

Identifying Post-Translational Modification Crosstalks for Breast Cancer

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Abstract

Post-translational modifications (PTMs) of proteins play substantial roles in the gene regulation of cell physiological functions and in the generation of major diseases. However, the majority of existing studies only explored a certain PTM of proteins, while very few have investigated the PTMs of two or more domains and the effects of their interactions. In this study, after collecting data regarding a large number of breast cancer-related and validated PTMs, a sequence and domain analysis of breast cancer proteins was carried out using bioinformatics methods. Then, protein-protein interaction network-related tools were applied in order to determine the crosstalks between the PTMs of the proteins. Finally, statistical and functional analyses were conducted to identify more modification sites of domains and proteins that may interact with at least two or more PTMs. In addition to exploring the associations between the interactive effects of PTMs, the present study also provides important information that would allow biologists to further explore the regulatory pathways of biological functions and related diseases.

Keyword : Post-translational modification; Crosstalk; Sequence analysis; Breast cancer