

MSCA PF 2026 HOSTING OFFER

Name of the host institution	<u>ELTE Eötvös Loránd University</u>
Faculty	<u>Faculty of Science</u>
Name of the supervisor	<u>Eszter Ari</u> , PhD
Organisational Unit / Research Group	<u>Institute of Biology, Department of Genetics, Evolutionary Bioinformatics Research Group</u>
Research Team	- <u>Eszter Ari</u>, associate professor, group leader - Ágoston Hunya, graduate student - András Asbóth, graduate student - Csenge Gázsó, master student - Norbert Kada, master student Research interests: - evolution - bioinformatics - phylogenetics - microbiology - transcriptional regulation - CHIP-seq, ATAC-Seq
Project experiences (EU / international)	International project experiences: - Eszter Ari was a supervisor of a Visegrad 4 Eastern Partnership (V4Eap) 2014 – 2015 grant project, connected to the fellowship of Zeljko Popovic; Title: DORMANCYbase – developing a database on gene and protein expression during dormancy in animals; 3,000 EUR National project experiences: - Supported Research Groups Programme 2025 - 2028: Roles: Eszter Ari - co-applicant, Ágoston Hunya - researcher; Title: Genomic surveillance for precision therapies against antibiotic-resistant bacteria; PI: Papp Balázs; Number: TKCS-2024/66; amount awarded to ELTE: 30,000,000 HUF - ELTE international online courses 2025: the “Analysis of OMICS Data PR” was selected as a course in CHARM-EU; 500 000 HUF - Hungarian National Research Fund Grant – Postdoctoral Excellence Programme 2020 - 2023: Eszter Ari’s role: Principal investigator; Title: How do ‘superbugs’ emerge? - A systematic study of the mobility of resistance and virulence genes in human microbiota and pathogenic bacteria; Nr. 131839; 25,500,000 HUF
Research Interests	Research topics: - Investigating the mobility of antimicrobial resistance and virulence genes: Horizontal gene transfer between bacterial lineages is widespread and plays a key role in the evolution of antimicrobial resistance and virulence. Despite its clinical importance, however, we have only a limited understanding of (i) the general trends and impacts of gene exchange between virulent pathogens and multidrug-resistant commensal bacteria. We address these issues by analyzing the gene exchange networks of human microbiota, multidrug-resistant

	and pathogenic bacteria alike. We have published our previous works in <i>Cell</i> and <i>Nature Microbiology</i>. - Creating and maintaining the TFLink database, an integrated gateway to access transcription factor - target gene interactions for multiple species: We created and maintain the TFLink database that uniquely provides comprehensive and highly accurate information on transcription factor - target gene interactions, nucleotide sequences and genomic locations of transcription factor binding sites for human and six model organisms. We integrated the results of small- and large-scale approaches from ten different databases. We are working on to make the database organ, tissue, and cell specific using data obtained by various high-throughput methods. We published our results in the <i>Database</i> journal. - Developing python and R packages in the field of OMICS studies, epidemiology and phylogenetics: mulea, treepruner
ORCID (link)	https://orcid.org/0000-0001-7774-1067
Contact e-mail	arieszter@ttk.elte.hu