1.	Record Nr.	UNINA9910789705303321
	Autore	Davis Thadious M. <1944->
	Titolo	Southscapes [[electronic resource]] : geographies of race, region, and literature / / Thadious M. Davis
	Pubbl/distr/stampa	Chapel Hill, N.C., : University of North Carolina Press, c2011
	ISBN	1-4696-0255-5
		0-8078-6932-5
	Descrizione fisica	1 online resource (471 p.)
	Collana	New directions in southern studies
	Disciplina	810.9/896073075
	Soggetti	American literature - African American authors
		American literature - Southern States
		Geographical perception in literature
		African Americans - Race identity
		Place (Philosophy) in literature
	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	Introduction. A map of the territory -- Southscapes : race, region, and reclamation -- Poverty and porches: controversial Mississippi -- Power and profession : Richard Wright's Mississippi and its expatriate legacies -- Politics and paysans : multicultural Louisiana and the space of the Crolit -- Parishes and prisons : Ernest Gaines's Louisiana and its North Carolina kin space -- Alice Walker matters : the fruits of gendered space.
	Sommario/riassunto	In this innovative approach to southern literary cultures, Thadious Davis analyzes how black southern writers use their spatial location to articulate the vexed connections between society and environment, particularly under segregation and its legacies. Basing her analysis on texts by Ernest Gaines, Richard Wright, Alice Walker, Natasha Trethewey, Olympia Vernon, Brenda Marie Osbey, Sybil Kein, and others, Davis reveals how these writers reconstitute racial exclusion as creative black space, rather than a site of trauma and resistance. Utilizing the social and political separation epi

2.	Record Nr.	UNINA9910143885603321
	Titolo	DNA Computing : 8th International Workshop on DNA Based Computers, DNA8, Sapporo, Japan, June 10-13, 2002, Revised Papers / / edited by Masami Hagiya, Azuma Ohuchi
	Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2003
	ISBN	3-540-36440-4
	Edizione	[1st ed. 2003.]
	Descrizione fisica	1 online resource (XII, 344 p.)
	Collana	Lecture Notes in Computer Science, , 0302-9743 ; ; 2568
	Disciplina	511.3
	Soggetti	Logic, Symbolic and mathematical
		Computers
		Algorithms
		Artificial intelligence
		Bioinformatics
		Mathematical Logic and Foundations
		Computation by Abstract Devices
		Algorithm Analysis and Problem Complexity
		Artificial Intelligence
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	Bibliographic Level Mode of Issuance: Monograph
	Nota di bibliografia	Includes bibliographical references and index.
	Nota di contenuto	Self-assembly and Autonomous Molecular Computation -- Self-assembling DNA Graphs -- DNA Nanotubes: Construction and Characterization of Filaments Composed of TX-tile Lattice -- The Design of Autonomous DNA Nanomechanical Devices: Walking and Rolling DNA -- Cascading Whiplash PCR with a Nicking Enzyme -- Molecular Evolution and Application to Biotechnology -- A PNA-mediated Whiplash PCR-based Program for In Vitro Protein Evolution -- Engineering Signal Processing in Cells: Towards Molecular Concentration Band Detection -- Applications to Mathematical Problems -- Temperature Gradient-Based DNA Computing for Graph Problems with Weighted Edges -- Shortening the Computational Time of the Fluorescent DNA Computing -- How Efficiently Can Room at the Bottom Be Traded Away for Speed at the Top? -- Hierarchical DNA

Memory Based on Nested PCR -- Binary Arithmetic for DNA Computers -- Implementation of a Random Walk Method for Solving 3-SAT on Circular DNA Molecules -- Version Space Learning with DNA Molecules -- DNA Implementation of Theorem Proving with Resolution Refutation in Propositional Logic -- Universal Biochip Readout of Directed Hamiltonian Path Problems -- Nucleic Acid Sequence Design -- Algorithms for Testing That Sets of DNA Words Concatenate without Secondary Structure -- A PCR-based Protocol for In Vitro Selection of Non-crosshybridizing Oligonucleotides -- On Template Method for DNA Sequence Design -- From RNA Secondary Structure to Coding Theory: A Combinatorial Approach -- Stochastic Local Search Algorithms for DNA Word Design -- NACST/Seq: A Sequence Design System with Multiobjective Optimization -- A Software Tool for Generating Non-crosshybridizing Libraries of DNA Oligonucleotides -- Theory -- Splicing Systems: Regularity and Below -- On the Computational Power of Insertion-Deletion Systems -- Unexpected Universality Results for Three Classes of P Systems with Symport/Antiport -- Conformons-P Systems -- Parallel Rewriting P Systems with Deadlock -- A DNA-based Computational Model Using a Specific Type of Restriction Enzyme -- Time-Varying Distributed H Systems of Degree 2 Can Carry Out Parallel Computations.

Sommario/riassunto	Biomolecular computing has emerged as an interdisciplinary ?eld that draws - gether chemistry, computer science, mathematics, molecular biology, and physics. Our knowledge on DNA nanotechnology and biomolecular computing increases exponentially with every passing year. The international meeting on DNA Based Computers has been a forum where scientists with di?erent backgrounds, yet sharing a common interest in biomolecular computing, meet and present their latest results. Continuing this tradition, the 8th International Meeting on DNA Based Computers (DNA8) focuses on the current theoretical and experimental results with the greatest impact. Papers and poster presentations were sought in all areas that relate to b- molecular computing, including (but not restricted to): algorithms and appli-tions, analysis of laboratory techniques/theoretical models, computational p- cesses in vitro and in vivo, DNA-computing-based biotechnological applications, DNA devices, error evaluation and correction, in vitro evolution, models of biomolecular computing (using DNA and/or other molecules), molecular - sign, nucleic acid chemistry, and simulation tools. Papers and posters with new experimental results were particularly encouraged. Authors who wished their work to be considered for either oral or poster presentation were asked to select from one of two submission "tracks": – Track A - Full Paper – Track B - One-Page Abstract For authors with late-breaking results, or who were submitting their manuscript to a scienti?c journal, a one-page abstract, rather than a full paper, could be submitted in Track B. Authors could (optionally) include a preprint of their full paper, for consideration only by the program committee.