

December 22th 2022

h 14.00

Seminar

New proteomic tools to model proteome relationships

ABSTRACT: Protein relationships, defined as physical and chemical protein associations, are major effectors and regulators of cellular functions. Hence, the knowledge of protein organization can be applied in clinical and pharmaceutical contexts to describe and discriminate physiological and pathological states. In this seminar, a panel of MS based proteomics tools will be presented¹⁻³: the aim is to investigate (plasma) proteome relationships, generate models to describe protein organization and, as ultimate goal, identify a new class of protein biomarkers which can be interpretable as direct proxies ("sentinels") of pathological events in the system.

1.Ciuffa, R. Uliana, F. et al. Novel biochemical, structural, and systems insights into inflammatory signaling revealed by contextual interaction proteomics. *Proc. Natl. Acad. Sci.* 119, e2117175119 (2022).

2.Uliana F., et al. Systematic dissection of phosphorylation-dependent YAP1 complex formation elucidates a key role for PTPN14 in Hippo signal integration (*Molecular System Biology*, in revision). *bioRxiv* 2022.03.13.484137.

3.Uliana, F. Vizovisek, M. et al. Mapping specificity, cleavage entropy, allosteric changes and substrates of blood proteases in a high-throughput screen. *Nat. Commun.* 12, 1693 (2021).

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