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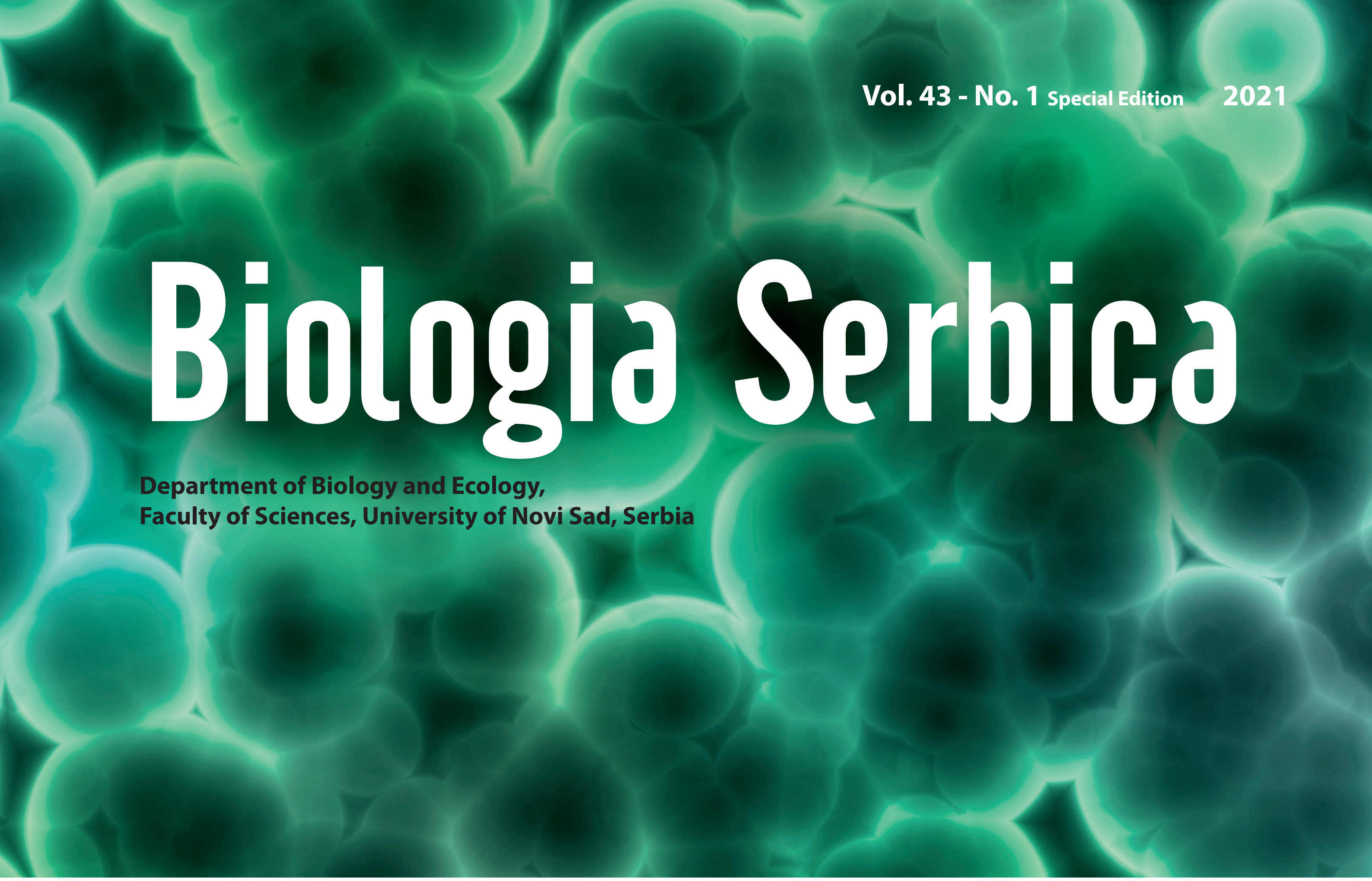

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PREFACE

The Belgrade Bioinformatics conference is a biennial event since 2016. This year, we are hosting the third **Belgrade Bioinformatics 2021 conference – BelBI2021**. The aim of the BelBI2021 is to provide a forum for exchange of knowledge and new ideas between scientists in the field, as well as, to include young scientists in this process and provide educational opportunities for them. Previously, we had the pleasure to welcome participants in Belgrade, but the situation with COVID-19 pandemia during 2020. made us postpone our conference and hold it this year as a virtual event. Nevertheless, the research presented in the abstracts available in this book is outstanding and it was an honor to edit it.

