

1. Record Nr.	UNISALENTO991003706329707536
Autore	Crespellani, Teresa
Titolo	Dinamica dei terreni per le applicazioni sismiche : [stati di sforzo e deformazione indotti nei terreni dalle azioni sismiche, comportamento del terreno in presenza di carichi dinamici e ciclici, caratterizzazione geotecnica ai fini sismici, misura dei parametri dinamici] / Teresa Crespellani, Johann Facciorusso
ISBN	9788857900421
Descrizione fisica	xii, 355 p. ; 28 cm
Collana	Collana di geotecnica e ingegneria geotecnica ; 1
Altri autori (Persone)	Facciorusso, Johannauthor
Disciplina	624.15
Soggetti	Engineering geology - Seismic zones
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes bibliography

2. Record Nr.	UNISA996465927103316
Titolo	Advances in Computer Games [[electronic resource]] : 12th International Conference, ACG 2009, Pamplona, Spain, May 11-13, 2009, Revised Papers / / edited by H. Jaap van den Herik, Pieter Spronck
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38646-0 9786613564382 3-642-12993-5
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XIV, 233 p. 75 illus.)
Collana	Theoretical Computer Science and General Issues, , 2512-2029 ; ; 6048
Disciplina	794.81526
Soggetti	Computer programming Algorithms Artificial intelligence Computer science Computer networks Computer science—Mathematics Discrete mathematics Programming Techniques Artificial Intelligence Theory of Computation Computer Communication Networks Discrete Mathematics in Computer Science Taipei <2005>
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographic references and index.
Nota di contenuto	Adding Expert Knowledge and Exploration in Monte-Carlo Tree Search -- A Lock-Free Multithreaded Monte-Carlo Tree Search Algorithm -- Monte-Carlo Tree Search in Settlers of Catan -- Evaluation Function Based Monte-Carlo LOA -- Monte-Carlo Kakuro -- A Study of UCT and Its Enhancements in an Artificial Game -- Creating an Upper-

Confidence-Tree Program for Havannah -- Randomized Parallel Proof-Number Search -- Hex, Braids, the Crossing Rule, and XH-Search -- Performance and Prediction: Bayesian Modelling of Fallible Choice in Chess -- Plans, Patterns, and Move Categories Guiding a Highly Selective Search -- 6-Man Chess and Zugzwangs -- Solving Kriegspiel Endings with Brute Force: The Case of KR vs. K -- Conflict Resolution of Chinese Chess Endgame Knowledge Base -- On Drawn K-In-A-Row Games -- Optimal Analyses for 3×n AB Games in the Worst Case -- Automated Discovery of Search-Extension Features -- Deriving Concepts and Strategies from Chess Tablebases -- Incongruity-Based Adaptive Game Balancing -- Data Assurance in Opaque Computations.

3. Record Nr.	UNINA9910132410403321
Autore	Barnett Michael
Titolo	2013 3rd International Workshop on Developing Tools as Plug-Ins (TOPI) / / Michael Barnett
Pubbl/distr/stampa	Piscataway, NJ : , : IEEE, , 2013
ISBN	1-4673-6288-3
Descrizione fisica	1 online resource (vi, 52 pages)
Disciplina	005.1
Soggetti	Computer software - Development Database management Plug-ins (Computer programs)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

