

Curriculum Vitae of Eszter Ari



Bioinformatic Researcher, University Teacher

arieszter@ttk.elte.hu

Websites

- Lab website: [Evolutionary Bioinformatics Research Group at Eötvös Loránd University \(ELTE\), Budapest, H](#)
- Personal website at [ELTE, Budapest, H](#)
- Personal website at [Biological Research Centre, Szeged, H](#)
- Public pages:       

Positions

Present

Associate professor - Eötvös Loránd University (ELTE), Department of Genetics

H-1117, Pázmány Péter stny. 1/C, Budapest, Hungary

- 2025 - present: *Role:* Teaching various bioinformatics courses to biology master and graduate students. Supervising undergraduate and graduate students. Coordinating the Molecular Genetics, Cell- and Developmental Biology specialisation.
- 2019 - 2025: assistant professor
- 2009 - 2019: assistant lecturer

- 2007 - 2009: scientific research associate

Research fellow – HUN-REN¹ Biological Research Centre (BRC), Institute of Biochemistry, Szeged

H-6726, Temesvári krt. 62, Szeged, Hungary

- 2016 - : Investigating the evolution of antibiotic resistance and virulence using phylogenetic and comparative genomics approaches in Balázs Papp's Lab, from 2020 as a project leader.

Research fellow – Hungarian Centre of Excellence for Molecular Medicine (HCEMM), Metabolic Systems Biology Research Group, Szeged

- 2019 -

Research fellow – HUN-REN Office for Supported Research Groups, Budapest

- 2025 -

Formerly

Postdoctoral researcher – Univ. of Veterinary Medicine (Vet-Med Uni), Institut für Populationsgenetik, Vienna, A

- 2012 - 2014: Analysing the RNA-seq data of thermal adapted fruit fly populations in Christian Schlötterer's Lab.

Diplomas & Degrees

- **Habilitation:** ELTE, Budapest, H, 2023
- **PhD:** Biology Doctoral School, Theoretical and Evolutionary Biology Doctoral Programme, ELTE, Budapest, H, 2012
- **Bachelor and Master:** Majoring in Applied Zoology, Faculty of Veterinary Sciences², Szent István University, Budapest, H, 1999 - 2004

¹Formal names: Research Network of the Hungarian Academy of Science (HAS); Eötvös Loránd Research Network (ELKH)

²Formal and actual name: University of Veterinary Medicine

Awards & Scholarships

- Outstanding scientific publication award from Excellence Fund of Eötvös Loránd University, 2024 and 2022, Budapest, H
- Junior fellowship at Collegium Budapest – Institute for Advanced Study, 2009, Budapest, H
- Scholarship of the Fac. Veterinary Sci., Szent István Univ., 2003 - 2004, Budapest, H
- 2nd Prize of the Conference for Student Scientists at Fac. Veterinary Sci., Szent István Univ., 2003, Budapest, H

Grants

- **Supported Research Groups Programme 2025 - 2027:** *Role:* co-applicant; *Title:* Genomic surveillance for precision therapies against antibiotic-resistant bacteria; *PI:* Balázs Papp; Number: TKCS-2024/66; amount awarded to ELTE: 30,000,000 HUF
- **ELTE international online courses 2025 and 2026:** the “Analysis of OMICS Data PR” was selected as a course in [CHARM-EU](#); 2 × 500 000 HUF
- **Hungarian National Research Fund Grant – Postdoctoral Excellence Programme 2020 - 2023:** *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
- **Promoting Excellence in Education, ELTE 2020:** *Role:* Principal investigator; *Title:* Development of the infrastructure of the computer practical room; 4,000,000 HUF
- **Visegrad 4 Eastern Partnership (V4Eap) 2014 - 2015;** *Role:* Supervisor; Connected to the fellowship of Zeljko Popovic; *Title:* DORMANCYbase – developing a database on gene and protein expression during dormancy in animals; 3,000 EUR

