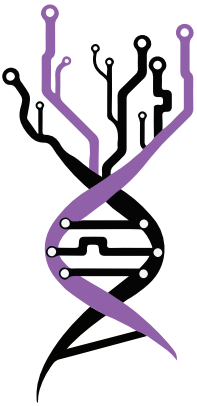
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE **2023**

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Dr. Ivana Morić
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ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title 4th 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/

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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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Possible role of estrogen metabolism and aldo-keto reductase activity in chemoresistance of ovarian cancer

Nika Marolt[1], Andrew Walakira[1], Tadeja Režen[1], Damjana Rozman[1] and Tea Lanišnik Rižner[1]

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High-grade serous ovarian cancer (HGSOC) is the most aggressive and chemoresistant form of epithelial ovarian cancer (OC) and is responsible for ~80% of OC-related deaths. OC is associated with disturbed estrogen action. In postmenopausal patients, estrogens are formed locally from steroid precursors. Enzymes of the AKR1C subfamily are associated with resistance to chemotherapeutic agents and are involved in the biosynthesis and metabolism of steroid hormones, thus may contribute to the growth of hormone-dependent tumors. To date, the interplay of estrogen synthesis and aldo-keto reductase activity in HGSOC chemoresistance remains unclear.

The aim of this study was to investigate the differences in targeted transcriptomics of HGSOC cell lines with different sensitivity to carboplatin: OVSAHO, OVCAR-3, Kuramochi, OVCAR-4, Caov-3, and COV362, and to evaluate the differences in correlation patterns between targeted gene expression profiles in platinum-sensitive and -resistant patients using publicly available data (PAD) (cBioPortal).

We first determined the expression of genes involved in estrogen biosynthesis/metabolism (*STS*, *SULT1E1*, *HSD17B1*, *HSD17B2*, *HSD17B14*, *PAPSS1*, *PAPSS2*), steroid transport (*SLCO1A2*, *SLCO1B3*, *SLCO2B1*, *SLCO4A1*, *SLCO4C1*, *ABCC1*, *ABCC4*, *ABCC11*, *ABCG2*, *SLC51A*, *SLC51B*), estrogen action (*ESR1*, *ESR2*, *GPER*) and oxidative metabolism (*CYP1A1*, *CYP1A2*, *CYP1B1*, *SULT1A1*, *SULT2B1*, *SULT1E1*, *UGTB7*, *COMT*, *NOQ1*, *NOQ2*, *GSTP1*), *NFE2L2* and *AKR1C1-3* by qPCR. Next, by using PAD we conducted a correlation analysis using the Pearson correlation coefficient for gene expression data of targeted genes in OC patients. The patients were classified into two groups based on their response to platinum treatment: sensitive and resistant. The correlation matrix was computed independently for each group.

Expression analysis revealed that the estrogen receptor *ESR2,* the efflux transporter *ABCG2* and aldo-keto reductase *AKR1C1* were highly expressed in the most resistant cell lines COV362 and Caov-3. The mRNA levels of estrogen biosynthesis and oxidative metabolism genes *STS*, *HSD17B14*, *NOQ1*, and *GSTP1* increased with carboplatin resistance in the HGSOC cell lines. These results indicate the potential of *ESR2, STS*, *HSD17B14*, *NOQ1*, *GSTP1*, and *ABCG2* as predictive markers for HGSOC chemoresistance. Furthermore, analysis of PAD revealed different correlation profiles between genes in sensitive and resistant patients. In chemoresistant were found a moderately to strong positive correlations ($p<0.001$) between gene pairs including *AKR1C1–AKR1C3, AKR1C1 – NFE2L2, AKR1C1 – SULT1E1, NOQ1 – HSD17B14, COMT – SULT1A1, ABCG2 – SLC515.* In chemosensitive patients was found a strong positive correlation ($p<0.001$) between gene pair *CYP1B1 – SULT1E1.* The correlation differences between sensitive and resistant OC patients suggest possible gene regulatory networks or molecular interactions contributing to the heterogeneity of response to platinum in OC. Further studies are ongoing to elucidate the mechanism of the interplay between local estrogen metabolism and aldo-keto reductase activity in HGSOC chemoresistance.

We gratefully acknowledge dr. Maja Zagorščak for her valuable assistance in implementing the R code used in this study.

ISBN: 978-86-82679-14-1