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RESEARCH AREA

Structural mass spectrometry (MS) analysis of proteins is a cutting-edge research field that combines mass spectrometry with structural biology to study the architecture and dynamics of proteins and protein complexes. This approach includes techniques like native MS, hydrogen-deuterium exchange MS (HDX-MS), and cross-linking MS, which provide detailed insights into protein structures, interactions, and modifications.

Native MS maintains proteins in their native state, allowing the study of non-covalent interactions and complex assemblies. HDX-MS measures the exchange of hydrogen atoms with deuterium in protein backbones, revealing solvent accessibility and conformational changes. This technique is particularly useful for studying protein folding, dynamics, and interactions. Cross-linking MS identifies spatial relationships within proteins by chemically linking interacting regions.

These methods are crucial for understanding protein function, mechanisms, and pathways in biological systems. They are applied in various fields, including drug discovery, disease research, and biotechnology, offering a comprehensive view of the proteome and its functional dynamics.

TECHNIQUES AVAILABLE IN THE LAB

- Heterologous protein expression in E. coli
- Mass spectrometric sample preparation of protein samples
- Protein sequence analysis by mass spectrometry
- Chemical cross-linking for characterization of protein suspensions
- Fluorescence labeling based interaction study and determination of dissociation constants
- Use of circular dichroism to verify correct unfolding of proteins

SELECTED PUBLICATIONS

Szabo, E., Nagy, B., Czajlik, A., Komlodi, T., **Ozohanics, O.**, Tretter, L., & Ambrus, A. (2024). Mitochondrial alpha-keto acid dehydrogenase complexes: recent developments on structure and function in Health and Disease. **Subcell Biochem 104:** 295–381.

Tóth, Z. S., Leveles, I., Nyíri, K., Nagy, G. N., Harmat, V., Jaroentomeechai, T., **Ozohanics, O.**, et al. (2024). The homodimerization domain of the Stl repressor is crucial for efficient inhibition of mycobacterial dUTPase. **Sci Rep 14(1):** 27171.

Ozohanics, O., Zhang, X., Nemeria, N. S., Ambrus, A., & Jordan, F. (2023). Probing the E1o-E2o and E1a-E2o interactions in binary subcomplexes of the human 2-oxoglutarate dehydrogenase and 2-oxoadipate dehydrogenase complexes by chemical cross-linking mass spectrometry and molecular dynamics simulation. **Int J Mol Sci 24(5):** 4555.

Piroli, G. G., Manuel, A. M., McCain, R. S., Smith, H. H., **Ozohanics, O.**, Mellid, S., Cox, H. et al. (2023). Defective function of α-ketoglutarate dehydrogenase exacerbates mitochondrial ATP deficits during complex I deficiency. **Redox Biol 67:** 102932.

Szabo, E., Nemes-Nikodem, E., Vass, K. R., Zambo, Z., Zrupko, E., Torocsik, B., **Ozohanics, O.,** Nagy, B., Ambrus, A. (2023). Structural and Biochemical Investigation of Selected Pathogenic Mutants of the Human Dihydrolipoamide Dehydrogenase. **Int J Mol Sci 24(13):** 10826.