



Colloquium

Clinical Colloquium Regenerative Medicine

Monday, February 24th, 13:00 – 14:00

Institute for Regenerative Medicine - IREM

Wagistrasse 12, 8952 Schlieren

Seminar room 9th floor

Prof. Paola Picotti

Institute of Molecular Systems Biology, ETH Zurich

Proteomes in 3D

Protein structural changes induced by external perturbations or internal cues can profoundly influence protein activity and thus modulate cellular physiology. Mass spectrometry (MS)-based proteomic techniques are routinely used to measure changes in protein abundance, post-translational modification and protein interactors, but much less is known about protein structural changes. In my talk, I will present a structural proteomics method that enables analysis of protein structural changes on a proteome-wide scale and directly in complex biological extracts. The approach relies on the coupling of limited proteolysis (LiP) tools and MS. LiP-MS can detect subtle alterations in secondary structure content, larger scale movements such as domain motions, and more pronounced transitions such as the switch between folded and unfolded states. I will describe how we are applying this approach to study the molecular bases of protein aggregation diseases and to the identification of protein-small molecule interactions (e.g. drug targets). I will also propose that monitoring protein structural states on a proteome-wide scale can serve as a new powerful readout to pinpoint altered protein functional states and the (de)regulation of biochemical pathways. Last, I will discuss the power and limitations of the new approach.