

Proteome Biology

Ruedi Aebersold

ETH Zürich, Institute of Molecular Systems Biology, Switzerland
aebersold@imsb.biol.ethz.ch

Biological processes can be viewed as networks of interacting components, whereby the structure and dynamics of the network determines the properties of the process. Different types of such networks concurrently exist in the cell and many consist of or contain proteins. Examples include protein:protein interaction networks, networks of enzymes and their substrates, networks of microRNA's and their targets, protein:DNA interaction networks etc. The study of such networks requires proteomic technologies that are capable of detecting and quantifying any protein of a given network, to determine the network connections and their dynamic change and to relate the results of measurements made on cell or tissue extracts back to the living cell.

In this presentation we will discuss technical and conceptual advances in proteomics that support proteome biology. These include the ability to detect reliably and quantify essentially any protein in a yeast cell by targeted, SRM based high sensitivity mass spectrometry, the ability to determine the true composition of protein complexes that exist in the cell and to visualize them in near life cells, and the ability to measure phosphorylation modulated regulatory networks. The technical advances will be illustrated with suitable examples.