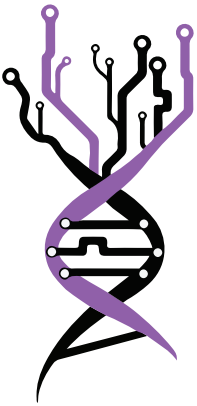
#BelBi2023 • Belgrade, Serbia

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

Pathway analysis of CD8+ T cell transcriptome in glioblastoma patients reveales multiple sclerosis signaling pathway as the top rated upregulated disease pathway in tumor infiltrating cells

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The significance of CD8+ T cell central nervous system migration and activation in the progression of glioblastoma is well documented. However, molecular signaling pathways regulation related to migration and activation in CD8+ cells in glioblastoma is scarce. Therefore we have analyzed the molecular pathway regulation in differentially expressed mRNAs of tumor infiltrating vs. peripheral blood CD8+ T cells from glioblastoma patients. Tumor-infiltrating vs. peripheral blood differentially expressed mRNAs were obtained by analyzing the FASTAQ files on the Galaxy platform using the LimmaVoom tool with filtering low count mRNAs (CPM > 2). We used publically avaliable FASTAQ files with CD8+ T cells mRNA sequencing data deposited at NCBI's GEO database (accession number GSE171197). The differentially expressed mRNA were analyzed with Qiagen's Ingenuity pathway analysis (p adj. cutoff 0.05). Protein-protein interaction network was constructed on the NetworkAnalyst platform using the IMeX database with minimal order parameters. The top rated disease canonical pathway was the multiple sclerosis (MS) signaling pathway, with 18 differentially expressed mRNA hits (out of possible 222), p adj. = 0.0009 and Z score = 2.828, implying significant upregulation of this pathway in tumor-infiltrating CD8+ T cells.

The MS signaling pathway describes the molecular cascade which leads to the autoimmune phenotype in lymphocytes, including activation and central nervous tissue infiltration. To further specify the aspects of the canonical MS signaling pathway which might influence tumor infiltrating phenotype we have constructed a minimal order protein-protein interaction network. Results showed a number of lymphocyte migration and activation KEGG terms within the network, such as: TNF signaling pathway (p adj. = 0.0000115), IL-17 signaling pathway (p adj. = 0.00000427), sphingolipid signaling pathway (p adj. = 0.00171), NF-kappa B signaling pathway (p adj. = 0.0000694) and TCR signaling pathway (p adj. = 0.0071).

We conclude that MS signaling pathway is an viable model for further understanding of the transcriptional phenotype of glioblastoma infiltrating CD8+ T killer cells, illustrating that same migration and activation mechanisms which mediate brain autoimmunity are essential for brain antitumor adaptive immunity.

Keywords: glioblastoma, multiple sclerosis, enrichment analysis, network analysis

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