Giancarlo Mauri

List of Publications by Year
in descending order

362	6,392	94269	128067
papers	citations	37	60
		h-index	g-index

400	400	400	6188
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Weeder Web: discovery of transcription factor binding sites in a set of sequences from co-regulated genes. Nucleic Acids Research, 2004, 32, W199-W203.	6.5	435
2	An algorithm for finding signals of unknown length in DNA sequences. Bioinformatics, 2001, 17, S207-S214.	1.8	279
3	USE-Net: Incorporating Squeeze-and-Excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets. Neurocomputing, 2019, 365, 31-43.	3.5	185
4	GAN-based synthetic brain MR image generation. , 2018, , .		173
5	Fuzzy Self-Tuning PSO: A settings-free algorithm for global optimization. Swarm and Evolutionary Computation, 2018, 39, 70-85.	4.5	171
6	Combining Noise-to-Image and Image-to-Image GANs: Brain MR Image Augmentation for Tumor Detection. IEEE Access, 2019, 7, 156966-156977.	2.6	138
7	MTGO: PPI Network Analysis Via Topological and Functional Module Identification. Scientific Reports, 2018, 8, 5499.	1.6	103
8	Uniform solutions to SAT and Subset Sum by spiking neural P systems. Natural Computing, 2009, 8, 681-702.	1.8	101
9	CAPRI: efficient inference of cancer progression models from cross-sectional data. Bioinformatics, 2015, 31, 3016-3026.	1.8	90
10	MedGA: A novel evolutionary method for image enhancement in medical imaging systems. Expert Systems With Applications, 2019, 119, 387-399.	4.4	85
11	Solving NP-Complete Problems Using P Systems with Active Membranes. , 2001, , 289-301.		82
12	From protein-protein interactions to protein co-expression networks: a new perspective to evaluate large-scale proteomic data. Eurasip Journal on Bioinformatics and Systems Biology, 2017, 2017, 6.	1.4	81
13	Algorithmic methods to infer the evolutionary trajectories in cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4025-34.	3.3	80
14	DYNAMICAL PROBABILISTIC P SYSTEMS. International Journal of Foundations of Computer Science, 2006, 17, 183-204.	0.8	79
15	In silico representation and discovery of transcription factor binding sites. Briefings in Bioinformatics, 2004, 5, 217-236.	3.2	74
16	Cellular automata: From a theoretical parallel computational model to its application to complex systems. Parallel Computing, 2001, 27, 539-553.	1.3	71
17	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. PLoS Computational Biology, 2019, 15, e1006733.	1.5	70
18	MoD Tools: regulatory motif discovery in nucleotide sequences from co-regulated or homologous genes. Nucleic Acids Research, 2006, 34, W566-W570.	6.5	67

#	Article	IF	Citations
19	A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect. PLoS Computational Biology, 2017, 13, e1005758.	1.5	64
20	Cellular automata in fuzzy backgrounds. Physica D: Nonlinear Phenomena, 1997, 105, 105-120.	1.3	57
21	Inferring Tree Causal Models of Cancer Progression with Probability Raising. PLoS ONE, 2014, 9, e108358.	1.1	57
22	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	1.3	54
23	Integration of mRNA Expression Profile, Copy Number Alterations, and microRNA Expression Levels in Breast Cancer to Improve Grade Definition. PLoS ONE, 2014, 9, e97681.	1.1	53
24	Social media and mobile applications in chronic disease prevention and management. Frontiers in Psychology, 2015, 6, 567.	1.1	53
25	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. International Journal of Molecular Sciences, 2017, 18, 274.	1.8	50
26	RNAProfile: an algorithm for finding conserved secondary structure motifs in unaligned RNA sequences. Nucleic Acids Research, 2004, 32, 3258-3269.	6.5	48
27	RESEARCH FRONTIERS OF MEMBRANE COMPUTING: OPEN PROBLEMS AND RESEARCH TOPICS. International Journal of Foundations of Computer Science, 2013, 24, 547-623.	0.8	48
28	Automated Prostate Gland Segmentation Based on an Unsupervised Fuzzy C-Means Clustering Technique Using Multispectral T1w and T2w MR Imaging. Information (Switzerland), 2017, 8, 49.	1.7	48
29	Modeling and stochastic simulation of the Ras/cAMP/PKA pathway in the yeast Saccharomyces cerevisiae evidences a key regulatory function for intracellular guanine nucleotides pools. Journal of Biotechnology, 2008, 133, 377-385.	1.9	46
30	Infinite Brain MR Images: PGGAN-Based Data Augmentation forÂTumor Detection. Smart Innovation, Systems and Technologies, 2020, , 291-303.	0.5	46
31	Modelling metapopulations with stochastic membrane systems. BioSystems, 2008, 91, 499-514.	0.9	45
32	Biochemical parameter estimation vs. benchmark functions: A comparative study of optimization performance and representation design. Applied Soft Computing Journal, 2019, 81, 105494.	4.1	45
33	GPU-accelerated simulations of mass-action kinetics models with cupSODA. Journal of Supercomputing, 2014, 69, 17-24.	2.4	44
34	A novel framework for MR image segmentation and quantification by using MedGA. Computer Methods and Programs in Biomedicine, 2019, 176, 159-172.	2.6	43
35	An excursion in reaction systems: From computer science to biology. Theoretical Computer Science, 2012, 454, 95-108.	0.5	42
36	A comparison of machine learning techniques for survival prediction in breast cancer. BioData Mining, 2011, 4, 12.	2.2	41

