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Nota di contenuto	Title page; Copyright page; Contents; Foreword; Preface; Contributors; 1: Classical Strain Improvement; 1.0 Introduction; 1.1 The Approach Defined; 1.2 Mutagenesis; 1.2.1 Numerical Considerations in Screen Design; 1.2.2 Random Genetic Drift; 1.2.3 Forced Mutagenesis; 1.2.4 Strain Mating; 1.3 Genotypic Landscapes; 1.4 Screening; 1.4.1 Rational Screens; 1.4.2 Random Screens; 1.4.3 Screening Platforms; 1.5 Conclusions; References; 2: Tracer-Based Analysis of Metabolic Flux Networks; 2.0 Introduction; 2.1 Setting Up a Stoichiometric Network Model; 2.2 Small-Scale Models versus Genome Scale Models 2.3 Network Analysis: Maximum Theoretical Yield2.4 (Stoichiometric) Metabolic Flux Analysis; 2.5 Carrying Out a Labeling Experiment; 2.6 MEASURING ISOTOPE LABELING PATTERNS; 2.7 Tracer-Based MFA; 2.8 Validating Metabolic Flux Networks; 2.9 Conclusions; Acknowledgments; References; 3: Integration of "Omics" Data with Genome-Scale Metabolic Models; 3.0 Introduction; 3.1 Genome-Scale

Metabolic Networks; 3.2 Constraint-Based Modeling Theory; 3.3 Current Analysis of Omics Data; 3.4 New Approaches to Developing Model Constraints; 3.5 Use of Gene Expression Data in Metabolic Models
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Sommario/riassunto

This book highlights current trends and developments in the area of engineering strains. The book details the current and future tools used in the production of bulk chemicals and biofuels from renewable biomass using green technologies. Complex phenotypes are traits in a microbe that requires multiple genetic changes to be modulated simultaneously in the microorganism's DNA. Knowing what those genetic changes are for a given trait and how to make those changes in the most efficient way forms the motivation behind writing this book. This book explains the newer tools to develop and enable engi
