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Commentary

Detection Methods for Analysis of Protein-Protein Interactions

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DESCRIPTION

Proteins are controller of all biological systems in a cell, and while many proteins work on their own, the great majority of proteins interact with one another to ensure correct biological activity. Most biological functions in a cell, such as gene expression, cell growth, proliferation, nutrition uptake, morphogenesis, motility, intercellular communication, and apoptosis, are facilitated by proteins. Protein-protein interaction is important in predicting target protein function as well as molecule drug ability. The bulk of genes and proteins use a series of interactions to achieve their phenotypic roles. The study of signal transduction pathways is substantially aided by the discovery of protein interaction networks. PPIs regulate a wide range of biological activities, including cell-to-cell interactions, metabolic control, and developmental control.

Types

Protein interactions can be classified as either persistent or transient, with both types of interactions being strong or weak. Stable interactions are those that are linked with proteins isolated as multi-subunit complexes, the subunits of which can be same or different. Multi-subunit interactions that generate stable complexes include haemoglobin and core RNA polymerase. The majority of cellular functions are believed to be controlled by transient interactions. Fleeting contacts, as their name implies, are transient in nature and often necessitate a series of conditions that encourage the interaction, such as phosphorylation, conformational changes, or localization to certain parts of the cell. Strong or weak, fast or slow, transient interactions might occur.

PPIs identification methods

Methods for detecting protein-protein interactions can be divided into three categories: *in vitro, in vivo,* and *in silico.*

In vivo: An example of an *in vivo* identification approach is the yeast two hybrid system. This approach assesses protein-protein interaction by measuring the transcriptional activity. Many site-specific transcriptional activators, which are made up of a DNA-binding domain and a transcriptional activation domain, are modular. The activator's DNA-binding domain is used to direct it to the genes that will be expressed. To allow transcription to take place, the activation domain interacts with other proteins in the transcriptional machinery.

In vitro: An example of an *in vivo* identification method is co-immunoprecipitation. The most difficult method is co-immunoprecipitation (coIP). Co-immunoprecipitation (co-IP) is a common method for discovering protein interactions. Co-IP is similar to immunoprecipitation (IP) of a single protein, except that the antibody-precipitated target protein, also known as the "bait," is used to co-precipitate a binding partner/protein complex.

In silico: Several *in silico* methods have been developed to support interactions discovered using an experimental methodology. Sequence-based approaches, structure-based approaches, chromosome proximity, gene fusion, *in silico* 2 hybrid, mirror tree, phylogenetic tree, gene ontology, and gene expression-based approaches are some of the computational methods for *in silico* prediction. A PPI network is a heterogeneous network of proteins connected by interactions as edges. The visualization of the PPI network arrangement is the first step in the computational study of PPI networks. The most basic sketch is made up of nodes and edges in the shape of a mathematical graph. The huge amount of experimental PPI data being created on a regular basis has necessitated the creation of computer-readable biological databases to organize and process it. The Biomolecular Interaction Network Database (BIND), for example, is built on an extensible specification framework that allows for a detailed explanation of how the PPI data was obtained experimentally. Another library of experimentallydetermined protein-protein binary interactions is the Database Of Interacting Proteins (DIP). BioGRID (Biological General Repository for Interaction Datasets) is a database that provides protein and genetic interactions between thirteen species. Another resource of empirically derived PPI data taken from the literature is the Molecular Interaction (MINT) database.

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