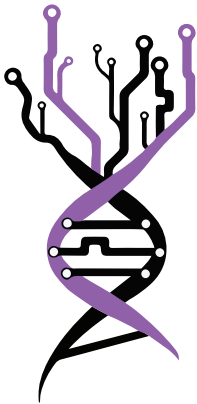


#BelBi2023 • Belgrade, Serbia

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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Single cell 3' transcriptome profiling

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Whole 3' transcriptome profiling at the single cell level opens up new abilities for researchers to answer complex questions. Thousands of individual cells per sample are Barcoded separately to index the transcriptome of each cell individually. It is done by partitioning thousands of cells into nanoliter-scale Gel Beads-in-emulsion (GEMs), where cells are delivered at a limiting dilution, such that the majority (~90-99%) of generated GEMs contain no cell. The 16 bp 10x Barcode and 12 bp UMI are encoded in Read 1, while the poly(dT) primers are used in this protocol for generating Single Cell 3' Gene Expression libraries. After GEM generation, copartitioned cells are lysed and reverse transcription (RT) was performed after which all cDNA from single cell share a common Barcode. Full-length cDNA was amplified via PCR to generate sufficient mass for library construction. This is followed by enzymatic fragmentation and size selection to optimize the cDNA amplicon size. Library construction was finished via End Repair, A-tailing, Adaptor Ligation, and PCR. P5, P7, i7 and i5 sample index, and TruSeq Read 2 (read 2 primer sequence) were added. TruSeq Read 1 and TruSeq Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing. The library prepared in this way, containing the P5 and P7 primers, is ready for Illumina amplification.

Keywords: single-cell analysis, mRNA, bioinformatics, transcriptome, sequencing

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