Several research institutions, faculties and scientific societies from Serbia have joined their forces to organize this international conference focused on different aspects of bioinformatics. Four Universities participated in the organization – Universities of Belgrade, Novi Sad, Niš and Kragujevac. The Conference is organized by the Vinča Institute of Nuclear Sciences – National Institute of the Republic of Serbia, University of Belgrade, as the the main organizer, and Faculty of Mathematics, University of Belgrade, Faculty of Biology, University of Belgrade, Institute of Molecular Genetics and Genetic Engineering University of Belgrade, Mathematical Institute of SASA and Serbian Society for Bioinformatics and Computational Biology, as co-organizing institutions, in cooperation with several other institutions and societies from Serbia.

This Book of Abstracts covers a wide range of various topics in bioinformatics, including Big data analytics, Machine learning in biological data analysis, Biological networks, Data mining methods and their applications in biology and medicine, Protein structure and function prediction, and much more. Special session of the BelBI2021 is dedicated to the bioinformatics in the field of COVID-19 analysis, which emerged as an immensely important research topic during the previous year, and these abstracts are also included in this book.

The Book of Abstract is printed as a Special Issue of Biologia Serbica, a journal published by the Faculty of Sciences, Department of Biology, University of Novi Sad, one of the Conference co-organizes, and thus, I would like to thank Prof. Željko D. Popović, Managing Editor, for all his effort to bring this enormous work successfully to the finish.

I would like to thank all members of the International Advisory, the International Program and the Local Organizing Committees for their efforts and help to make this event successful. Also, on behalf of the Local Organizing Committee, I would like to express my deepest gratitude to all attendees, and especially to all presenters for their interesting and much appreciated talks. In addition, we owe many thanks to the Ministry of Education, Science and Technological Development of the Republic of Serbia, as well as to the International Centre for Genetic Engineering and Biotechnology (ICGEB) that supported attendance of many students and early stage researchers. Also, the Local Organizing Committee is very grateful to all Conference's sponsors and donors, especially Factory World Wide d.o.o. and Seven Bridges Genomics, with the hope that they will be with us for many years to come.

This book contains 101 abstracts of presentations at the third Belgrade Bioinformatics 2021 conference – BelBI2021. Authors from 21 countries from almost all continents will present their work at the conference. There will be six keynote lectures, forty one invited lectures, twenty seven contributed talks and thirty two poster presentations.

Belgrade, June 2021.
Branislava Gemović
On behalf of BelBI2021

De Novo Transcriptome Sequencing of *Ramonda serbica*: Identification of Late Embryogenesis Abundant Proteins

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Abstract

An extreme loss of cellular water or desiccation (5-10% of relative water content) leads to protein denaturation, aggregation and degradation, and affects the fluidity of membrane lipids resulting in loss of membrane integrity [1]. The essential constituents of vegetative desiccation tolerance in so-called resurrection plants are late embryogenesis abundant proteins (LEAPs). This heterogeneous group of anhydrobiosis-related intrinsically disordered proteins forms mostly random conformation when fully hydrated, turning into compact α-helices during desiccation [2]. Based on *in vitro* studies, LEAPs can be involved in water binding, ion sequestration, stabilization of both membrane and enzymes during freezing or drying, while by forming intracellular proteinaceous condensates they increase structural integrity and intracellular viscosity of cells during desiccation.

Here, we identify 164 members of LEA gene family in endemic and relict resurrection species *Ramonda serbica* by integrating previously done *de novo* transcriptome and homologues protein motifs. Identified LEAPs were classification into six groups according to Protein family (PFAM) database and the most populated group was LEA4 containing 47% of total identified LEAPs. By using four secondary structure predictors, we showed that this group exhibited a high propensity to form amphipathic α-helices (81% of total sequence length is predicted to form α-helical structure). This implies that charged residues might be exposed to the solvent, while hydrophobic amino acids might interact with lipid bilayers or with other target proteins in the cell. In addition, as predicted by several bioinformatics tools, more than 70% of identified LEAPs were found to be highly disordered. Structural characterization of LEAPs is a key to understand their function and regulation of their intrinsic structural disorder-to-order transition during desiccation. These findings will promote transformative advancements in various fields, such as the development of new strategies in neurodegenerative disorders, cell preservation technology and the improvement of crop drought tolerance.

Keywords:

desiccation tolerance, intrinsically disordered proteins, liquid-liquid phase separation, resurrection plants, secondary structure prediction, water stress

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