Teaching Activities

Present

- [Bioinformatics](#) (L, P; EN) – for Master students
- [Analysis of Omics data](#) (P; EN) – for Master students. The course has also been included in the [CHARM-EU Course Catalogue](#).
- Bioinformatic seminars (L; EN) – for PhD students
- [Advanced R programming](#) (P; EN) – for Master students
- Phylogenetics (L, P; EN)

Formerly

- Introduction to Bioinformatics (L; HU) – for Bachelor students
- Genetic lab. practices (selected P; EN, HU) – for Bachelor students
- Genomics (selected L; EN, HU) – for Master students
- Molecular evolution (selected L; HU) – for Master students
- Evolutionary biology (selected L; HU) – for Master students
- Discrete mathematical methods in biology (L, P; HU) – for Master and PhD students

Course Book

- Genetics Exercises: Chapter 7 – Bioinformatics: Genetic Disease Recognition and Detection (HU)

Supervising & Mentoring

- [The personal site at the website of Hungarian Doctoral Council](#)
- **At present:** Co-supervising 2 PhD students, supervising 2 Master students, and 1 Scientific Student Association student
- **Graduated students:** 4 co-supervised PhD, 6 Master, 14 Bachelor, and 9 Scientific Student Association students
- **Mentoring:** 1 with Support for summer internships for Hungarian students studying abroad grant, [Szent-Györgyi Mentoring Program](#) mentoring

Main Workshops

As Lecturer

- *ELTE Carpathian Basin Hungarian Summer University*, 2022: Genetic analysis of the virus variants determining the COVID epidemic in Hungary
- [Practical Course on Next Generation Sequencing for Population Genetics and Experimental Evolution](#), 2014 Vet-Med Uni Vienna, A: Practicals about RNA-seq data analysis

As Participant

- *EMBO Training: Laboratory Leadership Course*, 2024, Budapest, H
- *An R Reproducibility Toolkit for the practical researcher*, 2022, online

- *8th International Course in Microbial Ecology – Microbiome Metagenome Analysis*, 2017, CNR-ISE, Verbania, I
- *EMBO course: Bioinformatics and Comparative Genome Analyses*, 2011, Inst. Pasteur Paris, F
- *Computational Phyloinformatics Course*, 2008, Duke Univ., Durham, NC, USA
- *Workshop on Molecular Evolution*, 2006, Marine Biological Lab., Woods Hole, MA, USA

Memberships

- [Hungarian Society for Bioinformatics](#): 2016 – **member of the directory board**; 2006 – member
- Hungarian Academy of Sciences, Interdepartmental Scientific Committee on Bioinformatics: 2021 – **committee member**
- Hungarian node of the [Elixir Europe](#): 2023 – **lead researcher**
- [Institute of Scientific Computing, Society](#) (SciComp): 2024 – member
- Public Body of the Hungarian Academy of Sciences: 2013 – member (ID: 31344)

Languages

- Hungarian – mother tongue
- English – C1 level
- Italian – A1 level

Areas of Interest

- Bioinformatics
- Evolutionary Biology
- Antibiotic Resistance
- Comparative genomics
- Molecular phylogenetics
- Metagenomics
- Transcriptomics
- Transcriptional regulation
- Data analysis

Professional Skills

- Developing and using different bioinformatic methods, software and pipelines.
- *R* programming language – professional level
- *Linux Shell* scripting – intermediate level

Editing, Reviewing, & Organizing Conferences

- Topic editor in [Frontiers in Systems Biology](#)
- Reviewer in journals: *Brief. Bioinformatics* (3); *Evol. Biol.* (1); *Genome Biol. Evol.* (1); *J. Math. Chem.* (4); *Mol. Ecol.* (1); *Mol. Phylogenetics Evol.* (1); *Sci. Rep.* (1); *Opusc. Zool.* (1); *Plos One* (2)
- Reviewing: PhD Theses (4), Grant proposals: Hungarian Scientific Research Fund Grant (4)
- Conference organization as a member of the scientific organizing committee: [The Joint Conference of the Hungarian Physiological Society, the Hungarian Biophysical Society, the Hungarian Society for Microcirculation and Vascular Biology, and the Hungarian Bioinformatics Society](#), Sep. 2–5, 2025, Szeged, H

