

# BEÁTA VÉRTESSY



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## RESEARCH AREA

How much do we know actually about the true structure, composition and sequence of DNA? We work to answer these fundamental questions. It is well known that in addition to the four canonical DNA bases, many additional components occur in DNA. These remain hidden in the usual DNA sequencing procedures. We focus on the uracil base in DNA (deoxyuridine) to understand the physiological and pathophysiological role of uracil-DNA in normal developmental processes and in various cancers. We have shown that uracil in DNA is interpreted in a regulated manner, both as an error to be repaired and as a signal for transmission. Our main activity is basic research - we want to answer the big unknown questions. Meanwhile, our results present an important contribution to new therapies in cancer and various infectious diseases (tuberculosis, malaria). Our group also has several structural biology / enzymology projects underway. Our toolbox encompasses methods from biochemistry, enzymology, molecular biology, structural biology (X-ray crystallography), cell biology and bioinformatics (development of new sequencing methods). We also work with several animal models (zebrafish, mouse, fruit fly).

## TECHNIQUES AVAILABLE IN THE LAB

Molecular biology (cloning, creation of transgenic organisms, insertion of mutations, Crispr genome editing), structural biology (spectroscopy methods, macromolecular X-ray diffraction, solving 3D structures), biochemistry (protein expression, protein purification, investigation of protein-ligand interactions, gel electrophoresis, Western blotting, other blotting techniques), enzymology, enzyme kinetics, bioinformatics (DNA and RNA sequencing, management of large databases), cell biology (management of cell lines and genome editing, confocal and super-resolution microscopy)

## SELECTED PUBLICATIONS

Situ, K., Duan, H., Godin, S. K., Yang, J., McCloskey, G. Q., Naeem, B., Gillis, M. K., Zeb, M. H., Salhotra, S., Rawal, P., Patel, N., Mouliere, S. K., Chen, J., Békési, A., Pálinkás, H. L., Venkatesan, S., Green, A. M., Birkbak, N. J., **Vértessy, B. G.**, Swanton, C., ... Pathania, S. (2025). BRCA2 deficiency and replication stress drive APOBEC3-Mediated genomic instability. *Nat Commun* **16**(1): 9544.

Tóth, O., Rácz, G. A., Oláh, E., Tóth, M., Szabó, E., Várady, G., **Vértessy, B. G.**, & Nagy, N. (2025). Identification of new reference genes with stable expression patterns for cell cycle experiments in human leukemia cell lines. *Sci Rep* **15**(1): 1052.

Ubhi, T., Zaslaver, O., Quaile, A. T., Plenker, D., Cao, P., Pham, N. A., Békési, A., Jang, G. H., O’Kane, G. M., Notta, F., Moffat, J., Wilson, J. M., Gallinger, S., **Vértessy, B. G.**, Tuveson, D. A., Röst, H. L., & Brown, G. W. (2024). Cytidine deaminases APOBEC3C and APOBEC3D promote DNA replication stress resistance in pancreatic cancer cells. *Nat Cancer* **5**(6): 895–915.

Pálinkás, H. L., Békési, A., Róna, G., Pongor, L., Papp, G., Tihanyi, G., Holub, E., Póti, Á., Gemma, C., Ali, S., Morten, M. J., Rothenberg, E., Pagano, M., Szűts, D., Györffy, B., & **Vértessy, B. G.** (2020). Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. *eLife* **9**: e60498.

Rácz, G. A., Nagy, N., Tóvári, J., Apáti, Á., & **Vértessy, B. G.** (2021). Identification of new reference genes with stable expression patterns for gene expression studies using human cancer and normal cell lines. *Sci Rep* **11**(1): 19459.

Babai, R., Izrael, R., & **Vértessy, B. G.** (2022). Characterization of the dynamics of Plasmodium falciparum deoxy-nucleotide-triphosphate pool in a stage-specific manner. *Sci Rep* **12**(1): 19926.

Nagy, K. K., Takács, K., Németh, I., Varga, B., Grolmusz, V., Molnár, M., & **Vértessy, B. G.** (2024). Novel enzymes for biodegradation of polycyclic aromatic hydrocarbons identified by metagenomics and functional analysis in short-term soil microcosm experiments. *Sci Rep* **14**(1): 11608.