

Preface

More than 612 bacterial, 51 archaeal, 1283 mitochondrial, 122 plastid, 47 fungal, and 82 higher eukaryote genomes have now been fully sequenced (<http://www.genomeonline.org/>), and in consequence, a wealth of sequence data has become available in the various public and private data banks. Notwithstanding the massively accumulated genome sequence information, an impressive number of additional pro- and eukaryotic genomes are currently being sequenced (some 1752 bacterial, 91 archaeal, and 908 eukaryotic genomes, plus an additional 116 metagenomes). The speed of whole genome sequencing is ever-increasing and will surpass any predictions of the past, given the available series of novel second- and third-generation sequencing technologies such as picoliter pyrosequencing (454 Life Sciences, see *Nature* (2005) 437: 376–380), the 1G Genetic Analyzer System manufactured by Solexa, the SOLiD system developed by Applied Biosystems, or the truly single-molecule sequencing platform produced by Helicos Biosciences, to name but a few. And with the increased speed of sequencing, more and more sequence data will swamp the data banks.

While the genome sequences will inform us of the precise genome size, the gross and fine genome architecture, various parameters such as e.g. the GC content, the distribution of various sequence elements (e.g. microsatellites, transposons and retrotransposons) and putative open reading frames (among many other features), the identification of regulatory sequences (promoters, enhancers, silencers) and of genes themselves still poses an extraordinary, mostly bioinformatic challenge. However, the functions of the various sequence elements still remain largely obscure. For example, of the 20–25 000 putative human genes, only about 30% encode proteins with known functions. The situation looks much worse for other animals, not to mention plants. Therefore, a great deal of analyses will necessarily be devoted to the *functions of all sequence elements* of a genome, and this enormous task will be handled by what has been coined *functional genomics*, and will be the focus of the so-called post-genomic era.

The present book *The Handbook of Plant Functional Genomics (Concepts and Protocols)* follows the unexpectedly successful and well received first book *The Handbook of Plant Genome Mapping* in the Wiley-VCH series of *Handbooks of Plant*

Genome Analysis. The present second handbook compiles all techniques presently developed for the various functional genomics approaches, presents informative introductions to each chapter, and robust and ready-to-go laboratory protocols written by internationally renowned experts in their research fields. Although the Handbook focuses on *plant* functional genomics, some promising techniques that have been successfully introduced into the field of medicine are also included, some of which may be new to plant biologists. Yet the potential of these technologies may well catalyze plant research. In any case, they reflect the present state-of-the-art in functional genomics generally.

The editors very much appreciate that all the authors have contributed excellent chapters, and expect that this book *The Handbook of Plant Functional Genomics (Concepts and Protocols)* will reproduce the worldwide success of the first handbook in this series.

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