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## Preface

We would like to use this opportunity to say a few words about how and why this book emerged. Our story goes back to the early 2000s at Integrated Genomics Inc., in Chicago, when we embarked on a project fostered by Michael Fonstein to establish a high-throughput approach to systematically probe the relative importance (contribution to fitness) of genes in *Escherichia coli* under a variety of growth conditions. Since Fred Blattner's and, later, Hirotada Mori's groups were pursuing the gene-by-gene knockout strategy, we chose to adopt a complementary "transposomics" approach. This technique, if successfully implemented in set conditions, could be expanded toward comparative studies in multiple conditions and potentially in other species of clinical and industrial importance. We were convinced that a *comparative approach* would become a key to the successful analysis of gene essentiality data, just as it had proved to be valuable in other genomic techniques. This triggered the idea for this book, which was to bring together various research groups that developed and applied a variety of techniques for genome-scale analysis of gene essentiality in diverse microorganisms. We believed that it would not only provide guidance for future studies but also further the establishment of comparative analysis of gene essentiality as an important addition to the Systems Biology toolbox.

This book sends a message to new investigators that gene essentiality technology already exists in various implementations, ready for immediate application to numerous fundamental and practical tasks. Despite remaining hurdles, many technical problems have already been addressed and resolved due to ingenuity and persistence of pioneering research groups, many of which have contributed to this book. Still, this technology is not yet available as an off-the-shelf service. Hence, this book provides researchers with a first-stop guide for choosing the most appropriate strategy for their planned essentiality studies. Experimental and computational aspects are equally important in genome-scale gene essentiality analysis, as in all other genomic technologies, and we attempted to reflect both of these aspects in the book.

We are deeply grateful to all contributors who agreed to share their valuable experience in developing and applying this revolutionary methodology. We hope that their efforts (as well as patience and tolerance during the entire time between inception and publication of this book) will be rewarded by the utility and impact of this volume on the anticipated rapid progress of gene essentiality studies. We would especially like to thank John Walker for his inspiration and guidance in preparation of this book and Cindy Cook for her valuable help with technical editing and handling the manuscripts.

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