Popularising Science

- Presenting at the Festival of ELTE: Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*. 2022, Budapest, H
- Creating a website for The genomic epidemiology of SARS-CoV-2 in Hungary
- Presenting at Capital of Science “Tudományok Fővárosa”: The genomic epidemiology of SARS-CoV-2 in Hungary, 2020, Budapest, H
- Presenting at Night of Scientists “Kutatók Éjszakája”, 2018 and 2020

Scientific Websites

- Supervising the creation of the [TFLink](#), a transcription factor - target gene database.
- Supervising the creation of the [mulea](#) and the [muleaData](#) *R* packages for functional enrichment analysis and dataset.
- Supervising the creation of the [treepruner](#) *R* and *Python* packages for pruning too long branches of phylogenetic trees.

Publications



- Nr. of published papers: **28** (D1: **18** + Q1: **5**)
- Nr. of first, last or corresponding author publications: **8**
- Cumulative impact factor of first, last or corresponding author publications: **47.22**
- Cumulative impact factor of all publications (IF): **234.26**
- Independent citations of all publications (IC): **789**
- h-index: **17**

Preprints

- Zsichla L, Adravecz L, Müller D, Lemey P, Lakatos Á, **Ari E**, Kusejko K, Kouyos R, Szlávik J, Lakatos B, Áy É & Müller V (2025) Molecular epidemiology of HIV-1 in Hungary: an evolving contact zone of colliding virus subtypes *Frontiers in Microbiology*, under review.

Published

- Balogh GM, Koncz B, Asztalos L, **Ari E**, Papp B, Szebeni GJ, Gémes N, Pál C & Manczinger M (2025) [C>U mutations generate immunogenic peptides in SARS-CoV-2](#). *Nature Communications*, 16: 10156. **D1, IF: 15.70, IC: 0**
- Daruka L, Czikkely MS, Szili P, Farkas Z, Balogh D, Maharramov E, Vu TH, Sipos L, Vincze BD, Grézal G, Juhász Sz, Dunai A, Daraba A, Számel M, Sári T, Stirling T, Vásárhelyi BM, **Ari E**, Christodoulou C, Manczinger M, Enyedi MZs, Jaksa G, van Houte S, Pursey E, Papp CG, Szilovics Z, Pintér L, Haracska L, Gácser A, Kintses B, Papp B & Pál Cs (2025) [ESKAPE pathogens rapidly develop resistance against antibiotics in development](#). *Nature Microbiology*, 10(2): 313-331. **D1, IF: 20.50, IC: 42**
- Koncz M, Stirling T, Mehdi HH, Méhi O, Eszenyi B, Asbóth A, Apjok G, Tóth Á, Orosz L, Vásárhelyi BM, **Ari E**, Daruka L, Polgár TF, Schneider Gy, Zalokh SA, Számel M, Fekete G, Bohár B, Nagy Varga K, Visnyovszki Á, Székely E, Licker MS, Izmendi O, Costache C, Gajic I, Lukovic B, Molnár Sz, Szőcs-Gazdi UO, Bozai Cs, Indreas M, Kristóf K, Van der Henst C, Breine A; Pál C, Papp B & Kintses B (2024) [Genomic surveillance as a scalable framework for precision phage therapy against antibiotic-resistant pathogens](#). *Cell*, 187(21): 5901 - 5918.e28. **D1, IF: 45.50, IC: 25**
- Turek C, Ölbei M, Stirling T, Fekete G, Tasnádi E, Gul L, Bohár B, Papp B, Jurkowski W & **Ari E*** (2024) [mulea - an R package for enrichment analysis using various ontologies and empirical false discovery rate](#). *BMC Bioinformatics*, 25(1): 334. **Q1, IF: 2.90**,

IC: 1 “Impactful paper” according to [OOIR Observatory of International Research](#). (*corresponding author)

