

Metabolite-Related Protein, Cell Cycle, and Kinome Networks in Yeast

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Proteins bind to each other to form stable complex and to contribute cellular responses. At a complex system, protein complexes interact with other proteins weakly, transiently, or conditionally to form a biological module that serves a specific function in cells and systems as well. With the sufficiency of protein-protein interaction data obtained by genome projects, it is possible to create a widespread representation of the protein network of the yeast cells and human cells. Protein networks are currently investigated in terms of topology, motifs, correlation structure, and modular properties that are related to function. A functional module is defined as a group of proteins that its function is separable from other modules. We have been constructed kinome, metabolite-related protein, and cell cycle protein networks and analyzed structural characterization and functional modules of the networks. Since large scale protein-protein interaction database contains random false positives, we employed cellular localization concept to construct highly purified metabolite-related protein network of the yeast cells in here. From functional modules of the networks, we derive tentative functions for unannotated proteins and identify several hub proteins and significant linkers regarding the lethality of the null mutants. We also elucidate lethality and robustness of the protein networks. Therefore, protein network is a useful tool for identifying unknown functions of proteins and prediction of hub or lethal proteins that highly connected with proteins to form modules.