GÁBOR TUSNÁDY

HUN-REN Research Centre for Natural Sciences
Institute of Molecular Life Sciences

Address: Magyar Tudósok körútja 2.,
H-1117 Budapest, Hungary

RESEARCH AREA

Our research group's main area of investigation is transmembrane proteins. To study these proteins, which are experimentally very difficult to investigate, we primarily develop bioinformatics tools and, more recently, artificial intelligence-based methods that can be used to estimate the structure, occurrence, interactions, and other properties of transmembrane proteins. In order to develop these methods, it is important to start from reliable, up-to-date databases containing accurate data, which is why we have compiled and maintain a number of such databases. In addition to bioinformatics tools, we are also working on several laboratory developments that will allow us to obtain topological information on hundreds or even thousands of transmembrane proteins at once, or to determine their exact abundance on the cell surface. These developments could be extremely important in identifying new targets for immunotherapy and in the fight against various pathogens.

TECHNIQUES AVAILABLE IN THE LAB

Programming (Python, C++, PHP), database management (MySQL), artificial intelligence-based processes, cell culture, cell surface labeling processes, mass spectrometry

SELECTED PUBLICATIONS

Bajtai, E., Kiss, C., Bakos, É., Langó, T., Lovrics, A., Schád, É., Tisza, V., Hegedűs, K., Fürjes, P., Szabó, Z., **Tusnády, G. E.**, Szakács, G., Tantos, Á., Spisák, S., Tóvári, J., & Füredi, A. (2025). Therapy-induced senescence is a transient drug resistance mechanism in breast cancer. **Mol Cancer 24**(1): 128.

Tusnády, G. E., & Gerdán, C. (2025). TmDet 4.0: determining membrane orientation of transmembrane proteins from 3D structure. **Nucleic Acids Res 53**:(W1), W542–W546.

Dobson, L., Gerdán, C., Tusnády, S., Szekeres, L., Kuffa, K., Langó, T., Zeke, A., & **Tusnády, G. E.** (2024). UniTmp: unified resources for transmembrane proteins. **Nucleic Acids Res 52**:(D1), D572–D578.

Dobson, L., Szekeres, L. I., Gerdán, C., Langó, T., Zeke, A., & **Tusnády, G. E.** (2023). TmAlphaFold database: membrane localization and evaluation of AlphaFold2 predicted alpha-helical transmembrane protein structures. **Nucleic Acids Res 51**:(D1), D517–D522.

Dobson, L., & **Tusnády, G. E.** (2021). MemDis: Predicting Disordered Regions in Transmembrane Proteins. **Int J Mol Sci 22**(22): 12270.