

Biochemical approaches to biomolecular networks

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Since the sequencing of the first eukaryotic genome, *Saccharomyces cerevisiae*, some 10 years ago, our understanding of the basic building blocks that make up a cell has spectacularly improved. The explosion of new analytical tools in the fields of genomics, proteomics and metabolomics contributes ever-growing molecular repertoires of a cell. Biology does not rely on biomolecules acting in isolation. Biological function depends on the concerted action of molecules acting in protein complexes, pathways or networks. Biomolecular interactions are central to all biological functions. In human, for example, impaired or deregulated protein–protein or protein–metabolite interaction often leads to disease. Recent strategies have been designed that allow the study of interactions more globally at the level of entire biological systems. We will discuss the use of these biochemical approaches to genome-wide scale screen in model organisms.