

Centre de Neurosciences Psychiatriques

CNP SEMINAR

ANNOUNCEMENT

Friday June 14th 2024, 11:00 12:00 am

Quantitative mass spectrometry to map the structural and functional diversity of proteins.

By: Tatjana Sajic

Summary :

Over the past century, synthetic and catalytic principles have been established for many individual enzymes, improving our understanding of the basis of life and transforming modern medicine and biotechnology. However, the biochemical processes of the living cell depend on the coordinated regulation of the activity of multiple enzymes or proteins, e.g. those of a metabolic pathway or caspase cascades. Mass spectrometry (MS) has become the method of choice for the parallel quantitative measurement of biomolecules and their interactions, including proteins, metabolites, and trace elements (OMICS approaches). Here we discuss the advanced MS techniques used to systematically profile the functional and structural diversity of proteins, the activity of enzymes in cells and tissues in different states, and to identify protein and small molecule modulators of enzyme activity. In this context, we also present the study of functional and standard 'expression' proteomics of blood serum in traumatic brain injury (TBI), including paediatric abusive head trauma (AHT), which is the leading cause of death and disability in children and young adults worldwide.

Invited by : benjamin.boutrel@unil.ch



Short Bio :

Dr Sajic has an interdisciplinary background including a degree in Pharmacy, a PhD in Pharmaceutical Sciences and a Master in Bioinformatics and Proteomics at the Swiss Institute of Bioinformatics (SIB), which she completed as a Swiss Government Scholar at the University of Geneva (UniGE). During her PhD studies at the UnGE, from 2008 to 2013, she worked on metabolic questions on the link between inflammatory cell metabolism and diabetes/obesity. In May 2013, she joined the ETH Zurich, in prof. Aebersold's lab, where she is a postdoctoral fellow until October 2019.

Most recently, she was employed as a permanent researcher at the University Centre for Legal Medicine (CURML), where she established a platform for chemical proteomics working in the fields of cancer, obesity-related environmental metabolic changes and, in particular, paediatric abusive head trauma (AHT), the leading cause of traumatic brain injury (TBI) death in infants.

Publications :

Sajic, T.*, Liu, Y., Arvaniti, E., et al. (2018). Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. *Cell Rep*, 23(9), 2819-2831 • Stier, A., Gilberto, S., Mohamed, W. I., Royall, L. N., Helenius, J., Mikicic, Sajic, T., Beli, P., Muller, D. J., Jessberger S. and Peter, M. (2023). The CUL4B-based E3 ubiquitin ligase regulates mitosis and brain development by recruiting phospho-specific DCAFs. *EMBO J*, 42(17) • Maret, E., Wiskott, K., Shipley, T., Gilardi, F., Augsburg, M., Thomas, A., Fracasso, T*, Sajic, T.* (2024). Activity based proteome profiling of serum serine hydrolases: application in pediatric abusive head trauma. Manuscript number prca.202400022 Proteomics - Clinical Applications. (In revision). Open Access. • Wiskott, K., Gilardi, F., Hainard, A., Sanchez, J.-C., Thomas, A., Sajic, T.*, Fracasso, T* (2023). Blood proteome of acute intracranial hemorrhage in infant victims of abusive head trauma. *Proteomics*, 23(3-4). • Sajic T.*, V. M., Arni C., Ciuffa R., Mehnert M., Lenglet S., Buljan M., Thomas A., Weder W., Hillinger S.*, Aebersold R.* (2024). Depletion-dependent Activity-Based Protein Profiling coupled to SWATH/DIA Mass Spectrometry detects serine hydrolase lipid remodeling in lung adenocarcinoma progression (under revision *Nature Communications*-NCOMMS-23-55691T)

Salle de séminaire 1er étage - CNP