Preface

Often defined as "the unicellular human" and "everybody's favorite fungus," the baker's yeast *Saccharomyces cerevisiae* has long been considered one of the most highly studied model organisms in the study of basic cellular processes. Along with this notion, yeast-based functional genomics and proteomics technologies, developed over the past decade, have contributed greatly to our understanding of bacterial, yeast, fly, worm, and human gene functions. More than 1,000 different papers and hundreds of reviews dealing with functional genomics and proteomics in yeast have appeared, but no comprehensive yeast-based functional genomics and proteomics textbook has yet been written and published. This book aims to be the standard textbook in the field of yeast-based functional genomics and proteomics and should serve as a stand-alone protocols handbook suitable for daily use in research laboratories. It includes recent advanced protocols in addition to major basic yeast-based functional genomics and proteomics techniques. In this way, both yeast researchers and those who wish to use yeast as a model system for functional genomics and proteomics will find this book useful.

Chapter "Comparative Genome Hybridization on Tiling Microarrays to Detect Aneuploidies in Yeast" serves as an introduction in how to use DNA microarrays to detect copy number variations in yeast. Chapter "Identification of Transcription Factor Targets by Phenotypic Activation and Microarray Expression Profiling in Yeast" describes in detail a methodology showing how overexpression of all yeast transcription factors combined with DNA microarray expression profiling and data analysis can be used to identify DNA-binding sequences for transcription factors. Chapter "SGAM: An Array-Based Approach for High-Resolution Genetic Mapping in *Saccharomyces cerevisiae*" contains state-of-the-art protocols for one of the best-known yeast functional genomics techniques, the synthetic genetic array (SGA) analysis, and focuses on a specific SGA application for high-resolution genetic mapping, referred to as SGA mapping (SGAM). Chapter "Reporter-Based Synthetic Genetic Array Analysis: A Functional Genomics Approach for Investigating the Cell Cycle in *Saccharomyces cerevisiae*" describes a modification of the SGA, termed reporter-based SGA (R-SGA) analysis, and its application in studying the expression of all yeast genes under a particular condition. Chapter "The Fidgety Yeast: Focus on High-Resolution Live Yeast Cell Microscopy" gives an excellent insight into experimental strategies for live yeast cell imaging, geared towards imaging-based large-scale screens, whereas Chapter "A Genomic Approach to Yeast Chronological Aging" describes a novel functional genomics approach for quantitatively measuring the yeast chronological life span. Chapters "Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways" and "Identification of Inhibitors of Chromatin Modifying Enzymes Using the Yeast Phenotypic Screens" contain series of protocols that were essentially invented to study drug action in yeast and thus set up a foundation for yeast-based chemical genomics approaches. Chapter "Exploiting Yeast Genetics to Inform Therapeutic Strategies for Huntington's Disease" shows a perfect example of how yeast functional genomics approaches can efficiently be used to study a devastating human neurodegenerative disorder, Huntington's disease. Chapter "Global Proteomic Analysis of *Saccharomyces cerevisiae*

Identifies Molecular Pathways of Histone Modifications" describes a proteomics method, the global proteomic analysis in *S. cerevisiae* (GPS), for the global analysis of the molecular machinery required for proper histone modifications. Chapters "Systematic Characterization of the Protein Interaction Network and Protein Complexes in *Saccharomyces cerevisiae* Using Tandem Affinity Purification and Mass Spectrometry," "Protein Microarrays," "Analysis of Protein–Protein Interactions Using Array-Based Yeast Two-Hybrid Screens," and "Analysis of Membrane Protein Complexes Using the Split-Ubiquitin Membrane Yeast Two-Hybrid System" contain a collection of protocols for studying protein complexes and protein–protein interactions such as tandem affinity purification (TAP) linked to mass spectrometry, protein microarrays, the array-based yeast two-hybrid approach, and membrane yeast two-hybrid (MYTH) system. Protocols described in the last chapter aim to describe how computational analyses help us to understand the yeast proteome.

Finally, I wish to take this opportunity to thank all authors for their great commitment, cooperation, and contributions that made my first editing job easier. I also wish to express my sincere thanks to Dr. John M. Walker for providing guidance on how to generate this book.

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