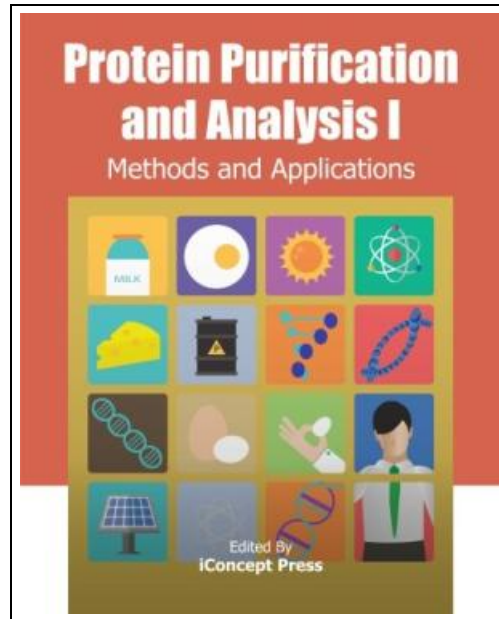


Protein Purification and Analysis I: Methods and Applications



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Createspace, United States, 2013. Paperback. Book Condition: New. 254 x 203 mm. Language: English . Brand New Book ***** Print on Demand *****.Chapter 1 is a review of the bioinformatics literature on protein-protein interactions (PPIs). A protein-protein interaction network (PPIN) is a collection of PPIs, often deposited in online databases. PPINs may complement other datasets, such as protein structural information. Chapter 2 describes the usability and advantages of the micro-patterning technique to study protein-protein interactions in a live cell context. It summarizes results achieved so far, discusses latest technical developments and describes potential future applications. Chapter 3 describes a strategy for identification of protein peptides cross-linked to radiolabeled RNA derivatives in specific complexes of proteins or ribonucleoproteins with these derivatives. This strategy is alternative to the identification based on mass-spectrometry and can be used for determination of protein sites involved in interactions with specific RNAs when mass-spectrometry is not applicable. Chapter 4 describes biochemical methods for assessing interaction between distinct ligand-gated channels. This chapter proposes also methods to examine functional impact of these receptor-receptor interactions in the nervous system. Chapter 5 proposes a statistical approach based on Structural Equation Modeling, in combination with step-wise factor analysis, to infer protein-DNA interactions for gene transcriptional control in the absence of protein information. Such approach only uses gene expression profiles. Chapter 6 describes procedures for the biochemical analysis of amyloid proteins in transgenic *Drosophila*, specifically the prion protein. The authors show that protocols from the mammalian literature can be easily adapted and scaled to these small flies and by ensuring robust expression of the prion protein and proper handling of these delicate samples. Chapter 7 discusses DEAD-box proteins. DEAD-box protein family members participate in many aspects of RNA metabolism, particularly in the ATP-driven disruption of secondary structures of RNA. Genes coding for these...



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