

# GÁBOR APJOK



**HUN-REN Biological Research Centre  
Institute of Biochemistry**

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## RESEARCH AREA

I am a postdoctoral researcher working on the improvement of phage therapy, applying synthetic biological and genome engineering techniques, as the senior of a group of talented individuals. I am involved in projects investigating and altering the interactions between phages and the human body, the gut and the blood-brain barrier in particular. Furthermore, I regularly carry out phage hunts upon request and already isolated and provided therapeutically applicable phages to hospitals in Switzerland, Portugal and the United Kingdom.

## TECHNIQUES AVAILABLE IN THE LAB

- Basic and advanced molecular biological techniques
- Routine handling of MDR pathogenic bacteria
- Bioinformatics (Processing and characterizing sequencing data, coding etc.)
- Phage isolation, characterization, genetic analysis
- Handling of mammalian cell cultures
- Advanced genome engineering skills:
- Phage engineering: display techniques, mutagenesis, recombineering, construction of transducing particles etc.
- CRISPR/Cas9 and derivative methods e.g. pEvolVR, dCas9
- MAGE-based applications: pORTMAGE, DivERGE

## SELECTED PUBLICATIONS

**Apjok, G., Számel, M., Christodoulou, C., Seregi, V., Vásárhelyi, B.M., Stirling, T., Eszenyi, B., Sári, T., Vidovics, F., Nagrand, E. et al. (2023) Characterization of antibiotic resistomes by reprogrammed bacteriophage-enabled functional metagenomics in clinical strains. *Nat Microbiol* 8: 410-423.**

Visnyovszki, Á., Orosz, L., Kintsés, B., Stirling, T., Vásárhelyi, B.M., Ari, E., Kiss, E., Papp, B., **Apjok, G.**, Vidovics, F. et al. (2021) A covid-19 pandémiához társulóan előfordult multirezisztens acinetobacter baumannii törzsek molekuláris jellemzése. **Magyar Infektológiai és Klinikai Mikrobiológiai Társaság 48. Kongresszusa** 2021-09-30 [Debrecen, Magyarország], (előadás)

**Apjok, G., Boross, G., Nyerges, A., Fekete, G., Lazar, V., Papp, B., Pál, C., Csörgő, B. (2019) Limited evolutionary conservation of multidrug resistance and collateral sensitivity. *Mol Biol Evol* 38: 3029-3029.**

Dunai, A., Spohn, R., Farkas, Z., Lázár, V., Györkei, Á., **Apjok, G.**, Boross, G., Szappanos, B., Grézal, G., Faragó, A. et al. (2019) Rapid decline of bacterial drug-resistance in an antibiotic-free environment through phenotypic reversion. **ELIFE** 8 Paper: e47088.

**Apjok, G., Boross, G., Nyerges, Á., Fekete, G., Lázár, V., Papp, B., Pál, C., Csörgő, B. (2019) Limited evolutionary conservation of the phenotypic effects of antibiotic resistance mutations. *Mol Biol Evol* 36: 1601-1611.**

Nyerges, A., Csörgő, B., Nagy, I., Balint, B., Bihari, P., Lazar, V., **Apjok, G.**, Umenhoffer, K., Bogos, B., Posfai, G. et al. (2016) A highly precise and portable genome engineering method allows comparison of mutational effects across bacterial species. **Proc Natl Acad Sci U S A** 113: 2502-2507.