, University of Novi Sad

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
Organizing Committee

ORGANIZER

Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

MAIN CO-ORGANIZERS

Faculty of Biology, University of Belgrade

Faculty of Mathematics, University of Belgrade

Mathematical Institute of SASA, Belgrade

Vinča Institute of Nuclear Sciences, University of Belgrade

Serbian Society for Bioinformatics and Computational Biology

CO-ORGANIZERS

Faculty of Sciences, University of Novi Sad

BioIRC - Bioengineering Research and Development Center

Faculty of Engineering, University of Kragujevac

Centre for the Fourth Industrial Revolution in Serbia

Serbian Society for Molecular Biology

Biophysical Society of Serbia

TABLE OF CONTENT

KEYNOTE LECTURES

INVITED LECTURES

ORAL PRESENTATION

POSTER PRESENTATION

Poster presentation

Determinants of CRISPR array non-canonical adaptation mechanism

Marko Tumbas[1]* and Marko Đorđević[1]

[1] Quantitative 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