

## Special Seminar Invitation

# Probing protein structural changes on a proteome-wide scale

Speaker [Prof. Dr. Paola Picotti](#)  
*Institute of Molecular Systems Biology ETHZ*

When **May 9, 14.00 – 15.00**

Where **Forum Chriesbach, room D24, Eawag Dübendorf**

Abstract 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 recently developed 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 different applications of the approach, including the unbiased identification of protein-small molecule interactions and the monitoring of amyloidogenic proteins involved in neurodegenerative diseases. I will describe how we recently used the approach to build a map of protein-metabolite interactions and binding sites in *E. coli* and how this enabled the unbiased identification of novel allosteric events. Last, I will discuss the power and limitations of the new approach.