Journal of Proteomics & Bioinformatics

ISSN: 0974-276X

Editorial

Editorial on Protein-Protein Interactions

Susan Williams

Managing Editor, Journal of Proteomics & Bioinformatics, Spain

EDITORIAL

Protein-protein interactions (PPIs) or multi-protein complexes perform central roles in the cellular systems of all living organisms. They control variety of biological phenomena including development, cell to cell interactions and metabolic processes [1].

Identifying protein–protein interactions through methods such as co-immunoprecipitation (co-IP), pull-down assays, crosslinking, label transfer, and far–western blot analysis is critical to understand protein function and the biology of the cell.

It is required to understand the function of a protein includes: Protein sequence and structure, Evolutionary history and conserved sequences, Expression profile, Post-translational modifications, Interactions with other proteins, Intracellular localization.

The PPIs can be classified into different groups based upon their functional and structural properties i.e. stable or transient, and both types of interactions can be either strong or weak. Hemoglobin and core RNA polymerase are examples of stable interactions. These are associated with the proteins that are purified as multi-subunit complexes, and the subunits of these complexes can be identical or different. Transient interactions are expected to control the majority of cellular processes (Heavy BAD protein–protein interaction).

The quantitative effects of protein interactions have been outlined as follows:

Alter the kinetic properties of enzymes, which may be the result of subtle changes in substrate binding or allosteric effects, Create a new binding site, typically for small effector molecules, Inactivate or destroy a protein, Allow for substrate channeling by moving a substrate between domains or subunits, resulting ultimately in an intended end product, Serve a regulatory role in either an upstream or a downstream event, Change the specificity of a protein for its substrate through the interaction with different binding partners, e.g., demonstrate a new function that neither protein can exhibit alone [2].

Common methods to analyze the various types of protein interactions are given below:

Co-immunoprecipitation (co-IP): Co-IP is conducted in essentially the same manner as an immunoprecipitation (IP) of a single protein, except that the target protein precipitated by the antibody called “bait” is used to co-precipitate a binding partner, or "prey", from a lysate.

Pull-down assays: These assays are very similar in methodology to co-immunoprecipitation because of the use of beaded support to purify interacting proteins.

Crosslinking protein interaction analysis: Crosslinking interacting proteins is an approach to stabilize or permanently adjoin the components of interaction complexes.

Label transfer protein interaction analysis: It crosslinking interacting molecules (i.e., bait and prey proteins) with a labeled crosslinking agent and then cleaving the linkage between the bait and prey so that the label remains attached to the prey.

Far–western Blot Analysis: Protein–protein interactions are detected by incubating electrophoresed proteins with a purified, tagged bait protein instead of a target protein-specific antibody, respectively [2,3].

REFERENCES

1. https://genomemedicine.biomedcentral.com/articles/10.1186/gm441
2. https://www.thermofisher.com/in/en/home/life-science/protein-biology/protein-biology-learning-center/protein-biology-resource-library/pierce-protein-methods/overview-protein-protein-interaction-analysis.html
3. https://www.intechopen.com/books/protein-protein-interaction-assays/introductory-chapter-protein-protein-interactions-and-assays

Correspondence to: Susan Williams, Managing Editor, Journal of Proteomics & Bioinformatics, Spain, Tel: +44 7480022449; E-mail: proteomics@peerreviewedjournals.com

Received Date: August 10, 2020, **Accepted Date:** August 17, 2020, **Published Date:** August 24, 2020

Citation: Williams S (2020) Editorial on Protein-Protein Interactions. J Proteomics Bioinform 10: 8. doi: 10.35248/0974-276X.1000517