

#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE 2023

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ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title	4 th 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 Đorđević
Technical editor	Dušan Radojević
ISBN	978-86-82679-14-1
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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

Two contrasting late embryogenesis abounded protein family groups of *Ramonda serbica* Panc.

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Ramonda serbica Panc. is an ancient resurrection plant, that survives a long desiccation period and fully recovers metabolic functions upon watering. The main characteristic of desiccation-tolerant plant species is their ability to accumulate protective late embryogenesis abounded protein (LEAPs). To propose their role in *R. serbica* desiccation tolerance we structurally analysed LEAPs in hydrated and desiccated leaves.

According to transcriptomics, 318 LEAPs were identified and classified into seven family groups based on protein BLAST analysis and conserved motifs (Pfam). The largest LEAPs belonged to the LEA2 and LEA4 protein family groups. We employed online tools to analyse physicochemical characteristics (ExPasy, ProtParam, BioPython, GRAVY calculator), disorder propensity, and characterization protein structures (FELLS, JPred, SOPMA, PsiPred, Phyre2, Espritz-DisProt, Espritz-X, Iupred, TMHMM, +Heliquist).

The most abundant, atypical LEA2 group containing 127, mostly hydrophobic proteins, was divided into five subgroups. Members of this group were predicted to fold into globular domains, β -barrel at the C-terminus, followed by transmembrane hydrophobic-helices and disordered N-terminal regions. Results indicated the possible involvement in the protection of the chloroplastic membranes.

The LEA4 group exhibited an exceptionally high tendency to form amphipathic α -helices and simultaneously had a high disorder propensity. This group is made of 96 proteins, classified into 3 subgroups. The high content of polar and charged amino acids (lysine, glutamate, and aspartate) is characteristic of this group. Motifs corresponding to the *R. serbica* LEA4 protein family group folded into A-type α -helices that contained positive, negative, and hydrophobic surfaces. Based on previous knowledge, the possible functions of the LEA2 and LEA4 groups are discussed with significant implications on cell preservation technology and the improvement of crop drought tolerance.

Keywords: LEA proteins, secondary structure prediction, IDPs, resurrection plants

Acknowledgements: This work was funded by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contract No. 451-03-47/2023-01/200042) and by the Science Fund of the Republic of Serbia-RS (PROMIS project LEAPSyn-SCI, grant no. 6039663).



ISBN: 978-86-82679-14-1