4. Record Nr.	UNINA9910776386903321
Autore	Küster, Ernst <botanico ; 1874-1953>
Titolo	Anatomie des panaschierten Blattes / von Ernst Kuster
Pubbl/distr/stampa	Berlin, : Gebruder Borntraeger, 1927-
Descrizione fisica	v. : ill. ; 26 cm
Collana	Handbuch der Pflanzenanatomie / begründet von K. Linsbauer ; 8
Disciplina	581.22
Locazione	FAGBC
Collocazione	A PAT 1228-8
Lingua di pubblicazione	Francese
Formato	Materiale a stampa
Livello bibliografico	Monografia
5. Record Nr.	UNINA9911020041503321
Autore	Kaltashov Igor A
Titolo	Mass spectrometry in structural biology and biophysics : architecture, dynamics, and interaction of biomolecules / / Igor A. Kaltashov, Stephen J. Eyles
Pubbl/distr/stampa	Wiley, 2012
ISBN	9786613620118 9781280590283 1280590289 9781118232118 1118232119 9781118232125 1118232127
Edizione	[2nd ed.]
Descrizione fisica	1 online resource (312 p.)
Collana	Wiley series on mass spectrometry
Altri autori (Persone)	EylesStephen J
Disciplina	610.28/4
Soggetti	Mass spectrometry Biophysics Biomolecules - Spectra
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	MASS SPECTROMETRY IN STRUCTURAL BIOLOGY AND BIOPHYSICS: Architecture, Dynamics, and Interaction of Biomolecules; CONTENTS; Preface to the Second Edition; Preface to the First Edition; 1 General Overview of Basic Concepts in Molecular Biophysics; 1.1 Covalent Structure of Biopolymers; 1.2 Noncovalent Interactions and Higher Order Structure; 1.2.1 Electrostatic Interaction; 1.2.2 Hydrogen Bonding; 1.2.3 Steric Clashes and Allowed Conformations of the Peptide Backbone: Secondary Structure; 1.2.4 Solvent--Solute Interactions, Hydrophobic Effect, Side-Chain Packing, and Tertiary Structure; 1.2.5 Intermolecular Interactions and Association: Quaternary Structure; 1.3 The Protein Folding Problem; 1.3.1 What Is Protein Folding?; 1.3.2 Why Is Protein Folding So Important?; 1.3.3 What Is the Natively Folded Protein and How Do We Define a Protein Conformation?; 1.3.4 What Are Non-Native Protein Conformations?: Random Coils, Molten Globules, and Folding Intermediates; 1.3.5 Protein Folding Pathways; 1.4 Protein Energy Landscapes and the Folding Problem; 1.4.1 Protein Conformational Ensembles and Energy Landscapes: Enthalpic and Entropic Considerations; 1.4.2 Equilibrium and Kinetic Intermediates on the Energy Landscape; 1.5 Protein Dynamics and Function; 1.5.1 Limitations of the Structure--Function Paradigm; 1.5.2 Protein Dynamics under Native Conditions; 1.5.3 Is Well-Defined Structure Required for Functional Competence?; 1.5.4 Biomolecular Dynamics and Binding from The Energy Landscape Perspective; 1.5.5 Energy Landscapes Within a Broader Context of Nonlinear Dynamics: Information Flow and Fitness Landscapes; 1.6 Protein Higher Order Structure and Dynamics from A Biotechnology Perspective; References; 2 Overview of Traditional Experimental Arsenal to Study Biomolecular Structure and Dynamics; 2.1 X-Ray Crystallography; 2.1.1 Fundamentals; 2.1.2 Crystal Structures at Atomic and Ultrahigh Resolution; 2.1.3 Crystal Structures of Membrane Proteins; 2.1.4 Protein Dynamics and X-Ray Diffraction; 2.2 Solution Scattering Techniques; 2.2.1 Static and Dynamic Light Scattering; 2.2.2 Small-Angle X-Ray Scattering; 2.2.3 Cryo-Electron Microscopy; 2.2.4 Neutron Scattering; 2.3 NMR Spectroscopy; 2.3.1 Heteronuclear NMR; 2.3.2 Hydrogen Exchange by NMR; 2.4 Other Spectroscopic Techniques; 2.4.1 Cumulative Measurements of Higher Order Structure: Circular Dichroism; 2.4.2 Vibrational Spectroscopy; 2.4.3 Fluorescence: Monitoring Specific Dynamic Events; 2.5 Other Biophysical Methods to Study Macromolecular Interactions and Dynamics; 2.5.1 Calorimetric Methods; 2.5.2 Analytical Ultracentrifugation; 2.5.3 Surface Plasmon Resonance; 2.5.4 Size Exclusion Chromatography (Gel Filtration); 2.5.5 Electrophoresis; 2.5.6 Affinity Chromatography; References; 3 Overview of Biological Mass Spectrometry; 3.1 Basic Principles of Mass Spectrometry; 3.1.1 Stable Isotopes and Isotopic Distributions; 3.1.2 Macromolecular Mass: Terms and Definitions
Sommario/riassunto	The definitive guide to mass spectrometry techniques in biology and biophysics The use of mass spectrometry (MS) to study the architecture and dynamics of proteins is increasingly common within the biophysical community, and Mass Spectrometry in Structural Biology and Biophysics: Architecture, Dynamics, and Interaction of

Biomolecules, Second Edition provides readers with detailed, systematic coverage of the current state of the art. Offering an unrivalled overview of modern MS-based armamentarium that can be used to solve the most challenging problems in biophysics, structural biol
