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| 1. Record Nr.           | UNISA996465328903316   |
| Titolo                  | DNA Computing [[electronic resource] ] : 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                | Mathematical logic<br>Computers<br>Algorithms<br>Artificial intelligence<br>Bioinformatics<br>Mathematical Logic and Foundations<br>Computation by Abstract Devices<br>Algorithm Analysis and Problem Complexity<br>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.

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### Sommario/riassunto

Biomolecular computing has emerged as an interdisciplinary field that draws together 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 different 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 biomolecular computing, including (but not restricted to): algorithms and applications, analysis of laboratory techniques/theoretical models, computational processes 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 design, 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 scientific 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.

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