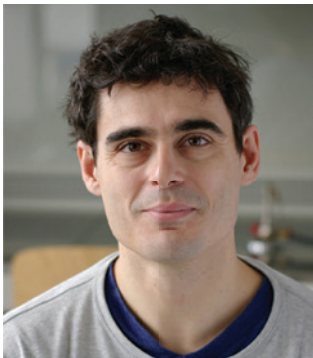


## CSABA PÁL



Biological Research Centre  
Institute of Biochemistry  
Synthetic and Systems Biology Unit

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## RESEARCH AREA

We focus on bacterial pathogens and the problem of antibiotic resistance. We found that multidrug resistance mutations in bacteria simultaneously enhance sensitivity to other unrelated antibiotics (collateral sensitivity). This finding has led to the design of new antibiotic cocktails. Using bacterial genome engineering, we aim to develop novel resistance-free antibiotics. Finally, we study the evolution of adaptive immune system in response to pathogens and cancer.

More details: <http://www.brc.hu/sysbiol>

## TECHNIQUES AVAILABLE IN THE LAB

Bacterial genome engineering, laboratory evolution, systems biology, bioinformatics.

## SELECTED PUBLICATIONS

Kintsés, B., Méhi, O., Ari, E., Számel, M., Györkei, Á., Jangir, P.K., Nagy, I., Pál, F., Fekete, G., Tengölics, R., Nyerges, Á., Likó, I., Bálint, A., Molnár, T., Bálint, B., Vásárhelyi, B.M., Bustamante, M., Papp, B., **Pal, C.** (2019) Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. **Nature Microbiology** 4: 447–458.

Lázár, V., Martins, A., Spohn, R., Daruka, L., Grézal, G., Fekete, G., Számel, M., Jangir, P.K., Kintsés, B., Csörgő, B., Nyerges, Á., Györkei, Á., Kincses, A., Dér, A., Walter, F.R., Deli, M.A., Urbán, E., Hegedűs, Z., Olajos, G., Méhi, O., Bálint, B., Nagy, I., Martinek, T. A., Papp, B., **Pal C.** (2018) Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. **Nature Microbiology** 3: 718–731.

**Pal, C.**, Papp, B., Pósfai, G (2014) The dawn of evolutionary genome engineering. **Nature Reviews Genetics** 15: 504–512.

**Pal, C.**, Macia, M., Oliver, A., Schacher, I., Buckling, A. (2007) Coevolution with viruses drives the evolution of bacterial mutation rates. **Nature** 450: 1079–81.

**Pal, C.**, Papp, B., Lercher, M.J., Csermely, P., Oliver, S.G., Laurence, D. Hurst. (2006) Chance and necessity in the evolution of minimal metabolic networks. **Nature** 440: 667–670.