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Nota di contenuto	Pathogenomics; Foreword; Contents; Preface; List of Contributors; Color Plates; I Methods; 1 Bioinformatics: Data Mining Among Genome Sequences; 1.1 Systematic Genome Analysis of Pathogens as a Basis for Pharmacogenomic Strategies; 1.2 Direct Sequence Annotation Tools for Functional Genomics; 1.3 Identification of Protein Function; 1.4 Obtaining Protein Information from a Domain Server; 1.5 Pathway Analysis; 1.6 Network Analysis; 1.7 Adaptation in Time and to Stimuli; 1.7.1 Experimental Design for Microarray Analysis; 1.7.2 Data Analysis; 1.8 Pathogen-Specific Challenges 1.9 Pathogen Adaptation Potential1.10 The Fight Against Resistance; 1.11 Drug Design and Antibiotics; 1.12 Annotation Platforms Suitable for Pathogenomics; 1.13 Conclusions; 2 Transcriptome Analysis: Towards a Comprehensive Understanding of Global Transcription Activity; 2.1 Introduction; 2.2 Development of Transcriptomics; 2.2.1

From Genomics to Functional Genomics; 2.2.2 From Gene to Whole Genome; 2.3 Introducing the Microarray; 2.3.1 What Is a Microarray?; 2.3.2 The Affymetrix Gene Chip; 2.3.3 The Spotted Microarray; 2.4 Microarray Methods; 2.4.1 Experimental Design 2.4.1.1 Type of Experiment 2.4.1.2 Replicates; 2.4.2 RNA Extraction; 2.4.3 Labeling/Reverse Transcription; 2.4.4 Hybridization; 2.4.5 Scanning; 2.5 Data Normalization and Analysis; 2.5.1 Image Quantification; 2.5.2 Data Processing; 2.5.3 Data Analysis; 2.5.3.1 Detection of Differential Expression; 2.5.3.2 Pattern Recognition; 2.5.3.3 Graphical Representations; 2.5.6 Microarray Analysis Tools; 2.5.7 Microarray Follow-Up; 2.5.8 Data Storage and Reanalysis; 2.6 Transcriptomics: Where We Are Now and What's to Come 3 Physiological Proteomics of *Bacillus subtilis* and *Staphylococcus aureus*: Towards a Comprehensive Understanding of Cell Physiology and Pathogenicity 3.1 Introduction; 3.2 Proteomics of *Bacillus subtilis*: The Gram-positive Model Organism; 3.2.1 The Vegetative Proteome; 3.2.2 Proteomes of Nongrowing Cells: Proteomic Signatures of Stress/Starvation Stimuli; 3.3 Physiological Proteomics of *Staphylococcus aureus*; 3.3.1 The Postgenome Era of *S. aureus*; 3.3.2 Proteomes of Growing and Nongrowing Cells; 3.3.3 Extracellular Proteins and Pathogenicity Networks 3.4 Outlook: Second Generation Proteomics and New Fields in *S. aureus* Physiology and Infection Biology 4 Impact of Genome Sequences on Mutational Analysis of Fungal and Bacterial Pathogens; 4.1 The Long Road from Sequence to Function; 4.2 Classical Genetics Still at the Forefront in the Postgenome Era; 4.2.1 Reverse Genetics; 4.2.2 Transposon Mutagenesis; 4.3 Genome-Scale Mutational Analyses; 4.3.1 *Saccharomyces cerevisiae*; 4.3.2 Bacterial Workhorses: *E. coli* and *Bacillus subtilis*; 4.3.3 Bacterial Pathogens; 4.3.3.1 *Mycoplasma* Species; 4.3.3.2 *Pseudomonas aeruginosa* 4.3.3.3 *Staphylococcus aureus*

Sommario/riassunto

The first book on this young, highly dynamic, and expanding field. This comprehensive, interdisciplinary text focuses on those pathogenic bacteria that are of high scientific and public health interest, yet which also display great potential for the development of new diagnostic, prophylactic and therapeutic procedures. The authors cover all aspects of pathogenomics, including methods, genomics and applications. In addition, the ongoing development of genome, transcriptome, proteome and bioinformatic analyses of pathogenic microorganisms and their host interactions makes for a comprehens