Methods in ENZYMOLOGY

Volume 350

Guide to Yeast Genetics and Molecular and Cell Biology Part B

Edited by

Christine Guthrie

Gerald R. Fink

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Volume 350

GUIDE TO YEAST GENETICS AND MOLECULAR AND CELL BIOLOGY

Part B

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Guide to Yeast Genetics and Molecular and Cell Biology

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Preface

Volumes 350 and 351 of *Methods in Enzymology,* "Guide to Yeast Genetics and Molecular and Cell Biology," Parts B and C, reflect the enormous burst of information on *Saccharomyces cerevisiae* since publication of Part A, Volume 194. The ten years between these publications witnessed the emergence of *Saccharomyces cerevisiae* as the most technically advanced experimental organism, extending its versatility as a system to drug discovery, cancer research, and aging. As the first eukaryotic genome to be completely sequenced (April 1996), yeast provided the inaugural view of the basic functions common to all nucleated cells. The availability of the complete yeast genome sequence (∼13 mbp) coupled with facile databases that are easily accessible on the internet quickly fueled the discovery of new techniques such as two hybrid analysis, transcriptional and protein arrays, and sophisticated microscopic techniques, all of which have completely changed the landscape of today's biology. Because of these neoteric advances, Volumes 350 and 351 contain chapters on proteomics and genomics that provide convenient links to reliable sites on the internet. These information-based tools extend the power intrinsic to the traditional yeast genetic system. This vibrancy is evident in the creation of a library containing a null allele for each of the 6100 yeast genes predicted to encode a protein of 100 amino acids or more. This library permits a comprehensive screen of all such genes in the genome for any loss of function phenotype without the biases of random mutant hunts.

These remarkable advances like a searchlight in a cave also reveal many unexplored areas. Some are technical; there is still no reliable method for obtaining pure yeast nuclei. And of the 6000 genes in the genome there are ∼35% whose function is not known. Other unexplored areas are of a more theoretical nature. Though we know much about the information coding capacity of yeast genomic DNA there are many molecules whose information content is unknown. The work on yeast prions shows that some proteins contain heritable information not coded in the DNA. How widespread is this phenomenon? Do the lipids, polysaccharides, and RNA molecules passed mitotically from mother to daughter cell or through meiosis to the progeny also exist in alternative states that influence phenotype? It is our hope that the techniques recounted in these volumes will help answer these many questions.

CHRISTINE GUTHRIE
GERALD R. FINK

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