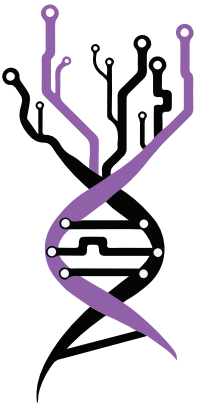
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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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Elongation factor P (-like) protein and polyproline motifs

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Two or more consecutive prolines induce ribosome stalling during translation. In bacteria the elongation factor P (EF-P) efficiently rescues the ribosome stalling and allows the protein biosynthesis to continue. A seven amino acids long loop between beta-strands β3/β4 is crucial for EF-P function. The residue at the tip of the loop is subjected to the post-translational modifications: lysine is lysylated or arginine is rhamnosylated. We have demonstrated that only those enzymes that are needed for specific post-translational modification of the tip are coded in the bacterial genome (EpmA, EpmB and EpmC proteins for EF-P with lysine and EarP- for those with arginine). Phylogenetic analysis has also unveiled an invariant proline in the -2 position of the tip of the loop in EF-Ps that utilize lysine modifications such as *Escherichia coli*. Bacteria with the arginine modification like *Pseudomonas putida* on the contrary have selected against it. Combining these observations with experimental evidence, we conclude that β3/β4 loop composition is important for functionalization of EF-P by chemically distinct modifications.
Some bacterial genomes also code the elongation factor P-like (EfpL) protein that shares the same domain architecture with EF-P and has an extended loop of eight amino acid residues long. The evolution, sequence and the structure of EfpL protein have been extensively characterized. Using the assay based on luminescence emission and ribosomal profiles we have shown that EfpL can also relieve the arrest of the ribosome induced by polyproline motifs.
We have also observed the negative correlation between the occurrence of the motif in the proteome of *Escherichia coli* and its stalling strength measured in luminescence assay. We hypothesize that motifs that cause strong ribosome stalling are disfavored in the protein sequences during evolution due to their impact on the dynamics of translation.

Keywords: polyproline motifs, translation, post-translational modifications, evolution, ribosome profiling, ribosome stalling

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