

1. Record Nr.	UNISA996387151703316
Titolo	A new declaration of the Lords and Commons in Parliament, in answer to His Majesties letter, dated the 14 day of June; and sent to the lord major, aldermen, and sheriffs of the city of London [[electronic resource]] : as also, concerning His Majesties declaration published at Heyworth-Moore. Together with the vindication of the Parliament, from scandalls which are cast upon them
Pubbl/distr/stampa	London, : Printed for E. Husbands and J. Franck, [June 21, 1642]
Descrizione fisica	7 p
Soggetti	Great Britain History Civil War, 1642-1649 London (England) History 17th century Great Britain Politics and government 1642-1649
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	At head of title: June 21. 1642. Other editions have title: A declaration of the Lords and Commons in Parliament in answer to His Majesties letter. Reproduction of original in: British Library.
Sommario/riassunto	eebo-0018

2. Record Nr.	UNISALENTO991001403889707536
Autore	Agnati, Ulrico
Titolo	Il commento di Bartolo di Sassoferrato alla lex quod Nerva (D. 16,3,32) : introduzione, testi e annotazioni / Ulrico Agnati
Pubbl/distr/stampa	Torino : Giappichelli, c2004
ISBN	8834846680
Descrizione fisica	190 p. ; 24 cm
Disciplina	346.3702
Soggetti	Responsabilit� contrattuale - Diritto romano Bartolo da Sassoferrato Bartolo da Sassoferrato
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

3. Record Nr.	UNISALENTO991003963699707536
Autore	Guarda, Gabriele
Titolo	Guida al giudice unico nella nuova geografia giudiziaria in materia civile : le norme relative all'istituzione del giudice unico di primo grado (D. lgs. 19/2/98 n. 51) coordinate con il D. lgs. 138/99, il D.L. 145/99 e le recentissime disposizioni di attuazione dettate dal Ministero di grazia e giustizia : i nuovi uffici, le nuove competenze, le nuove modalit professionali / Gabriele Guarda ; in allegato un CD-ROM contenente il software per la ricerca dell'ufficio giudiziario competente
Pubbl/distr/stampa	Milano : Giuffrè, 1999
ISBN	8814077401
Descrizione fisica	xii, 212 p. ; 24 cm + 1 CD-ROM
Collana	Cosa & come. Professioni
Disciplina	347.4502
Soggetti	Giudice unico di primo grado - Legislazione
Lingua di pubblicazione	Non definito
Formato	Materiale a stampa
Livello bibliografico	Monografia

4. Record Nr.	UNINA9910791679703321
Autore	Zak Albin
Titolo	I don't sound like nobody : remaking music in 1950s America / / Albin J. Zak III
Pubbl/distr/stampa	Ann Arbor : , : University of Michigan Press, , 2010
ISBN	1-282-88296-1 9786612882968 0-472-02454-X
Descrizione fisica	1 online resource (325 p.)
Collana	Tracking pop
Disciplina	781.640973/09045
Soggetti	Music - United States - 20th century - History and criticism Music trade - United States
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, index, and discography.
Nota di contenuto	Records on the radio -- Shifting currents in the mainstream -- Hustlers and amateurs -- Crossing over -- Surface noise -- "Hail! hail! rock and roll" -- New traditions.
Sommario/riassunto	A definitive study of the most important decade in post-World War II popular music history

5. Record Nr.	UNINA9910484962603321
Titolo	Algorithms for Computational Biology : 8th International Conference, AICoB 2021, Missoula, MT, USA, June 7–11, 2021, Proceedings / / edited by Carlos Martín-Vide, Miguel A. Vega-Rodríguez, Travis Wheeler
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2021
ISBN	3-030-74432-9
Edizione	[1st ed. 2021.]
Descrizione fisica	1 online resource (177 pages)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 12715
Disciplina	570.285
Soggetti	Data structures (Computer science) Information theory Artificial intelligence Image processing - Digital techniques Computer vision Computer science - Mathematics Mathematical statistics Discrete mathematics Numerical analysis Data Structures and Information Theory Artificial Intelligence Computer Imaging, Vision, Pattern Recognition and Graphics Probability and Statistics in Computer Science Discrete Mathematics in Computer Science Numerical Analysis
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Learning Molecular Classes from Small Numbers of Positive Examples Using Graph Grammars -- Can We Replace Reads by Numeric Signatures? Lyndon Fingerprints as Representations of Sequencing Reads for Machine Learning -- Exploiting Variable Sparsity in Computing Equilibria of Biological Dynamical Systems by Triangular

Decomposition -- A Recovery Algorithm and Pooling Designs for One-Stage Noisy Group Testing Under the Probabilistic Framework -- Novel Phylogenetic Network Distances Based on Cherry Picking -- Best Match Graphs with Binary Trees -- Scalable and Accurate Phylogenetic Placement Using pplacer-XR -- Comparing Methods for Species Tree Estimation with Gene Duplication and Loss -- Reversal Distance on Genomes with Different Gene Content and Intergenic Regions Information -- Reversals Distance Considering Flexible Intergenic Regions Sizes -- Improved DNA-versus-Protein Homology Search for Protein Fossils -- The Maximum Weight Trace Alignment Merging Problem.

Sommario/riassunto

This book constitutes the proceedings of the 8th International Conference on Algorithms for Computational Biology, AICoB 2020, was planned to be held in Missoula, MT, USA in June 2021. Due to the Covid-19 pandemic, AICoB 2020 and AICoB 2021 were merged and held on these dates together. AICoB 2020 proceedings were published as LNBI 12099. The 12 full papers included in this volume were carefully reviewed and selected from 22 submissions. They were organized in topical sections on genomics, phylogenetics, and RNA-Seq and other biological processes. The scope of AICoB includes topics of either theoretical or applied interest, namely: sequence analysis; sequence alignment; sequence assembly; genome rearrangement; regulatory motif finding; phylogeny reconstruction; phylogeny comparison; structure prediction; compressive genomics; proteomics: molecular pathways, interaction networks, mass spectrometry analysis; transcriptomics: splicing variants, isoform inference and quantification, differential analysis; next-generation sequencing: population genomics, metagenomics, metatranscriptomics, epigenomics; genome CD architecture; microbiome analysis; cancer computational biology; and systems biology.
