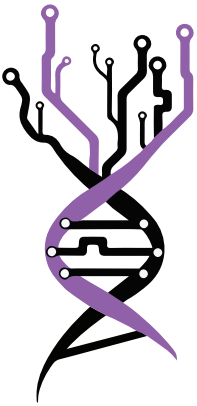
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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EDITORS
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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POSTER PRESENTATION

Mining for the data about glycosylation in the bovines-the analysis of the recently published studies

Anđelo Beletić[1]*, Ivana Duvnjak Orešković[1], Tea Pribić[1], and Gordan Lauc[1,2]

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Deciphering the glycosylation patterns and mechanisms in bovines (*Bos taurus*) holds the potential for improvement regarding reproduction, herd health management, and the quality and safety of milk and meat products. The PubMed database was searched for "glycosylation" and "B. taurus" using the following filters: full text available, the publication date of five years, and the preprints excluded. The search retrieved 244 results, and after the content analysis by the authors, 88 remained relevant. All publications were Research Articles except one Review. The assessment of the glycan profile composition was among the aims in 34, the functional aspects in 33, and the protein glycoforms in 12 studies. Ten studies brought data about the total glycome profile of the milk, tissue, or meat sample, while the other contained glycosylation-related features of the individual protein(s). Most often, the studies used milk (25), individual proteins (23), or tissue (20 studies) as the samples. Usually, the milk was material to analyze the glycosylation of casein, immunoglobulin G, or the total glycans. The studies involving the individual proteins most frequently analyzed fetuin, and the glycosylation of submaxillary gland mucin was the target in the studies using tissue samples. These pioneer data mining results allow for the conclusion on the availability of reliable data about glycosylation in the bovines, eligible as the starting point for further scientific efforts on their continuous appending, systematization, and multidisciplinary analyses.

Keywords: data mining, glycosylation, bovines

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