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Affinity-purification mass spectrometry and bioinformatic analysis for deciphering the protein interactome: looking for needles in a haystack?

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Abstract

In the last years, the study of protein interactomes, meaning the complex map of molecular interactions among proteins, genes, and RNA, has gained increasing popularity. The ability of mass spectrometry to identify thousands of proteins as well as to quantify protein expression and post-translational modifications using labelling technologies has proven the invaluable in deciphering the whole proteome of an organism. In order to study the protein interactome, researcher biologists need comprehensive tools that allow analysis of bias, reproducibility, statistical significance and biologically significant pattern in the data set. Thus, genomic catalogues of protein-protein interactions are a rich source of information to explore the relationships between proteins. A variety of bioinformatic software have been released to allow biologists to compile novel molecular pathways and networks. Here, two examples of protein interactome analysis are compared; the analysis of protein interacting with the interferon-induced, double-stranded RNA-activated protein kinase (PKR) and those interacting with the 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1, isoform b (PI-PLCβ1b), within the nuclear compartment. Advantages and limits of affinity purification mass spectrometry are discussed, along with data analysis redundancy and statistical reproducibility. Moreover, analysis of protein interaction networks, the integration of data and the comparison of results from different bioinformatic programs, are reported.

Biography

Manuela Piazzi received her Ph.D in 2009 from the University of Bologna. Following the completion of her PhD, she initiated her post-doctoral studies in Mass Spectrometry analysis in the laboratory of Anthony Whetton at the Universsity of Manchester, School of Enabling Science (UK), before returning to the University of Bologna, cellular Signaling laboratory, under the direction of Lucio Cocco. Currently, she is a Researcher Assistant Professor at the University of Bologna, where she is responsible for the Mass Spectrometry-Proteomic Unit of the Cell Biology Laboratory, Rizzoli Orthopedic Institute, Bologna. She has published more than 10 papers in peer-reviewed journals.