1. Record Nr. UNISALENTO991001044579707536

Autore	Oustinoff, Michael
Titolo	La traduction / Michael Oustinoff, maitre de conférences à l'Université de Paris III - Sorbonne Nouvelle
Pubbl/distr/stampa	Paris : Presses Universitaires de France, 2003
ISBN	2130534341
Edizione	[Prima edizione: 2003, novembre]
Descrizione fisica	127 p. ; 17 cm
Collana	Que Sais-Je?
Soggetti	Traduzione ed interpretazione
Lingua di pubblicazione	Francese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index

2. Record Nr. UNINA9910781195503321

Autore	Terzuolo Eric R
Titolo	Nato and weapons of mass destruction [[electronic resource]] : regional alliance, global threats / / Eric Terzuolo
Pubbl/distr/stampa	London ; ; New York, : Routledge, 2006
ISBN	1-134-18099-3 1-282-59587-3 9786612595875 0-203-96395-4
Descrizione fisica	1 online resource (224 p.)
Collana	Contemporary security studies
Disciplina	327.1745
Soggetti	Weapons of mass destruction
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	BOOK COVER; TITLE; COPYRIGHT; CONTENTS; ACKNOWLEDGMENTS; ABBREVIATIONS; INTRODUCTION; 1 A NEW COGNIZANCE OF THE WMD THREAT; 2 THE WASHINGTON SUMMIT INITIATIVE ON WMD; 3 FROM 11 SEPTEMBER TO THE PRAGUE SUMMIT; 4 NATO AND THE IRAQ INTERVENTION; 5 NATO'S FUTURE IN AN AGE OF NEW THREATS; NOTES; SELECTED BIBLIOGRAPHY; INDEX
Sommario/riassunto	NATO was hugely successful in facing off the Soviet Union during the Cold War. But has it been equally successful in addressing the ""new threats"" of the post-Cold War era? This new study assesses the organization's political and military initiatives, and how its outreach to Russia, Ukraine, and other countries in the Euro-Atlantic and Mediterranean regions, devoted considerable attention to WMD proliferation risks. It also probes the political factors, both inside and outside NATO, as well as resource constraints, which have limited the alliance's ""added value"" in the inte

3. Record Nr. UNINA9910817720203321

Autore	Nguyen Ken <1975->
Titolo	Multiple biological sequence alignment : scoring functions, algorithms and applications / / Ken Nguyen, Xuan Guo, Yi Pan
Pubbl/distr/stampa	Hoboken, New Jersey : , : John Wiley & Sons, Inc., , 2016
ISBN	1-119-27245-9 1-119-27375-7 1-119-27376-5
Descrizione fisica	1 online resource (286 p.)
Collana	Wiley series on bioinformatics: computational techniques and engineering
Disciplina	572.8
Soggetti	Sequence alignment (Bioinformatics)
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	Title Page; Copyright; Table of Contents; Preface; Chapter 1: Introduction; 1.1 Motivation; 1.2 The Organization of this Book; 1.3 Sequence Fundamentals; Chapter 2: Protein/DNA/RNA Pairwise Sequence Alignment; 2.1 Sequence Alignment Fundamentals; 2.2 Dot-Plot Matrix; 2.3 Dynamic Programming; 2.4 Word Method; 2.5 Searching Sequence Databases; References; Chapter 3: Quantifying Sequence Alignments; 3.1 Evolution and Measuring Evolution; 3.2 Substitution Matrices and Scoring Matrices; 3.3 GAPS; 3.4 Scoring Multiple Sequence Alignments; 3.5 Circular Sum Score; 3.6 Conservation Score Schemes 3.7 Diversity Scoring Schemes3.8 Stereochemical Property Methods; 3.9 Hierarchical Expected Matching Probability Scoring Metric (HEP); Chapter 4: Sequence Clustering; 4.1 Unweighted Pair Group Method with Arithmetic Mean - UPGMA; 4.2 Neighborhood-Joining Method - NJ; 4.3 Overlapping Sequence Clustering; Chapter 5: Multiple Sequences Alignment Algorithms; 5.1 Dynamic Programming; 5.2 Progressive Alignment; 5.3 Consistency and Probabilistic MSA; 5.4 Genetic Algorithms; 5.5 New Development in Multiple Sequence Alignment Algorithms; 5.6 Test Data and Alignment Methods; 5.7 Results Chapter 6: Phylogeny in Multiple Sequence Alignments6.1 The Tree of

Life; 6.2 Phylogeny Construction; 6.3 Inferring Phylogeny from Multiple Sequence Alignments; Chapter 7: Multiple Sequence Alignment on High-Performance Computing Models; 7.1 Parallel Systems; 7.2 Exiting Parallel Multiple Sequence Alignment; 7.3 Reconfigurable-Mesh Computing Models - (R-Mesh); 7.4 Pairwise Dynamic Programming Algorithms; 7.5 Progressive Multiple Sequence Alignment ON R-Mesh; Chapter 8: Sequence Analysis Services; 8.1 EMBL-EBI: European Bioinformatics Institute
8.2 NCBI: National Center for Biotechnology Information8.3 GenomeNet and Data Bank of Japan; 8.4 Other Sequence Analysis and Alignment Web Servers; 8.5 SeqAna: Multiple Sequence Alignment with Quality Ranking; 8.6 Pairwise Sequence Alignment and Other Analysis Tools; 8.7 Tool Evaluation; Chapter 9: Multiple Sequence for Next-Generation Sequences; 9.1 Introduction; 9.2 Overview of Next Generation Sequence Alignment Algorithms; Chapter 10: Multiple Sequence Alignment for Variations Detection; 10.1 Introduction; 10.2 Genetic Variants; 10.3 Variation Detection Methods Based on MSA
10.4 Evaluation Methodology10.5 Conclusion and Future Work; Chapter 11: Multiple Sequence Alignment for Structure Detection; 11.1 Introduction; 11.2 RNA Secondary Structure Prediction Based on MSA; 11.3 Protein Secondary Structure Prediction Based on MSA; 11.4 Conclusion and Future Work; References; Index; End User License Agreement