
Preface

Unicellular yeast cells have been traditionally used as models of lower eukaryotic organisms and the study of yeast has made tremendous contributions to our understanding of life and cellular metabolism. In particular, the budding yeast *Saccharomyces cerevisiae* is the first organism whose entire genome sequence was determined. This has greatly facilitated and expedited our efforts aiming at deciphering functions of the entire genome of approximately 6200 genes. As a consequence, the functionally unknown genes have decreased from two-thirds of the genome in 1994 to less than 40% today. We are confident that in another decade, the functions of the vast majority of yeast genes will be uncovered, with new functions added to previously described genes as well.

Technological advances are the major force driving yeast research in a race that out-competes perhaps any other rival organisms. Since publication of the first edition of *Yeast Protocols* in 1996, many new techniques have been invented and original protocols improved or refined. This second edition should serve as a stand-alone protocols handbook suitable for daily use in research laboratories. It includes recent advanced protocols in addition to the major basic techniques. Hence, both yeast research laboratories and those researchers who wish to use yeast as a host to study their favorite genes from other organisms will find this book useful.

Chapter 1 serves as a start-up kit for those who are not yet experienced with yeast to learn basic handling techniques. Chapters 2–6 describe how to isolate subcellular components, including organelles and macromolecules. Chapters 7–11 contain a collection of protocols for basic cellular and molecular analysis specific for yeast cells.

Perhaps the greatest advantages of using budding yeast for genetic analysis are its powerful genome manipulation and mutant selection systems. Chapters 12–15 describe both traditional and advanced protocols, as well as novel approaches that create conditional mutant phenotypes. Chapters 16–23 contain a series of protocols that were essentially invented in yeast cells to study genetic interactions, DNA and chromatin metabolism, and gene expression. I want to point out that some of the protocols in the above chapters are challenging, and may take time to develop proficiency in, but the authors have done an excellent job of providing sufficient details to make them reproducible. Protocols in the last four chapters aim to study foreign genes and gene products in yeast cells, although they can also be used to analyze native yeast genes and gene products.

Finally, I wish to take this opportunity to thank all authors for their initial commitment, cooperation, and contributions that made my first editing job a pleasant experience. I also wish to express my sincere thanks to Michelle

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