

Towards quantitative and conditional mapping of yeast and human protein-protein interactions

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The Genome Project is a powerful resource to the community but prediction of a protein's function and their impact on diseases remains a challenging task. To compensate this problem, many studies have been conducted to provide comprehensive information on proteins, including protein-protein interactions. However, these efforts cost a lot of time and resource; further, there is a lack of studies integrating the strength of interactions (a quantitative measurement) with the biological conditions where the interaction would naturally occur. Here, we developed a strategy, by which we construct a two-dimensional (quantitative and condition) map of budding yeast and human's protein interactome. Using the in-house Barcode Fusion Genetics-Yeast Two-Hybrid (BFG-Y2H) technique, we focused on mapping the quantitative interactions of ~6,000 yeast proteins and ~20,000 human proteins by fast and convenient single experiment and identified ~4,000 interactions for yeast. Further, we began to apply the same strategy to assess the protein-protein interactions in yeast but under six different physiological conditions like DNA damage and heat shock. The aforementioned map will be the first resource in a eukaryote to associate quantitative and biological conditions on proteins. In the long term, this tool will provide new clues for the development of complementary assays in multicellular organisms. Enabling the creation of this interaction screen will renew interest in the biomedical research field of protein-protein interactions and provide new resources for the development of diseases therapies.