



1st BALKAN CONFERENCE on BIOMEDICAL AND CANCER RESEARCH

Balkan.BMCR 2026

**ABSTRACT BOOK
KNJIGA SAŽETAKA**

September 03–05, Foča, Bosnia and Herzegovina

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Molecular and cellular medicine, Biology, Bioinformatics, Immunology, Microbiology, Oncology, Chemistry, Biotechnology, Experimental and clinical medicine

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ЦЕНТАР ЗА МОЛЕКУЛСКУ МЕДИЦИНУ И ИСТРАЖИВАЊЕ МАТИЧНИХ ЋЕЛИЈА



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FOREWORD

We present to you an abstract book of the 1st BALKAN CONFERENCE on BIOMEDICAL AND CANCER RESEARCH (Balkan.BMCR 2026), dedicated to the latest achievements, challenges, and perspectives in the fields of biomedicine and oncology. Held from September 03-05 2026, in Foca (Bosnia and Herzegovina), this meeting brought together leading scientists, clinicians, researchers, and young professionals from across the globe with a shared mission- to advance the fight against malignant diseases through the synergy of fundamental science and clinical practice.

The international character of this meeting, featuring participants from over 10 countries, underscores once again that cancer knows no borders. Global health challenges can only be overcome through collective efforts, open dialogue, and cross-border scientific collaboration. The exchange of ideas and the establishment of new research networks during this event represent an invaluable asset for the further advancement of medical science.

We believe that the conclusions we reach will make a significant contribution to our academic community.

The Organizing and Scientific Committees extend their deepest gratitude to all the authors for their exceptional scientific contributions, and to the institutions and sponsors whose support made this significant meeting possible.

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ПРЕДГОВОР

Представљамо вам збирку сажетака са научне конференције: 1st BALKAN CONFERENCE on BIOMEDICAL AND CANCER RESEARCH (Balkan.BMCR 2026), посвећене најновијим достигнућима, изазовима и перспективама у областима биомедицине и онкологије. Одржан од 3. до 5. септембра 2026. године у Фочи (Босна и Херцеговина), овај састанак је окупио водеће научнике, клиничаре, истраживаче и младе стручњаке из целог света са заједничком мисијом - да унапреде борбу против малигних болести кроз синергију фундаменталних наука и клиничке праксе.

Међународни карактер овог састанка, на којем учествују учесници из преко 10 земаља, још једном наглашава да „тумор не познаје границе“. Глобални здравствени изазови могу се превазићи само колективним напорима, отвореним дијалогом и међународном научном сарадњом. Размена идеја и успостављање нових истраживачких конекција током овог догађаја представљају непроцењиву предност за даљи напредак био-медицинских наука.

Верујемо да ће закључци до којих дођемо значајно допринети нашој академској заједници.

Организациони и Научни одбор изражавају најдубљу захвалност свим ауторима на њиховом изузетном научном доприносу, као и институцијама и спонзорима чија је подршка омогућила овај значајан скуп.

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P-048 Approaches to Identifying Clinically Significant SNPs in Cancer ResearchJasmina Obradovic*Institute for Information Technologies Kragujevac, University of Kragujevac, Kragujevac, Republic of Serbia*

Single nucleotide polymorphisms (SNPs) are single-base alterations (purine or pyrimidine) at specific DNA nucleotide. Unlike mutations, SNPs are generally defined as common germline variants present in at least 1% of the population. They are important targets in numerous clinical applications, including the assessment of disease susceptibility, the diagnostic and prognostic biomarkers, and the prediction of therapeutic response. Clinically significant SNPs located within coding regions may alter protein structure or function, whereas those in promoter regions can influence gene expression. The identification of clinically relevant SNPs in cancer involves a range of bioinformatic approaches, including database mining, literature review, and, where appropriate, experimental validation. Depending on the research objective, several public databases provide information on SNP location and functional annotation. For example, dbSNP, maintained by the National Center for Biotechnology Information (NCBI), is a widely used repository of genetic variation. ClinVar is an archive of genomic variants and their relationships to disease, including evidence regarding drug response; however, its data are intended for research rather than diagnostic use. The GWAS Catalog contains thousands of publications and tens of thousands of SNP–trait associations. OMIM (Online Mendelian Inheritance in Man) catalogs variants associated with Mendelian disorders across more than 16,000 genes and is a valuable resource for genotype–phenotype correlations. The 1000 Genomes Project provides comprehensive data on SNPs and structural variants across diverse populations, generated with high-throughput sequencing technologies. Bioinformatic tools such as SIFT, PolyPhen-2, GTE_x, and FASTSNP are commonly used to predict the functional impact of novel SNPs. Confirmation of clinical significance typically requires experimental validation, including PCR-based genotyping methods (e.g., TaqMan assays or high-resolution melting analysis), next-generation sequencing, and functional assays to assess effects on protein activity. All in all, these resources and approaches form a robust framework for identifying clinically significant SNPs in cancer research.



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