

## PREFACE

### IN ENZYMOLOGY

It has been 8 years since the last volumes on yeast genetics appeared in *Methods in Enzymology* (Guide to Yeast Genetics and Molecular and Cell Biology; Volumes 350, 351). At that time, *Saccharomyces cerevisiae* was already acknowledged to be the most advanced system for the exploration of basic questions in cell biology. The existence of a small, well-annotated genome, together with simple and facile genetics and a wealth of functional tools, was propelling new discoveries at an unprecedented rate. Predictably, the number of completely uncharacterized genes has since dwindled from roughly one-third to just a few handfuls. Harder to foresee then, however, was how these new tools would qualitatively change the way one could attack biological questions, rapidly ushering in the "postgenomic" era. Suddenly the experimental world became virtually finite. Interested in how the ER makes a particular lipid? One no longer had to carry out an open-ended search hoping to find a few key players and bootstrap one's way through the pathway. Instead, one could immediately focus on the systematic exploration of several hundred genes whose products localize to that organelle. This targeted exploration could in turn be enormously facilitated by the ready availability of comprehensive collections of null or compromised alleles and tagged genes, exploiting rapid methods for genetic crosses and quantitative phenotypic characterization of the candidates. Of comparable impact is the ability to then transition from a function-centered point of view (i.e., the identification of players important for a cellular process of interest) to one in which the full sets of processes that a given gene impacts can be systematically explored, derived from the functional and physical interactions with other gene products. This new paradigm has already pointed to many novel and unanticipated cellular functions.

In the present volume, we have documented many of the major experimental and analytical advances that have catalyzed this change. Additionally, we have highlighted a variety of powerful improvements in biochemical and cytological approaches. Finally, the volume concludes with basic primers on other yeasts, including *Schizosaccharomyces pombe* as well as the clinically relevant *Cryptococcus neoformans* and *Candida albicans*. Yeast is the best characterized eukaryotic cell and will likely remain so for the foreseeable future. The next exciting frontier to consider is how the availability of a complete wiring diagram will inform our understanding of how the cell functions as an integrated machine.