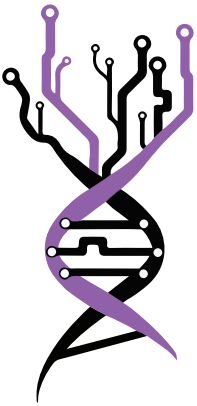
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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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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POSTER PRESENTATION

Transcriptomic profiling of white blood cells reveals new insights into the molecular mechanisms of thalidomide in children with inflammatory bowel disease

Marianna Lucafò[1]*, Letizia Pugnetti[2], Debora Curci[2], Carlotta Bidoli[1], Marco Gerdol[1], Fulvio Celsi[2], Sara Renzo[3], Monica Paci[3], Sara Lega[2], Paolo Lionetti[3], Alberto Pallavicini[1], Giuliana Decorti[2,4], Gabriele Stocco[2,4], Matteo Bramuzzo[2]

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Thalidomide has emerged as an effective immunomodulator in the treatment of pediatric patients with inflammatory bowel disease (IBD) refractory to standard therapies. Cereblon, a component of E3 protein ligase complex that mediates ubiquitination and proteasomal degradation of target proteins, has been identified as the primary target of thalidomide. Cereblon plays a crucial role in thalidomide teratogenicity, however it is unclear whether it is also involved in the therapeutic effects in IBD patients. This study aimed at identifying the mechanisms underpinning thalidomide action in pediatric IBD. Ten IBD pediatric patients clinically responsive to thalidomide were prospectively enrolled. RNA-sequencing and functional enrichment analysis was carried out on peripheral blood mononuclear cells obtained before and after treatment with thalidomide. RNA-sequencing analysis revealed 378 differentially expressed genes after treatment with thalidomide. The most deregulated pathways were cytosolic calcium ion concentration, cAMP-mediated signaling, eicosanoid signaling and inhibition of matrix metalloproteinases. Neuronal signaling mechanisms such as CREB signaling in neurons and axonal guidance signaling also emerged. Connectivity Map analysis revealed that thalidomide gene expression changes were similar to those induced by MLN4924, an inhibitor of NEDD8 activating enzyme, suggesting that thalidomide exerts its immunomodulatory effects by acting on the ubiquitin-proteasome pathway.
In vitro experiments on cell lines confirmed the effect of thalidomide on altered candidate pathways observed in patients. These results represent a unique resource for enhanced understanding of thalidomide mechanism in patients with IBD, providing novel potential targets associated with drug response.

Keywords: RNA-sequencing, thalidomide, pediatric, Crohn's disease, ulcerative colitis

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