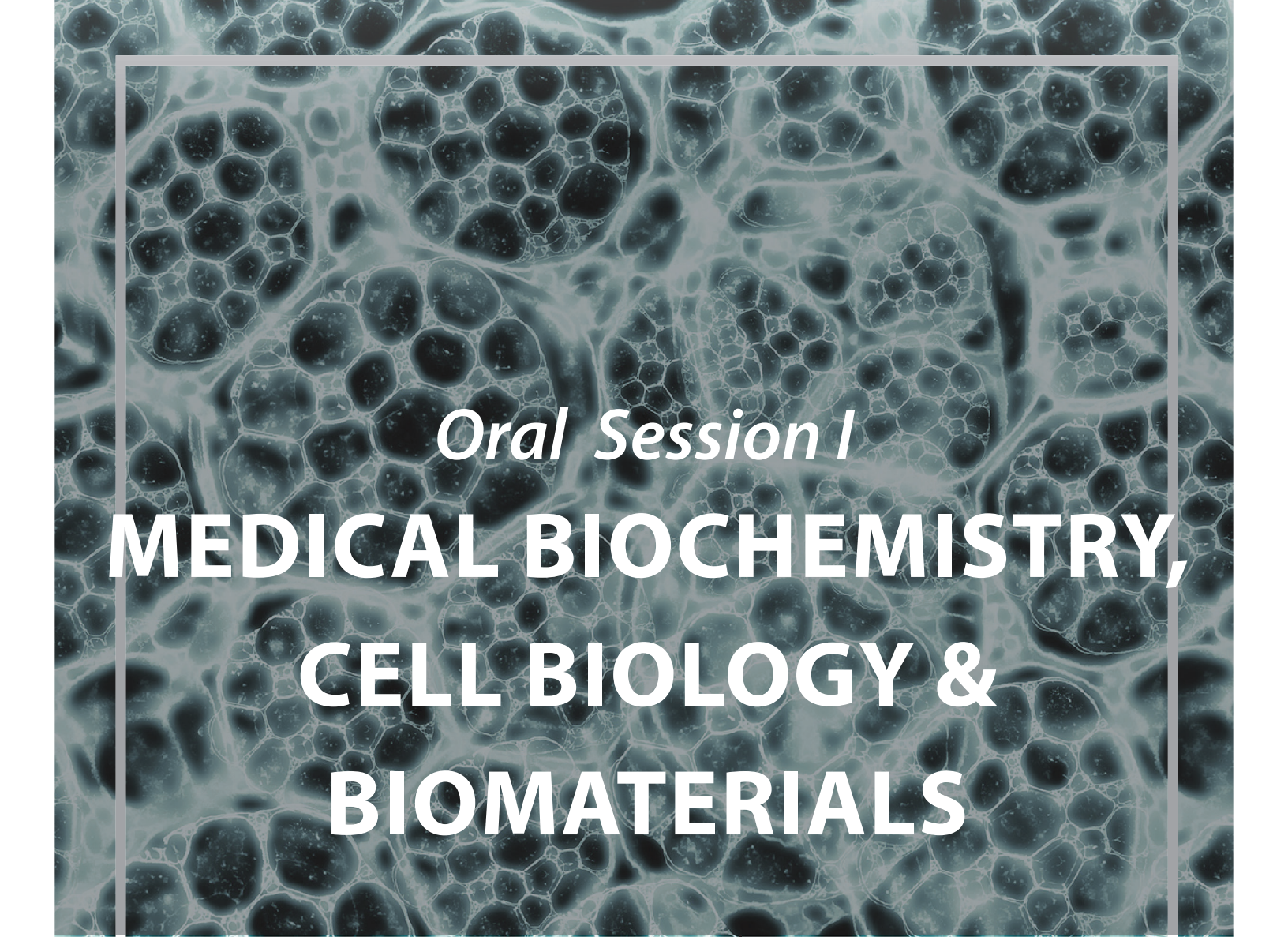


The background image is a composite of three photographs. The top portion shows a tall, ornate Gothic church tower with a green patinated roof, set against a blue sky with light clouds. The middle portion shows a large, multi-story brick building with many windows, partially obscured by lush green trees. The bottom portion shows a formal garden with intricate topiary hedges and a large, leafy tree. The text 'Book of Abstracts 2024' is overlaid on the top right of the image in a large, dark blue font.

Book of Abstracts 2024

31st International Student Congress of (bio)Medical Sciences

A microscopic image of cells, likely adipocytes, showing large, clear, circular lipid droplets surrounded by thin cell membranes. The image is in grayscale with a blue tint.

Oral Session I

MEDICAL BIOCHEMISTRY, CELL BIOLOGY & BIOMATERIALS

Presenters:

- Sem Geertsema
- Attila Tamás György
- Jiaqi Lin
- Joaquín Torres-Núñez
- Zhisheng Wu
- Jinling Zhong

Investigation of protein-protein interactions in the pathogenesis of colorectal and prostate cancer using artificial intelligence

Attila Tamás György

General Medicine

Romania

Introduction

Although several previous studies have highlighted the potential role of arylsulfatase B in the pathogenesis of malignant colorectal and prostate tumors, the exact pathomechanism of this remains unknown. In silico examinations of the protein-protein interactions can be very effective with the application of artificial intelligence in this field. The objective of our research is to investigate the potential involvement of arylsulfatase B in the development of colorectal and prostate cancer, using interaction predictions by artificial intelligence.

Method & Materials

The interaction network of arylsulfatase B was examined using the STRING database. The recommended confidence value of 0.400 was used to determine the strength of the interactions. Two bioinformatics tools based on artificial intelligence were used to analyze the interactions of the proteins in the most optimal pathway, using different methods. The proteins' amino acid sequence was inputted into the PEPPI system, and the HDock Server tool utilized their tertiary structure.

Results

The strongest interaction pathway between ARSB and proteins involved in tumor development was represented by GUSB (0.77) and HSP90AB1 (0.62) proteins. For colorectal cancer, the PEPPI system predicted the most likely interaction of HSP90AB1 with AKT1 ($\log(\text{LR}) = 1.78$), TP53 ($\log(\text{LR}) = 0.96$) and EGFR ($\log(\text{LR}) = 0.87$) proteins. Meanwhile, the HDock Server showed the highest confidence score for connection of HSP90AB1 with RAF1 (0.92), BRAF (0.91), and EGFR (0.90) proteins. For prostate cancer, the PEPPI system predicted the most likely interaction of HSP90AB1 protein with ERBB2 ($\log(\text{LR}) = 0.99$), TP53 ($\log(\text{LR}) = 0.96$) and EGFR ($\log(\text{LR}) = 0.87$) proteins. In contrast, the HDock Server showed the highest confidence score for connection of HSP90AB1 with BRAF (0.91), EGFR (0.90), and TP53 (0.87) proteins.

Conclusion

For both tumor types, the strongest association between ARSB and the proteins involved in tumorigenesis is found to be GUSB and HSP90AB1. Furthermore, TP53 and EGFR are the most likely interaction partners for HSP90AB1 according to the PEPPI system, while BRAF and EGFR according to the HDock Server. Our results illustrate the benefits of using artificial intelligence in the field of molecular biology and highlight the ways in which these analytical methods can help guide experimental research.