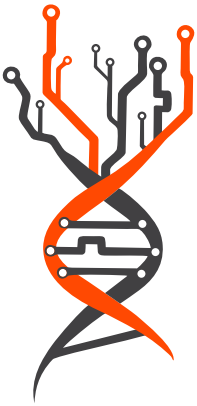
#BelBi2024 • Belgrade, Serbia

# BOOK OF ABSTRACTS



# 5th Belgrade Bioinformatics Conference

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EDITORS
**Dr. Ivana Morić**
**Dr. Valentina Đorđević**

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# FOREWORD

We are pleased to announce the successful conclusion of the 5th Belgrade Bioinformatics Conference - BelBi2024, where numerous high-quality scientific contributions were presented. We sincerely thank all participants and proudly present a book of abstracts that not only reflects the scientific richness and diversity of the conference, but also serves as a lasting memento of this remarkable event.

This international conference was jointly organized by several research institutions, faculties, and scientific societies from Serbia. It covered a wide range of topics from the fields of computational biology, bioinformatics, biomedical informatics, and health informatics. The main goal of BelBi 2024 was to promote contacts between scientists of all levels, provide a platform for the exchange of experiences and present the latest advances in their fields. We hope that BelBi2024 was a valuable platform for researchers from all over the world to meet, build new collaborations and expand professional networks.

We are grateful and proud that we were able to welcome over 250 researchers from 21 countries from three continents. The conference included 24 scientific sessions with more than 68 oral presentations (including eight keynote lectures), 54 poster presentations, three hands-on workshops and three satellite events – the MICOS-EU competition, the TranSYS final conference and Shere the IDEA session. We also organized two industry presentations and two panel discussions - "Building Skills for the Future: Masters 4.0 in Bioinformatics" and "BIO4 Campus: Transforming Science into Business". We also presented the first BelBi art exhibition inspired by scientific discoveries, entitled "IMGGE Magnificent Cell Dance". And finally, we are particularly proud of the "Future Keynote Speakers" program, which enabled students from faculties across Serbia to attend this year's keynote lectures and panel discussions for free.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help that contributed to the success of this event. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, the SAIGE project and the Chamber of Commerce and Industry of Serbia for their support. Finally, the local organizing committee is very grateful to all sponsors of the conference - BGI & MGI, Elta'90MS, PacBio & East Diagnostics, Alfa Genetics, Vivogen, LKB, Altium, Telekom Srbija, Labena, AlphaMed, Galen Fokus, Superlab, Kefo, RNIDS, Danau Lab Beograd, RTC and Biomedica, and we hope that they will stay with us for many years to come.

Thank you once again to all who contributed to the success of BelBi2024. We look forward to seeing you at future conferences.

Warm regards,
Belgrade, July 2024

*Dr. Valentina Đorđević*
*& Dr. Ivana Morić,*
On behalf of BelBi2024
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## Non-coding transcripts of protein-coding genes as novel biomarkers for colorectal cancer diagnosis

Jovana Despotović*, Sandra Dragičević, Tamara Babić, Dunja Pavlović, Jelena Karanović and Aleksandra Nikolić

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Recent research shows that non-coding RNA transcripts of protein-coding genes could be an emerging novel class of diagnostic biomarkers. This study aimed to identify the most promising biomarkers for colorectal cancer (CRC) screening among upregulated non-coding transcripts of protein-coding genes in malignant CRC cells in comparison to non-malignant cells grown in 3D. Malignant CRC cell lines HCT116, DLD-1 and SW620, and a non-malignant human colon epithelial cell line HCEC-1CT, were cultivated in 3D as spheroids in 24-well plates with low attachment surface for 7 days. RNA sequencing was performed on ribosomal-depleted total RNA using Illumina's NovaSeq6000 platform that generated paired-end 150bp reads. Highly upregulated transcripts (>10 FPKM) present in all malignant cell lines and absent in non-malignant cell line were filtered and analyzed by a set of in silico tools to filter the best candidates for further validation studies. The publicly available GSE164541 set consisting of triplicate tissue samples of normal, adenoma and primary CRC tissues collected from five patients with CRC was used for validation. As a result, 5 transcripts with retained introns ANXA3-204, LLGL2-207, KRT19-204, KRT18-206 and KRT8-213 were analyzed by in silico tools. Only ANXA3-204 was classified as non-coding according to both CPC2 and LGC online coding potential prediction tools. Nucleus was predicted as subcellular localization for ANXA3-204 by AnnoLnc2. Additionally, ANXA3-204 expression was upregulated in adenoma ($p=0.04$) and CRC tissue samples, although statistical significance was not reached for CRC, in comparison to normal tissue samples in the validation set. Transcriptomic analysis revealed that non-coding ANXA3-204 transcript was highly upregulated in malignant CRC cell lines and adenomas compared to control samples, making ANXA3-204 a potential candidate for early CRC screening. Further studies are needed to confirm diagnostic potential and regulatory role of ANXA3-204.

**Keywords:** non-coding RNA, colorectal cancer, biomarker, ANXA3, retained intron

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