- Gerber D, Szeifert B, Székely O, Egyed B, Gyuris B, Giblin JI, Horváth A, Köhler K, Kulcsár G, Kustár Á, Major I, Molnár M, Palcsu L, Szeverényi V, Fábián S, Mende BG, Bondár M, **Ari E***, Kiss V* & Szécsényi-Nagy A* (2023) [Interdisciplinary analyses of Bronze Age communities from Western Hungary reveal complex population histories](#). *Molecular Biology and Evolution*, 40(9): msad182. **D1, IF: 11.00, IC: 11 (*shared corresponding authorship)**
- Bacsur P, Rutka M, Resál T, Szántó K, Jójárt B, Bálint A, **Ari E**, Walliyulah A, Kintses B, Fehér T, Asbóth A, Pigniczki D, Bor R, Fábián A, Maléth J, Szepes Z, Farkas K & Molnár T (2023) [Effects of bowel cleansing on the composition of the gut microbiome in inflammatory bowel disease patients and healthy controls](#). *Therapeutic Advances in Gastroenterology*, 16: 17562848231174298. **Q1, IF: 3.90, IC: 17**
- Sturm Á, Saskői É, Hotzi B, Tarnóci A, Barna J, Bodnár F, Sharma H, Kovács T, **Ari E**, Weinhardt N, Kerepesi C, Perczel A, Ivics Z & Vellai T (2023) [Downregulation of transposable elements extends lifespan in *Caenorhabditis elegans*](#). *Nature Communications*, 14(1): 5278. **D1, IF: 14.70, IC: 24**
- **Ari E**, Vásárhelyi BM, Kemenesi G, Tóth GE, Zana B, Somogyi B, Lanszki Z, Röst G, Jakab F, Papp B & Kintses B (2022) [A single early introduction governed viral diversity in the second wave of SARS-CoV-2 epidemic in Hungary](#). *Virus Evolution*, 8(2): veac069. **D1, IF: 5.30, IC: 4**
- Csabai L, Fazekas D, Kadlecik T, Szalay-Bekő M, Bohár B, Madgwick M, Módos D, Ölbei M, Gul L, Sudhakar P, Kubisch J, Oyeyemi OJ, Liska O, **Ari E**, Hotzi B, Billes VA, Molnár E, Földvári-Nagy L, Csályi K, Demeter A, Pápai N, Koltai M, Varga M, Lenti K, Farkas IJ, Türei D, Csermely P, Vellai T & Korcsmáros T (2022) [SignaLink3: A multi-layered resource to uncover tissue-specific signaling networks](#). *Nucleic Acids Research*, 50(D1): 701-709. **D1, IF: 14.90, IC: 35**
- Liska O, Bohár B, Hidas H, Korcsmáros T, Papp B, Fazekas D & **Ari E*** (2022) [TFLink: An integrated gateway to access transcription factor - target gene interactions for multiple species](#). *Database*, 2022, baac083. **D1, IF: 5.80, IC: 118 “High impact paper” according to [scientometrics.org](#)**. (*corresponding author)
- Bálint A, Farkas K, Kintses B, Méhi O, Vásárhelyi BM, **Ari E**, Pál C, Madácsy T, Maléth J, Szántó KJ, Nagy I, Rutka M, Bacsur P, Szűcs D, Szepes Z, Nagy F, Fábián A, Bor R, Milassin Á & Molnár T (2020) [Functional anatomical changes in ulcerative colitis patients determine their gut microbiota composition and consequently the possible treatment outcome](#). *Pharmaceuticals*, 13(11): 346-362. **D1, IF: 5.68, IC: 25**
- Kintses B, Jangir PK, Fekete G, Számel M, Méhi O, Spohn R, Daruka L, Martins A, Hosseinnia A, Gagarinova A, Kim S, Phanse S, Csörgő B, Györkei Á, **Ari E**, Lázár V, Faragó A, Nagy I, Babu M, Pál C & Papp B (2019) [Chemical-genetic profiling reveals](#)

limited cross-resistance between antimicrobial peptides with different modes of action. *Nature Communications*, 10(1): 5731. **D1, IF: 12.12, IC: 41**

