

# ÁBEL FÓTHI



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## RESEARCH AREA

Psychiatric disorders and other complex diseases frequently occur together, suggesting shared genetic and epigenetic mechanisms underlying their development. Our research group works in the field of psychogenetics, aiming to identify genetic variants and epigenetic regulatory processes that contribute to disease susceptibility and help explain the overlap between conditions. We perform bioinformatic analyses of large-scale genomic and epigenomic datasets, with a particular emphasis on genome-wide association studies (GWAS) and their integrative interpretation, complemented by targeted molecular biology assays. Using this approach, we investigate disease mechanisms across multiple biological scales, from population genetics to molecular and regulatory processes.

## TECHNIQUES AVAILABLE IN THE LAB

Laboratory techniques: During the project, students can acquire hands-on experience with nucleic acid isolation (DNA and RNA), conventional PCR-based genotyping and real-time PCR techniques, as well as epigenetic assays including DNA methylation and microRNA analyses. In addition, tissue culture methods and reporter assays can be learned.

Bioinformatic and data analysis methods: The experimental work is complemented by bioinformatic analyses of large-scale genetic and epigenetic datasets, with a particular focus on genome-wide association studies (GWAS) and the analysis of DNA methylation data. Students will also gain experience in using genetic and epigenetic databases, performing statistical analyses, and applying basic programming skills.

## SELECTED PUBLICATIONS

Pagliarioli, L., **Fóthi, A.**, Nespoli, E., Liko, I., Veto, B., Devay, P., Szeri, F., Hengerer, B., Barta, C., & Aranyi, T. (2021). Riluzole Administration to Rats with Levodopa-Induced Dyskinesia Leads to Loss of DNA Methylation in Neuronal Genes. *Cells* **10(6)**: 1442.

**Fóthi, Á.**, Biró, O., Erdei, Z., Apáti, Á., & Orbán, T. I. (2021). Tissue-specific and transcription-dependent mechanisms regulate primary microRNA processing efficiency of the human chromosome 19 MicroRNA cluster. *RNA Biol* **18(8)**: 1170–1180.

**Fóthi, Á.**, Pintér, C., Pollner, P., & Lőrincz, A. (2022). Peripheral gene interactions define interpretable clusters of core ASD genes in a network-based investigation of the omnigenic theory. *NPJ Syst Biol Appl* **8(1)**: 28.

**Fóthi, Á.**, Liu, H., Susztak, K., & Aranyi, T. (2024). Improve-RRBS: a novel tool to correct the 3' trimming of reduced representation sequencing reads. *Bioinform Adv* **4(1)**: vbae076.

Fanelli, G., Franke, B., Fabbri, C., Werme, J., Erdogan, I., De Witte, W., Poelmans, G., Ruisch, I. H., Reus, L. M., van Gils, V., Jansen, W. J., Vos, S. J. B., Alam, K. A., Martinez, A., Haavik, J., Wimberley, T., Dalsgaard, S., **Fóthi, Á.**, Barta, C., Fernandez-Aranda, F., ... Bralten, J. (2025). Local patterns of genetic sharing between neuropsychiatric and insulin resistance-related conditions. *Transl Psychiatry* **15(1)**: 145.