
Preface

This book is an update of the previously published book *Microbial Essential Genes* in this series. In the first eight chapters, we cover two main types of approaches that have been widely used to determine essential genes: single-gene knockouts and transposon mutagenesis, in both prokaryotes and *Candida albicans*. Since the last edition was published, we have seen significant advancement in the computational predictions of microbial essential genes. In the next seven chapters, we cover four main types of approaches: comparative genomics, supervised machine learning, constraint-based methods, and corrections of transposon mutagenesis data. We also present databases and servers that are often used in studying gene essentiality.

Finally, I would like to thank all the authors for the contributions. I would also like to thank Dr. John Walker. Without his encouragement and guidance, I would not have been able to complete this book.

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