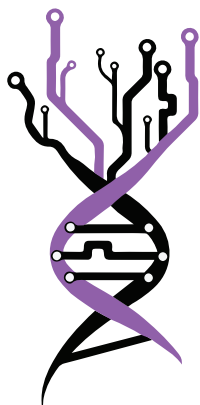


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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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Integration of differential transcriptomic and proteomic data in hydrated and desiccated leaves of *Ramonda serbica* Panc.

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The resurrection plant *Ramonda serbica* Panc. survives long desiccation periods and fully recovers metabolic functions within one day upon watering. We aimed to identify key candidates and pathways involved in desiccation tolerance in *R. serbica* by employing a systems biology approach, combining transcriptomics and proteomics.

A total of 68,694 differentially expressed genes (DEGs; p -value <0.005 and $\text{abs}(\log_2\text{FC})\geq 2$) were obtained in *R. serbica* leaves upon desiccation. Among them, 23,935 and 26,169 genes were upregulated and downregulated in desiccated leaves (DL) and hydrated leaves (HL), respectively. By differential TMT-based proteomic analysis 1192 different protein groups were identified after filtering with at least two unique peptides per protein. In total, 229 protein groups were more abundant in HL and 179 in DL (p -value <0.05 and $\text{abs}(\text{FC})\geq 1.3$). The majority of the DAPs and DEGs involved in photosynthesis, transport, secondary metabolism, and signaling, were less abundant in DL. On the other hand, proteins and transcripts associated with fermentation, N-metabolism, heme, protein synthesis, folding and assembly, C1-metabolism, and late embryogenesis abundant proteins, were more accumulated in DL.

A poor correlation between proteomic and transcriptomic results was detected for mitochondrial electron transport and ATP production, gluconeogenesis, glycolysis, tricarboxylic acid cycle, and enzymatic H_2O_2 scavengers due to different mRNA half-life, protein turnover, dynamic posttranscriptional and posttranslational modifications. Finally, desiccation tolerance in *R. serbica* is a species-specific process orchestrated by several metabolic pathways that are temporally and compartmentally regulated at several levels.

Keywords: differentially abundant proteins, differentially expressed genes, drought, resurrection plants

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