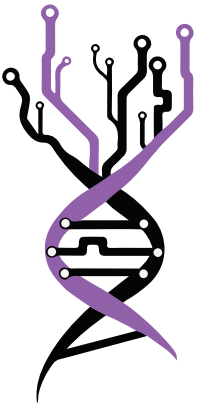
#BelBi2023 • Belgrade, Serbia

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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ORAL PRESENTATION

POSTER PRESENTATION

Shotgun metagenomics reveals gut microbiota features associated with the efficacy of myeloid derived suppressor cells in the prevention of neuroinflammation

Marina Bekić[2], Nataša Ilić[2], Jelena Đokić[1], Dušan Radojević*[1], Dragana Vučević[3], Saša Vasilev[2], and Sergej Tomić[2]

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Although genetic predisposition to Multiple Sclerosis (MS) may play an essential role in disease development, myeloid cell overactivation and gut microbiota dysbiosis are key contributors to MS pathogenesis. Myeloid-Derived Suppressor Cells (MDSC)s are immature myeloid cells with strong immunosuppressive functions which can be exploited in the treatment of autoimmune diseases. Considering the limited data on MDSCs application in MS therapy and their poorly studied effects on the gut microbiota, we have investigated the therapeutic potential of mice MDSC differentiated according to the standard protocol (MDSC) and modified with the addition of prostaglandin (PG) E2 (MDSC-PGE2) to ameliorate experimental autoimmune encephalomyelitis (EAE) induced with MOG35-55/CFA/PtX in C57BL/6 mice. Additionally, we analyzed the changes in gut microbiota features in control and MDSC-treated animals by using a shotgun metagenomics approach. In mice, PGE2-activated MDSC significantly inhibited the onset and clinical course of EAE. This effect correlated with increased IL-10, TGF-β, IL-4 production, and Arginase-1 level in MDSC-PGE2, as well as with reduced leukocyte infiltrates in the spinal cord. MDSC-PGE2 protective effect is also reflected in the maintenance of gut microbiota composition based on Kraken2/Bracken2 and LEfSe analysis. We observed an increase of MS-associated species *Romboutsia ilealis* in the control EAE group, while in both MDSC treatments the increase in relative abundances of *Muribaculum gordoncarteri* and *Duncaniella dubiosis*, associated with immunoregulatory properties, was observed. Microbial metabolic pathways profiling using Humann3 pipeline also reveals the increase in pathways involved in the production of potentially immunoregulatory metabolites in the MDSC-PGE2 group. In conclusion, we pointed to the significant association between the efficacy of MDSC-PGE2 treatment and gut microbiota features which can be further exploited in order to improve MDSC-based EAE therapy.

Keywords: Myeloid derived suppressor cells, gut microbiota, functional pathways, multiple sclerosis, immunoregulatory mechanisms

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