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Nota di contenuto	Proteomics of Microbial Pathogens; Table of Contents; Preface Proteomics of microbial pathogens; 1 Genome and proteome analysis of Chlamydia; 1.1 Introduction; 1.1.1 Chlamydia biology; 1.1.1.1 Diseases; 1.1.1.2 The developmental cycle; 1.2 Chlamydia genomes; 1.2.1 Sequenced Chlamydia genomes; 1.2.2 Chlamydial genes; 1.2.3 Genome comparison; 1.3 Proteome analysis of Chlamydia; 1.3.1 Early Chlamydia proteome studies; 1.3.2 C. trachomatis proteome studies; 1.3.3 C. pneumoniae proteome studies; 1.3.4 Identification of secreted proteins by comparative proteomics; 1.3.5 Proteome studies of comc 1.3.6 Proteome comparison of S. trachomatis serovars1.3.7 Proteome analysis of growth conditions; 1.3.8 Considerations in proteomics; 1.4 Concluding remarks; 2 Helicobacter pylori vaccine development based on combined subproteome analysis; 2.1 Introduction; 2.2 Classical whole-cell inactivated Helicobacter vaccines; 2.3 Subunit Helicobacter vaccines: Conventional antigen selection; 2.4 Subunit Helicobacter vaccines: Global antigen selection based on proteomics; 2.4.1 Proteomics as a tool for antigen characterization; 2.4.2 The Helicobacter proteome

2.4.3 Criteria for promising antigen candidates
2.4.4 Identification of protective antigens based on multiple criteria; 2.5 Concluding remarks;
3 Towards a comprehensive understanding of Bacillus subtilis cell physiology by physiological proteomics; 3.1 Introduction; 3.2 Subproteomes vs. the total theoretical proteome; 3.3 The vegetative proteome of growing cells; 3.4 Proteomes of nongrowing cells - the adaptational network; 3.5 Proteomic signatures - tools for microbial physiology and their practical application; 3.6 Transcriptomics vs. proteomics - towards a second generation of proteomics
3.7 The interactome
3.8 The secretome; 3.9 Post-translational modifications; 3.10 Protein quality control/protein degradation at a proteomic scale; 3.11 Gene expression network - horizontal and vertical approach; 3.12 Concluding remarks; 4 Web-accessible proteome databases for microbial research; 4.1 Introduction; 4.2 Materials and methods; 4.2.1 Data generation and data storage; 4.2.2 Software tools; 4.3 Results and discussion; 4.3.1 Data management, analysis and presentation; 4.3.2 2D-PAGE database; 4.3.3 ICAT-LC/MS database; 4.3.4 FUNC_CLASS database; 4.3.5 Data analysis and visualization
4.4 Concluding remarks
5 A targeted proteomics approach to the rapid identification of bacterial cell mixtures by matrix-assisted laser desorption/ionization mass spectrometry; 5.1 Introduction; 5.2 Materials and methods; 5.2.1 Chemicals; 5.2.2 Bacillus strains; 5.2.3 Vegetative cell digestion; 5.2.4 MALDI-TOF MS and unimolecular decomposition product ion analysis; 5.2.5 Database searches and identification of Bacillus species; 5.3 Results and discussion; 5.3.1 On-probe tryptic digestion of bacterial cells; 5.3.1.1 Bacillus subtilis 168; 5.3.1.2 Bacillus globigii and sphaericus 14577
5.3.1.3 Bacillus cereus Tand anthracis Sterne

Sommario/riassunto

Containing proven, high-quality research articles selected from the popular Proteomics journal, this is a current overview of the latest research into the proteomics analysis of microbial pathogens as well as several review articles.