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37	The Interplay of Intrinsic and Extrinsic Bounded Noises in Biomolecular Networks. PLoS ONE, 2013, 8, e51174.	1.1	41
38	NeXt for neuro‐radiosurgery: A fully automatic approach for necrosis extraction in brain tumor MRI using an unsupervised machine learning technique. International Journal of Imaging Systems and Technology, 2018, 28, 21-37.	2.7	41
39	Solving Numerical NP-Complete Problems with Spiking Neural P Systems. , 2007, , 336-352.		40
40	Evaluating performance and quality of knowledge-based systems: foundation and methodology. IEEE Transactions on Knowledge and Data Engineering, 1993, 5, 204-224.	4.0	39
41	Learning fuzzy rules with tabu search-an application to control. IEEE Transactions on Fuzzy Systems, 1999, 7, 295-318.	6.5	39
42	TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data. Bioinformatics, 2016, 32, 1911-1913.	1.8	39
43	A fully automatic approach for multimodal PET and MR image segmentation in gamma knife treatment planning. Computer Methods and Programs in Biomedicine, 2017, 144, 77-96.	2.6	39
44	Tumor size, stage and grade alterations of urinary peptidome in RCC. Journal of Translational Medicine, 2015, 13, 332.	1.8	38
45	Biowep: a workflow enactment portal for bioinformatics applications. BMC Bioinformatics, 2007, 8, S19.	1.2	36
46	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. Computational Biology and Chemistry, 2016, 62, 60-69.	1.1	36
47	Multilayered cellular automata. Theoretical Computer Science, 1999, 217, 99-113.	0.5	35
48	m-Asynchronous cellular automata: from fairness to quasi-fairness. Natural Computing, 2013, 12, 561-572.	1.8	33
49	Managing chronic pathologies with a stepped mHealth-based approach in clinical psychology and medicine. Frontiers in Psychology, 2015, 06, 407.	1.1	32
50	GTVcut for neuro-radiosurgery treatment planning: an MRI brain cancer seeded image segmentation method based on a cellular automata model. Natural Computing, 2018, 17, 521-536.	1.8	32
51	On-line construction of compact directed acyclic word graphs. Discrete Applied Mathematics, 2005, 146, 156-179.	0.5	31
52	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. Bioinformatics, 2017, 33, i311-i318.	1.8	31
53	Urinary Signatures of Renal Cell Carcinoma Investigated by Peptidomic Approaches. PLoS ONE, 2014, 9, e106684.	1.1	30
54	A GPU-Based Multi-swarm PSO Method for Parameter Estimation in Stochastic Biological Systems Exploiting Discrete-Time Target Series. Lecture Notes in Computer Science, 2012, , 74-85.	1.0	30

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55	Membership problems for regular and context-free trace languages. Information and Computation, 1989, 82, 135-150.	0.5	29
56	On three variants of rewriting P systems. Theoretical Computer Science, 2003, 301, 201-215.	0.5	29
57	Simulation of the Ras/cAMP/PKA pathway in budding yeast highlights the establishment of stable oscillatory states. Biotechnology Advances, 2012, 30, 99-107.	6.0	28
58	cuTauLeaping: A GPU-Powered Tau-Leaping Stochastic Simulator for Massive Parallel Analyses of Biological Systems. PLoS ONE, 2014, 9, e91963.	1.1	28
59	Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power. Journal of Biomedical Informatics, 2018, 87, 37-49.	2.5	28
60	Tau Leaping Stochastic Simulation Method in P Systems. Lecture Notes in Computer Science, 2006, , 298-313.	1.0	28
61	A framework for validating AI in precision medicine: considerations from the European ITFoC consortium. BMC Medical Informatics and Decision Making, 2021, 21, 274.	1.5	28
62	Algorithms for pattern matching and discovery in RNA secondary structure. Theoretical Computer Science, 2005, 335, 29-51.	0.5	27
63	Space complexity equivalence of P systems with active membranes and Turing machines. Theoretical Computer Science, 2014, 529, 69-81.	0.5	27
64	The role of feedback control mechanisms on the establishment of oscillatory regimes in the Ras/cAMP/PKA pathway in S. cerevisiae. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 10.	1.4	26
65	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26
66	Separating some splicing models. Information Processing Letters, 2001, 79, 255-259.	0.4	25
67	Multimodal medical image registration using Particle Swarm Optimization: A review. , 2016, , .		25
68	Monodirectional P systems. Natural Computing, 2016, 15, 551-564.	1.8	25
69	Cancer cell growth and survival as a system-level property sustained by enhanced glycolysis and mitochondrial metabolic remodeling. Frontiers in Physiology, 2012, 3, 362.	1.3	24
70	Membrane Division, Oracles, and the Counting Hierarchy. Fundamenta Informaticae, 2015, 138, 97-111.	0.3	24
71	A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems. Lecture Notes in Computer Science, 2009, , 116-127.	1.0	24
72	Experimenting an approximation algorithm for the LCS. Discrete Applied Mathematics, 2001, 110, 13-24.	0.5	23

