
Introduction

"Genome-scale analyses have allowed us to progress beyond the studies of gene expression, to the level of individual components of a given process by providing global information about functional connections between genes, mRNAs and their regulatory proteins. Such analyses have greatly increased our understanding of the interplay between different events in gene regulation that have previously highlighted unappreciated functional connections, including coupling between nuclear and cytoplasmic processes. Overall, these studies enhance our understanding of how the various components of the eukaryotic cell function as a system, to allow both coordination and versatility in gene expression" (Komili et al. 2008).

With the post-genome era, the proteomics study of direct analysis of proteins has become more and more important (James et al. 1997). Identification of the type of modification and its location in a protein structure often provides crucial information for understanding the function or regulation of a given protein in the biological pathways (Zhu et al. 2003).

Phosphorylation is one of the most important protein modifications, by which many different cellular responses and biological processes are regulated.

Protein-localization data provide valuable information in elucidating eukaryotic protein function (Zhu et al. 2003). Protein trafficking between nucleus and cytoplasm is fundamentally important in cell regulation. As such, the nuclear import and export are pivotal in orchestrating the activities of the key regulators of the cell cycle (Zhou et al. 2003).

"The discovery of regulatory networks is an important aspect in the post-genomic research. The process requires integrated efforts of experimental and computational strategies by employing the system's biology approach" (Li et al. 2008).

This book describes the new biochip nano-gold antibody-microarray tube, which was developed with the incorporation of protein localization and computation technologies for setting-up signaling pathways, where the information of discovery is also conveyed through various illustrations and tables, from which the reader can not only learn new technologies, but also gain knowledge about the protein localization, signaling pathways and protein relationships.