

Preface

In this laboratory manual, we have tried to capture basic techniques in yeast molecular genetics and cell biology, methodologies for functional genomics, some approaches to computational analysis, and the use of relevant databases. Our hope is that this information will serve as a starting point for the next phase of yeast analysis, which will include such areas as the emerging field of synthetic biology. We anticipate that the combination of the methods described here and new methods undoubtedly to come will allow the yeast community to assemble the first comprehensive and working model of a cell.

It is fitting that this book is published by Cold Spring Harbor Laboratory Press, given the critical role that Cold Spring Harbor Laboratory has long played in the yeast community. In particular, CSHL established the Yeast Genetics Course in 1970, which continues to this day. Many leaders in the field embarked on their careers as yeast geneticists after taking this course, catalyzing the growth of a remarkable community of researchers who focused on using yeast as a model system to understand the eukaryotic cell. Over the years, CSHL Press has produced several notable publications on budding yeast. The two-volume monograph *The Molecular Biology of the Yeast Saccharomyces*, published in 1981 and 1982, highlighted research advances in genome dynamics, metabolism, and gene expression—many of which were catalyzed by the then-recent development of robust methods for yeast transformation and genome manipulation. In the following decade, the monograph was updated with *The Molecular and Cellular Biology of the Yeast Saccharomyces*, a three-volume series published in 1991, 1992, and 1997 that provided an encyclopedia of fundamental knowledge of yeast biology.

Given the experimental tractability of budding yeast and the collaborative nature of the yeast community, *Saccharomyces cerevisiae* was unsurprisingly the first eukaryotic organism to have its genome sequenced, and that drove the development of numerous functional genomics methods and resources, including DNA microarrays, systematic reverse genetics with genome-wide mutant collections, and technologies for the analysis of the proteome. Throughout, the *Saccharomyces* Genome Database (SGD) led the effort to annotate the yeast genome and continues today to curate all aspects of its postgenome biology. With this history in mind, we hope that the experimental and computational methods described here will assist another generation of yeast researchers to make further progress on our understanding of this wonderful organism.

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