- Kintses B*, Méhi O*, **Ari E***, Számel M, Györkei Á, Jangir PK, Nagy I, Pál F, Fekete G, Tengölics R, Nyerges Á, Likó I, Bálint A, Molnár T, Bálint B, Vásárhelyi BM, Bustamante M, Papp B & Pál C (2019) *Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota*. *Nature Microbiology*, 4(3): 447-458. **D1, IF: 15.54, IC: 92** Craig MacLean recommended it in **F1000Prime** as being of special significance in its field. It was selected as a part of the **Nature Gut Microbiota core collection**. (*shared first authorship)
- Sudhakar P, Claire-Jacomin A, Hautefort I, Samavedam S, Fatemian K, **Ari E**, Gul L, Demeter A, Jones E, Korcsmaros T & Nezis JP (2019) *Targeted interplay between bacterial pathogens and host autophagy*. *Autophagy*, 15(9): 1620-1633. **D1, IF: 11.06, IC: 45**
- Sun D, Ren X, **Ari E**, Korcsmaros T, Csermely P & Wu L-Y (2019) *Discovering cooperative biomarkers for heterogeneous complex disease diagnoses*. *Briefings in Bioinformatics*, 20(1): 89-101. **D1, IF: 9.10, IC: 18**
- Nyerges Á, Csörgő B, Draskovits G, Kintses B, Szili P, Ferenc Gy, Révész T, **Ari E**, Nagy I, Bálint B, Vásárhelyi BM, Bihari P, Számel M, Balogh D, Papp H, Kalapis D, Papp B & Pál C (2018) *Directed evolution of multiple genomic loci allows the prediction of antibiotic resistance*. *Proceedings of the National Academy of Sciences of the United States of America*, 115(25): E5726-E5735. **D1, IF: 9.58, IC: 89**
- Fodor E, Sigmond T, **Ari E**, Lengyel K, Takács-Vellai K, Varga M & Vellai T (2017) *Methods to study autophagy in zebrafish*. *Methods in Enzymology*, 588: 467-96. **Q1, IF: 1.48, IC: 22**
- Métris A, Sudhakar P, Fazekas D, Demeter A, **Ari E**, Ölbei M, Branchu P, Kingsley RA, Baranyi J & Korcsmáros T (2017) *SalmoNet*, an integrated network of ten *Salmonella enterica* strains reveals common and distinct pathways to host adaptation. *Npj Systems Biology and Applications*, 3(1): s41540-17-34-NaN-17. **Q1, IF: 3.81, IC: 31**
- Ricotta C, **Ari E**, Bonanomi G, Giannino F, Heathfield D, Mazzoleni S & Podani J (2017) *Spatial analysis of phylogenetic community structure: New version of a classical method*. *Community Ecology*, 18(1): 37-46. **Q2, IF: 0.98, IC: 2**
- Ács É, **Ari E**, Duleba M, Dressler M, Genkal SI, Jakó É, Rimet F, Ector L & Kiss KT (2016) *Pantocsekiella*, a new centric diatom genus based on morphological and genetic studies. *Fottea*, 16(1): 56-78. **Q2, IF: 0.60, IC: 60**
- **Ari E*** & Jakó É (2016) *Classification of tRNA isoacceptor sequences by using graph-based molecular descriptors*. *Journal of Chemometrics*, 30(1): 182-187. **Q2, IF: 2.03, IC: 0** (*corresponding author)

