

Purification and separation of protein complexes

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Proteins perform their roles in biological systems by forming long term stable complexes, transient complexes necessary for cell function, and dynamic interactions for the transduction of different signals. The localization of proteins to specific compartments or to structural proteins can be key in defining protein interactions. Furthermore, proteins will have different interactions depending on their activation states. This is clearly illustrated by the signaling proteins that are involved in multiple pathways depending on their state of phosphorylation. Mapping protein interactions and their dynamicity is important for exploring individual proteins and, on a larger scale, for predictive modeling of biological systems at the molecular level. To date, only a few large-scale interaction mapping have been reported, and those are predominantly focused on protein-protein interactions. This session will review the main approaches for mapping protein-protein interactions, bioinformatic approaches to mine protein interactions at the individual protein level and at the network level. I will also discuss some selected examples of protein-protein interactions.

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3. A.C. Gavin, P. Aloy, P. Grandi *et al.*, Proteome survey reveals modularity of the yeast cell machinery, *Nature*, 440, 631-6, 2006.
4. M. Barrios-Rodiles, K.R. Brown, B. Ozdamar *et al.*, High-throughput mapping of a dynamic signaling network in mammalian cells, *Science*, 307, 1621-5, 2005.
5. P. Lamesch, N. Li, S. Milstein *et al.*, hORFeome v3.1: a resource of human open reading frames representing over 10,000 human genes, *Genomics*, 89, 307-15, 2007.