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RESEARCH AREA

The focus of my research is on long non-coding RNAs (lncRNAs), whose number in the human genome is estimated to be around 58,000. Non-coding RNAs are gene products that are not translated into proteins but still possess independent biological functions. Among the major groups of non-coding RNAs are microRNAs and lncRNAs.

LncRNAs play regulatory roles in numerous cellular processes, most commonly through molecular interactions. Their importance is well recognized in cell cycle regulation, DNA repair, stress responses, as well as in the regulation of gene expression and RNA processing. Abnormal expression of lncRNAs has been linked to the development and progression of various cancers; therefore, many of them represent not only potential drug targets but also promising biomarker candidates.

However, it is important to understand that these RNAs rarely act independently, and regulating a single lncRNA alone is unlikely to produce a significant therapeutic effect. Therefore, in my research group, we study lncRNAs using a network-based approach, taking into account both their protein and RNA interaction partners.

TECHNIQUES AVAILABLE IN THE LAB

In our research group, we apply molecular biology techniques and conduct experiments using both mammalian cell model systems and in vitro synthesized molecules.

The main techniques that can be mastered include:

- Maintenance and manipulation of mammalian cell cultures
- RNA immunoprecipitation
- Quantitative PCR
- Immunofluorescence assays
- Agarose and SDS gel electrophoresis
- Microscale thermophoresis (for characterizing molecular interactions)
- In vitro RNA transcription
- Recombinant protein expression and purification

SELECTED PUBLICATIONS

Amin, H. M., Abukhairan, R., Szabo, B., Jacksi, M., Varady, G., Lozsa, R., Schad, E., & **Tantos, A.** (2024). KMT2D preferentially binds mRNAs of the genes it regulates, suggesting a role in RNA processing. **Protein Sci 33**(1): e4847.

Amin, H. M., Szabo, B., Abukhairan, R., Zeke, A., Kardos, J., Schad, E., & **Tantos, A.** (2023). In Vivo and In Vitro Characterization of the RNA Binding Capacity of SETD1A (KMT2F). **Int J Mol Sci 24**(22): 16032.

Szabó, B., Murvai, N., Abukhairan, R., Schád, É., Kardos, J., Szeder, B., Buday, L., & **Tantos, Á.** (2018). Disordered Regions of Mixed Lineage Leukemia 4 (MLL4) Protein Are Capable of RNA Binding. **Int J Mol Sci 19**(11): 3478.

Szabó, C. L., Szabó, B., Sebák, F., Bermel, W., **Tantos, A.**, & Bodor, A. (2022). The Disordered EZH2 Loop: Atomic Level Characterization by $^{1}H^{N}$- and $^{1}H^{\alpha}$-Detected NMR Approaches, Interaction with the Long Noncoding HOTAIR RNA. **Int J Mol Sci 23**(11): 6150.

Zeke, A., Schád, É., Horváth, T., Abukhairan, R., Szabó, B., & **Tantos, A.** (2022). Deep structural insights into RNA-binding disordered protein regions. **Wiley Interdiscip Rev RNA 13**(5): e1714.