- Módos D, Brooks J, Fazekas D, **Ari E**, Vellai T, Csermely P, Korcsmáros T & Lenti K (2016) Identification of critical paralog groups with indispensable roles in the regulation of signaling flow. *Scientific Reports*, 6: 38588. **D1, IF: 4.62, IC: 7**
- Földvári-Nagy L, **Ari E**, Csermely P, Korcsmáros T & Vellai T (2014) Starvation-response may not involve Atg1-dependent autophagy induction in non-unikont parasites. *Scientific Reports*, 4: 5829. **D1, IF: 5.85, IC: 16**
- **Ari E***, Ittzés P, Podani J, Le Thi QC & Jakó É (2012) Comparison of Boolean analysis and standard phylogenetic methods using artificially evolved and natural mt-tRNA sequences from great apes. *Molecular Phylogenetics and Evolution*, 63(1): 193-202. **D1, IF: 4.42, IC: 5 (*corresponding author)**
- Boros G, Cech G, **Ari E** & Dózsa-Farkas K (2010) Extension of employing ITS region in the investigation of Hungarian *Fridericia* species (Oligochaeta: Enchytraeidae). *Zoology in the Middle East*, 51(sup2): 23-30. **Q3, IF: 0.30, IC: 2**
- Tihanyi B, Vellai T, Regős Á, **Ari E**, Müller F & Takács-Vellai K (2010) The *C. elegans* Hox gene *ceh-13* regulates cell migration and fusion in a non-colinear way. Implications for the early evolution of Hoxclusters. *BMC Developmental Biology*, 10(1): 78-92. **Q1, IF: 2.78, IC: 27**
- Jakó É, **Ari E**, Ittzés P, Horváth A & Podani J (2009) BOOL-AN: A method for comparative sequence analysis and phylogenetic reconstruction. *Molecular Phylogenetics and Evolution*, 52(3): 887-897. **D1, IF: 3.88, IC: 30**
- **Ari E**, Ittzés P, Podani J & Jakó É (2008) Phylogenetic tree reconstruction with a new discrete mathematical method. *Kitaibelia*, 13: 209-211. **Q2, IF: 0.23, IC: 0 (in Hungarian)**

Oral Presentations in Conferences

- Nr. of international conference talks: **9**
- Nr. of national conference talks: **7**
- As an invited speaker*: **4**
- Ari E*, Kada N (2025) Application of large language models for the standardization of DNA sequencing metadata. *2nd National HUN-REN Cloud Meeting*, 13 Nov, Budapest, H
- Ari E, *et al.* (2024) mulea - an R package for enrichment analysis using multiple ontologies and empirical false discovery rate. *Bioinformatika, a Magyar Tudomány Ünnepén*, 8 Nov, Budapest, H
- Ari E, *et al.* (2024) mulea - an R package for enrichment analysis using multiple ontologies and empirical false discovery rate. *SciComp24 Conference*, 17-19 Oct, Szeged, H

- Ari E, *et al.* (2023) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*. *3rd HCEMM PhD-POSTDOC Symposium*, 8-9 Nov, Keszthely, H
- Ari E, *et al.* (2022) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*. *1st Bioinformatics and Data Science in Genomic Studies (BDG2022)* online conference, 25 Nov, University of Debrecen, H
- Ari E, *et al.* (2022) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*. *Bioinformatics, Celebrating the Hungarian Science*, 11 Nov, HAS, Research Centre for Natural Sciences, Budapest, H
- Ari E*, Kintses B (2020) Methods to investigate the microbiome and understand the results. *Meeting of Hungarian Society for Gastroenterology, Section Colon*, 6-7 Mar, Visegrád, H
- Ari E, *et al.* (2019) Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. *EvolBiol Day*, 17 Apr, Szeged, H
- Ari E*, *et al.* (2018) How well do the antimicrobial peptide resistance genes spread? *Bioinformatics, Celebrating the Hungarian Science*, 16 Nov, HAS, Research Centre for Natural Sciences, Budapest, H
- Ari E: (2017) MulEA – A tool for multi-enrichment analysis. *2nd Interdisciplinary Signaling Workshop*, 17-21 Jul, Visegrád, H
- Ari E*: (2012) Molecular phylogenetic reconstructions with a discrete mathematical method, the Boolean analysis. *International Congress, Hungarian Society for Microbiology*, 24-26 Oct, Keszthely, H
- Ari E & Jakó É (2012) Comparison of Boolean analysis and standard phylogenetic methods using artificially evolved and natural mt-tRNA sequences from great apes. *9th Joint Conference on Mathematics and Computer Science*, 9-12 Feb, Siófok, H
- Ari E, *et al.* (2007) Boolean analysis: A new discrete mathematical method for phylogenetic reconstruction. *From Molecular Informatics to Bioinformatics – International Symposium*, 19-21 Apr, Collegium Budapest, H
- Ari E & Jakó É (2007) Testing a new discrete mathematical method for phylogenetic reconstruction. *Evolution 2007 Conference*, 16-20 Jun, Christchurch, NZ
- Ari E & Jakó É (2007) Testing a new discrete mathematical method for phylogenetic reconstruction. *The Dumont D'Urville Workshop on Applied Evolutionary Bioinformatics*, 24-27 Jun, Kaikoura, NZ
- Ari E, *et al.* (2007) Phylogenetic tree reconstruction with a new discrete mathematical method. *Molecular taxonomic, phylogenetic and phylogeographic researches in Hungary, Meeting in memory of Sámuel Diószegi*, 17 Nov, Debrecen, H
- Ari E (2006) Reconstructing the phylogenetic tree of great apes by using a new discrete mathematical method. *12th Annual European Meeting of PhD students in Evolutionary Biology*, 4-9 Sep, St. Andrews, UK

