# DÓRA TOMBÁCZ

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## RESEARCH AREA

Genomics is the study of the structure and function of genome. The genome sequences of many organisms have now been determined. It has also been described that the mammalian genomes contain approximately 22,000 protein-coding genes, however, they only represent about 1% of the genomes. It has also been demonstrated, that almost the entire genome is transcriptionally active at both DNA strands. More and more results show that the non-protein coding RNAs have a very important role on the regulation of gene expression, on various post-transcriptional processes and on the translation. Our research projects focus on the analysis of various viruses (e. g., Herpes simplex virus, Varicella Zoster virus, Vaccinia virus, etc.). We examine the gene expression profiles and transcriptional complexity of these viruses, and also use them as model organisms for the study of our Transcriptional Interference Network (TIN) hypothesis, which propose a novel layer of genetic regulation, and is based on the interactions between the gene activities via the mechanisms of transcriptional read-through between convergent, divergent and parallel gene pairs. For these, we apply state-of-the-art sequencing and bioinformatics techniques, as well as other cutting edge technologies such as the CrispR-Cas9/dCas9 techniques, with which we generate genetically modified viruses or inducible gene expression. Our group also has bacterial-fungal- and human genomics projects (analysis of the genetic background of major depression, Alzheimer's Disease) by applying exome-, transcriptome-, methyl- and ChIP-seq techniques.

## TECHNIQUES AVAILABLE IN THE LAB

We apply a wide variety of standard molecular biological methods and the most modern genomic approaches: DNA and RNA purification, propagation and maintaining various cell cultures, propagation of viruses, molecular cloning (homologous recombination and CrispR technique), PCR, quantitative (q)PCR, digital (d)PCR, Northern- and Western-blot, fluorescent and confocal microscopy. Next- and third generation sequencing (Illumina MiSeq, Oxford Nanopore MinION): genome-, transcriptome-, small RNA sequencing, analysis of epigenetic changes, preparation of sequencing libraries, bioinformatics and statistics. Pacific Biosciences RSII and Sequel data analysis and bioinformatics.

## SELECTED PUBLICATIONS

Boldogkői, Z., Moldován. N., Balázs. Z., Snyder, M., **Tombácz, D.** (2019) Long-Read Sequencing - A Powerful Tool in Viral Transcriptome Research. **Trends Microbiol 27:** 578-592.

**Tombácz, D.**, Prazsák, I., Szűcs, A., Dénes, B., Snyder, M., Boldogkői, Z. (2018) Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. **Gigascience 7:** giy139.

**Tombácz, D.**, Sharon, D., Szűcs, A., Moldován, N., Snyder, M., Boldogkői, Z. (2018) Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. **Sci Data 5:** 180119.

**Tombácz, D.**, Maróti, Z., Kalmár, T., Csabai, Z., Balázs, Z., Takahashi, S., Palkovits, M., Snyder, M., Boldogkői Z. (2017) High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. **Sci Rep 7:** 7106.

Boldogkői, Z., Balint. K., Awatramani. G.B., Balya, D., Busskamp,V., Viney, T.J., Lagali, P.S., Duebel, J., Pásti, E., **Tombácz, D.**, Tóth, J.S., Takács, I.F., Scherf, B.G., Roska, B. (2009) Genetically timed, activity-sensor and rainbow transsynaptic viral tools. **Nat Methods 6(2)**: 127-30.