

Talk abstract “Proteomes in 3D: Structural barcodes to probe protein functional alterations”

Proteomics has been broadly applied to detect changes in protein levels in response to perturbations and derive information on altered pathways. Beyond protein expression changes, however, biological processes are also regulated by events such as intermolecular interactions, chemical modification and conformational changes. These events do not affect protein levels and therefore escape detection in classical proteomic screens. I will present how a global readout of protein structure can detect various types of protein functional alterations concomitantly. The approach, relying on the LiP-MS technique, monitors structural changes in thousands of proteins simultaneously in situ. It captures enzyme activity changes, allosteric regulation, phosphorylation and protein complex formation and pinpoints regulated functional sites, thus substantially expanding the coverage of proteomic analyses and supporting the generation of mechanistic hypotheses. Applications of this approach include the study of complex phenotypes, the identification of disease biomarkers and drug target deconvolution.