LABORATORY OF PROTEOMICS RESEARCH

A BRC & HCEMM Research and Resource Facility.

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Group members

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Research

Proteomics has become one of the most exciting and dynamic research areas. Since the genomes sequenced failed to answer several questions, systems biology research started to target other biomolecules. Proteomic studies aim to decipher structural changes of proteins and protein complexes, their role in different interactions, biological functions and processes by characterizing the qualitative and quantitative changes in protein mixtures of varied complexity: up to cellular organelles, cell lines, tissues, or even individuals. Mass spectrometry has become the method of choice for such research. It is equally well suited for protein identification, *de novo* sequencing, for the characterization of post-translational modifications, or other covalent labeling. It can also be used for probing the 3D structure of proteins, the spatial organization of protein complexes, or studying intact protein populations. Last but not least, mass spectrometry can also deliver quantitative results.

We have extensive collaborations within the BRC and with academic organizations in Hungary and abroad. Biological samples are provided by our partners. Our tasks are the analytical sample preparation, chromatographic fractionation if necessary, mass spectrometry analysis as well as data interpretation. However, an ideal collaboration starts at the planning stage, designing the experiments together. Obviously our goal is to assure that the samples will be compatible with the following analyses, but also we have to agree on the number of biological and technical replicates and on the selection of the proper controls whenever it is necessary. We developed and regularly use a reliable protocol for the isolation of protein complexes. We also regularly perform the qualitative and (semi)quantitative characterization of the resulting mixtures, as well as other protein samples of different complexity. Such analysis may include the characterization of certain posttranslational modifications. We are experienced in the characterization of disulfide-bridges, proteolytic cleavage sites, ubiquitination, phosphorylation and glycosylation. For about a decade we have been successfully developing new methods for the characterization of mucin-type O-glycosylation.

Services

Selected Publications

1. Viczián, A., Ádám, É., Staudt, A. M., Lambert, D., **Klement, E.**, Romero Montepaone, S., Hiltbrunner, A., Casal, J., Schäfer, E., Nagy, F., & Klose, C. (2020). Differential phosphorylation of the N-terminal extension regulates phytochrome B signaling. *The New phytologist*, **225**(4), 1635–1650.
2. **Pap A**, Tasnadi E, **Medzihradszky KF, Darula Z**. (2020) Novel O-linked sialoglycan structures in human urinary glycoproteins. *Mol Omics*. **16**(2):156-164.
3. Lokdarshi, A., Papdi, C., **Pettkó-Szandtner, A.**, Dorokhov, S., Scheres, B., Magyar, Z., von Arnim, A. G., Bögre, L., & Horváth, B. M. (2020). ErbB-3 BINDING PROTEIN 1 Regulates Translation and Counteracts RETINOBLASTOMA RELATED to Maintain the Root Meristem. *Plant physiology*, **182**(2), 919–932.
4. Baba AI, Valkai I, Labhane NM, Koczka L, Andrási N, **Klement É, Darula Z, Medzihradszky KF**, Szabados L, Fehér A, Rigó G, Cséplő Á. (2019) CRK5 Protein Kinase Contributes to the Progression of Embryogenesis of Arabidopsis thaliana. *Int J Mol Sci.* **20**(24): 6120.
5. Lin King, J. V., Emrick, J. J., Kelly, M., Herzig, V., King, G. F., **Medzihradszky, K. F.**, & Julius, D. (2019). A Cell-Penetrating Scorpion Toxin Enables Mode-Specific Modulation of TRPA1 and Pain. *Cell*, **178**(6), 1362–1374.e16.
6. Andrási N, Rigó G, Zsigmond L, Pérez-Salamó I, Papdi C, **Klement E, Pettkó-Szandtner A,** Baba AI, Ayaydin F, Dasari R, Cséplő Á, Szabados L. (2019) The mitogen-activated protein kinase 4-phosphorylated heat shock factor A4A regulates responses to combined salt and heat stresses. *Exp Bot*. **70**(18): 4903-4918.
7. Letoha, T., Hudák, A., Kusz, E., **Pettkó-Szandtner, A.**, Domonkos, I., Jósvay, K., Hofmann-Apitius, M., & Szilák, L. (2019). Contribution of syndecans to cellular internalization and fibrillation of amyloid-β(1-42). *Scientific reports*, **9**(1), 1393.
8. Szél, E., Bozó, R., **Hunyadi-Gulyás, É.**, Manczinger, M., Szabó, K., Kemény, L., Bata-Csörgő, Z., & Groma, G. (2019). Comprehensive Proteomic Analysis Reveals Intermediate Stage of Non-Lesional Psoriatic Skin and Points out the Importance of Proteins Outside this Trend. *Scientific reports*, **9**(1), 11382.

9. Gyukity-Sebestyén E, Harmati M, Dobra G, Németh IB, Mihály J, Zvara Á, **Hunyadi-Gulyás É,** Katona R, Nagy I, Horváth P, Bálind Á, Szkalisity Á, Kovács M, Pankotai T, Borsos B, Erdélyi M, Szegletes Z, Veréb ZJ, Buzás EI, Kemény L, Bíró T, Buzás K. (2019) Melanoma-Derived Exosomes Induce PD-1 Overexpression and Tumor Progression via Mesenchymal Stem Cell Oncogenic Reprogramming. *Front Immunol.* **10**: 2459.
10. Schmitt LR, Henderson R, Barrett A, **Darula Z**, Issaian A, D'Alessandro A, Clendenen N, Hansen KC. (2019) Mass spectrometry-based molecular mapping of native FXIIIa cross-links in insoluble fibrin clots. *J Biol Chem.* **294**(22):8773-8778.
11. Laurinyecz, B., Vedelek, V., Kovács, A. L., Szilasi, K., Lipinszki, Z., Slezák, C., **Darula, Z.**, Juhász, G., & Sinka, R. (2019). Sperm-Leucylaminopeptidases are required for male fertility as structural components of mitochondrial paracrystalline material in Drosophila melanogaster sperm. *PLoS genetics*, **15**(2), e1007987.
12. **Darula Z, Pap Á, Medzihradszky KF**. (2019) Extended Sialylated O-Glycan Repertoire of Human Urinary Glycoproteins Discovered and Characterized Using Electron-Transfer/Higher-Energy Collision Dissociation. *J Proteome Res.* **18**(1):280-291.
13. **Darula Z, Medzihradszky KF**. (2018) Analysis of Mammalian O-Glycopeptides-We Have Made a Good Start, but There is a Long Way to Go. *Mol Cell Proteomics*. **17**(1):2-17.
14. Farkas Z, Kalapis D, Bódi Z, Szamecz B, Daraba A, Almási K, Kovács K, Boross G, Pál F, Horváth P, Balassa T, Molnár C, **Pettkó-Szandtner A, Klement É**, Rutkai E, Szvetnik A, Papp B, Pál C. (2018) Hsp70-associated chaperones have a critical role in buffering protein production costs. *Elife*. **7**: e29845.
15. Langó, T., Róna, G., **Hunyadi-Gulyás, É.,** Turiák, L., Varga, J., Dobson, L., Várady, G., Drahos, L., Vértessy, B. G., **Medzihradszky, K. F.**, Szakács, G., & Tusnády, G. E. (2017). Identification of Extracellular Segments by Mass Spectrometry Improves Topology Prediction of Transmembrane Proteins. *Scientific reports*, **7**, 42610.