

1. Record Nr.	UNINA9910449970503321
Autore	Foster James
Titolo	Programmer's ultimate security deskref [[electronic resource] /] / James C. Foster, Stephen C. Foster
Pubbl/distr/stampa	Rockland, MA, : Syngress Publishing, c2004
ISBN	1-281-05630-8 9786611056308 0-08-048045-4
Descrizione fisica	1 online resource (609 p.)
Altri autori (Persone)	FosterStephen C
Disciplina	005.8
Soggetti	Computer programming Computer security Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes index.
Nota di contenuto	Cover; About the Book; Contents; Foreword; Programmer's Ultimate Security DeskRef: ASP; Programmer's Ultimate Security DeskRef: C; Programmer's Ultimate Security DeskRef: C++; Programmer's Ultimate Security Desk Ref: C#; Programmer's Ultimate Security Desk Ref: ColdFusion; Programmer's Ultimate Security Desk Ref: JavaScript; Programmer's Ultimate Security DeskRef: JScript; Programmer's Ultimate Security DeskRef: LISP; Programmer's Ultimate Security DeskRef: Perl; Programmer's Ultimate Security DeskRef: PHP; Programmer's Ultimate Security DeskRef: Python Programmer's Ultimate Security DeskRef: VBAProgrammer's Ultimate Security DeskRef: VBScript; Related Titles
Sommario/riassunto	The Programmer's Ultimate Security DeskRef is the only complete desk reference covering multiple languages and their inherent security issues. It will serve as the programming encyclopedia for almost every major language in use.While there are many books starting to address the broad subject of security best practices within the software development lifecycle, none has yet to address the overarching technical problems of incorrect function usage. Most books fail to draw the line from covering best practices security principles to actual code

implementation. This book bridges that gap a

2. Record Nr.	UNIORUON00387649
Autore	Liddell, Henry George
Titolo	A Greek-English Lexicon / compiled by Henry George Liddell and Robert Scott
Pubbl/distr/stampa	Oxford, : at the Clarendon Press, 1968
ISBN	01-986421-4-8
Edizione	[Revised and augmented throughout by Sir Henry Stuart Jones]
Descrizione fisica	xlv, 2042, xi, 153 p. ; 30 cm
Altri autori (Persone)	Scott, Robert
Disciplina	483.21
Soggetti	Lingua greca - Dizionari inglesi
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Rist. della 9. ed. (1925-1940).

3. Record Nr.	UNINA9911020074103321
Autore	Kinter Michael
Titolo	Protein sequencing and identification using tandem mass spectrometry // Michael Kinter, Nicholas E. Sherman
Pubbl/distr/stampa	New York, : Wiley-Interscience, c2000
ISBN	9786610541669 9781280541667 1280541660 9780471231882 0471231886 9780471721987 0471721980
Descrizione fisica	1 online resource (321 p.)
Collana	Wiley-Interscience series on mass spectrometry
Altri autori (Persone)	ShermanNicholas E
Disciplina	572.8/5
Soggetti	Nucleotide sequence Proteins Mass spectrometry
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	PROTEIN SEQUENCING AND IDENTIFICATION USING TANDEM MASS SPECTROMETRY; CONTENTS; Series Preface; Preface; Chapter 1. An Introduction to Protein Sequencing Using Tandem Mass Spectrometry; 1.1. Introduction; 1.2. References; Chapter 2. The Primary Structure of Proteins and a Historical Overview of Protein Sequencing; 2.1. Protein and Peptide Structure; 2.2. Edman Degradation; 2.2.1. The Edman Reaction; 2.2.2. Incorporation of the Edman Degradation Reaction into Automated Protein Sequenators; 2.2.3. Edman Degradation in Proteomic Research; 2.3. Tandem Mass Spectrometry 2.3.1. A Brief History of the Application of Mass Spectrometry to Protein Sequencing2.3.2. Sequence Analysis of Peptides Using Electron Ionization Mass Spectrometry; 2.3.3. The Utilization of Fast Atom Bombardment with Tandem Mass Spectrometry to Sequence Peptides; 2.3.4. Internal Sequence Analysis of Proteins Using Electrospray Ionization-Tandem Mass Spectrometry and Matrix-Assisted Laser

Desorption/Ionization-Time-of-Flight Mass Spectrometry; 2.4. Summary; 2.5. References; Chapter 3. Fundamental Mass Spectrometry; 3.1. An Overview of the Instrumentation; 3.2. Ionization Methods 3.2.1. Electrospray Ionization 3.2.2. Nanospray and Microspray Ionization; 3.2.3. Matrix-Assisted Laser Desorption/Ionization; 3.3. Mass Analyzers; 3.3.1. Fundamental Parameters of Mass Analysis; 3.3.2. Quadrupole Mass Filters (3.20); 3.3.3. Ion Trap Mass Analyzers (3.21-3.23); 3.3.4. Time-of-Flight Mass Analyzers (3.5); 3.4. Tandem Mass Spectrometry; 3.4.1. Collisionally Induced Dissociation; 3.4.2. Tandem Mass Spectrometers; 3.4.3. Types of Tandem Mass Spectrometry Experiments; 3.5. Data Systems; 3.6. Summary; 3.7. References

Chapter 4. Collisionally Induced Dissociation of Protonated Peptide Ions and the Interpretation of Product Ion Spectra 4.1. Introduction; 4.2. Peptide Fragmentation Chemistry; 4.2.1. Collisionally Induced Dissociation of Peptide Ions Formed by Electrospray Ionization; 4.2.2. Fragmentation of Protonated Peptide Ions Formed by Matrix-Assisted Laser Desorption/Ionization; 4.3. Interpretation of the Product Ion Spectra of Tryptic Peptides; 4.3.1. Tabulated Values Used in the Interpretation; 4.3.2. A Strategy for the Interpretation of Product Ion Spectra of Tryptic Peptides 4.3.3. Sample Interpretation Problem Number One 4.3.4. Sample Interpretation Problem Number Two; 4.3.5. A Summary of Interpretation Problems One and Two; 4.3.6. Examples of More Difficult Product Ion Spectra That Cannot Be Completely Interpreted; 4.3.7. Interpretation of Product Ion Spectra from Triply Charged Ions; 4.4. Summary; 4.5. References; Chapter 5. Basic Polyacrylamide Gel Electrophoresis; 5.1. Introduction; 5.2. The Principles of Gel Electrophoresis; 5.2.1. Protein Movement and Separation; 5.2.2. Protein Detection 5.3. The Basic Steps in a Polyacrylamide Gel Electrophoresis Experiment

Sommario/riassunto

How to design, execute, and interpret experiments for protein sequencing using mass spectrometry The rapid expansion of searchable protein and DNA databases in recent years has triggered an explosive growth in the application of mass spectrometry to protein sequencing. This timely and authoritative book provides professionals and scientists in biotechnology research with complete coverage of procedures for analyzing protein sequences by mass spectrometry, including step-by-step guidelines for sample preparation, analysis, and data interpretation. Michael Kinter and Nicholas Sherman