Other Invited Talks

- Ari E* (2025) Pathoadaptive traits shape the spread of antibiotic resistance in *Escherichia coli*. Imperial College London, Faculty of Medicine, Korcsmáros Group, 20 May, London, UK
- Ari E* (2017) Investigating the antimicrobial peptide resistome in the human gut microbiome: a metagenomic approach. University of Graz, Institute of Zoology, 15 Nov, Graz, A
- Ari E*: (2015) Rapid evolution of phenotypic plasticity during experimental evolution of *Drosophila*. The Genome Analysis Centre, 23 Feb, Norwich, UK

Poster Presentations in Conferences

- Nr. of international conference posters: **10**
- Ari E, *et al.* (2025) Virulence gene content and ecological niche shape the spread of antibiotic resistance in *Escherichia coli*, *Applied Bioinformatics and Public Health Microbiology 2025*, 21-23 May, Hinxton, UK
- Ari E, *et al.* (2023) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*, *EMBO Workshop: Plasmids as vehicles of AMR spread*, 12-18 Sep, (Trieste, I) online
- Ari E, *et al.* (2023) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*, *EMBO Workshop: Predicting evolution*, 11-14 Jul, Heidelberg, D
- Ari E, *et al.* (2022) Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*. *Lake Arrowhead Microbial Genomics Conference*, 11-15 Sep, Lake Arrowhead, CA, USA
- Rutka M, Szántó K, Bacsur P, Resál T, Jójárt B, Bálint A, **Ari E**, Kintses B, Fehér T, Asbóth A, Pigniczki D, Bor R, Fábián A, Farkas K, Maléth J, Szepes Z & Molnár T (2022) **P713 Gut microbiota alterations after bowel preparation amongst inflammatory bowel disease patients**. *Journal of Crohn's and Colitis*, 16 (Supplement_1): i609. **Q1, IF: 9.07**
- Ari E, *et al.* (2019) Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. *Gordon Research Conference on Molecular Mechanisms in Evolution*, 9-14 Jun, Easton, MA, USA
- Ari E, *et al.* (2019) Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. *Gordon Research Seminar on Molecular Mechanisms in Evolution*, 8-9 Jun, Easton, MA, USA
- Ari E & Jakó É (2015) Graph-based generalized Boolean descriptors for classification of biological macromolecules. *Conferentia Chemometrica*, 13-16 Sep, Budapest, H

- Ari E *et al.* (2015) Rapid evolution of phenotypic plasticity during experimental evolution of *Drosophila*. *Annual Meeting of the Society for Molecular Biology and Evolution*, 12-16 Jul, Vienna, A
- Ari E, *et al.* (2006) Testing a new discrete mathematical method for reconstructing the great apes phylogeny based on mitochondrial tRNAs. *Evolution of Biomolecular Structure*, 25-27 May, Vienna, A