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73	Complexity classes for membrane systems. RAIRO - Theoretical Informatics and Applications, 2006, 40, 141-162.	0.5	23
74	Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach. Journal of Computational Biology, 2009, 16, 43-66.	0.8	23
75	A Comparative Study of Four Parallel and Distributed PSO Methods. New Generation Computing, 2011, 29, 129-161.	2.5	23
76	Proteomic profiles of thyroid tumors by mass spectrometry-imaging on tissue microarrays. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 817-827.	1.1	23
77	Evaluation of natural language processing systems: Issues and approaches. Proceedings of the IEEE, 1986, 74, 1026-1035.	16.4	22
78	Application of evolutionary algorithms to protein folding prediction. Lecture Notes in Computer Science, 1998, , 123-135.	1.0	22
79	On the dynamical behavior of chaotic cellular automata. Theoretical Computer Science, 1999, 217, 31-51.	0.5	22
80	An approximation algorithm for the shortest common supersequence problem. , 2001, , .		22
81	PSYSTEMS WITH ACTIVE MEMBRANES WORKING IN POLYNOMIAL SPACE. International Journal of Foundations of Computer Science, 2011, 22, 65-73.	0.8	22
82	Machine learning approaches in MALDI-MSI: clinical applications. Expert Review of Proteomics, 2016, 13, 685-696.	1.3	22
83	LASSIE: simulating large-scale models of biochemical systems on GPUs. BMC Bioinformatics, 2017, 18, 246.	1.2	22
84	Membrane Computing. Lecture Notes in Computer Science, 2004, , .	1.0	22
85	Introducing a Space Complexity Measure for P Systems. International Journal of Computers, Communications and Control, 2014, 4, 301.	1.2	22
86	Computational Intelligence for Parameter Estimation of Biochemical Systems. , 2018, , .		21
87	Detecting similarities among distant homologous proteins by comparison of domain flexibilities. Protein Engineering, Design and Selection, 2007, 20, 285-299.	1.0	20
88	P systems with active membranes: trading time for space. Natural Computing, 2011, 10, 167-182.	1.8	20
89	How interacting pathways are regulated by miRNAs in breast cancer subtypes. BMC Bioinformatics, 2016, 17, 348.	1.2	20
90	Characterising the complexity of tissue P systems with fission rules. Journal of Computer and System Sciences, 2017, 90, 115-128.	0.9	20

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91	Characterizing PSPACE with shallow non-confluent P systems. Journal of Membrane Computing, 2019, 1, 75-84.	1.0	20
92	An application of the theory of free partially commutative monoids: Asymptotic densities of trace languages. Lecture Notes in Computer Science, 1981, , 205-215.	1.0	20
93	Flattening in (Tissue) P Systems. Lecture Notes in Computer Science, 2014, , 173-188.	1.0	20
94	CNN-Based Prostate Zonal Segmentation on T2-Weighted MR Images: AÂCross-Dataset Study. Smart Innovation, Systems and Technologies, 2020, , 269-280.	0.5	20
95	A characterization of the class of functions computable in polynomial time on Random Access Machines. , 1981, , .		19
96	Different expression of Fibrinopeptide A and related fragments in serum of type 1 diabetic patients with nephropathy. Journal of Proteomics, 2010, 73, 593-601.	1.2	19
97	Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs. , 2012, , .		19
98	Computational complexity of finite asynchronous cellular automata. Theoretical Computer Science, 2017, 664, 131-143.	0.5	19
99	Area-based cell colony surviving fraction evaluation: A novel fully automatic approach using general-purpose acquisition hardware. Computers in Biology and Medicine, 2017, 89, 454-465.	3.9	19
100	Simulating Elementary Active Membranes. Lecture Notes in Computer Science, 2014, , 284-299.	1.0	19
101	Sublinear-Space PÂSystems with Active Membranes. Lecture Notes in Computer Science, 2013, , 342-357.	1.0	19
102	Parallel simulation of reactionâ€"diffusion phenomena in percolation processes. Future Generation Computer Systems, 2001, 17, 679-688.	4.9	18
103	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. Natural Computing, 2014, 13, 321-331.	1.8	18
104	Proactive Particles in Swarm Optimization: A self-tuning algorithm based on Fuzzy Logic. , 2015, , .		18
105	Top-k overlapping densest subgraphs: approximation algorithms and computational complexity. Journal of Combinatorial Optimization, 2021, 41, 80-104.	0.8	18
106	On-Line Construction of Compact Directed Acyclic Word Graphs*. Lecture Notes in Computer Science, 2001, , 169-180.	1.0	18
107	New Technologies for the Management and Rehabilitation of Chronic Diseases and Conditions. BioMed Research International, 2015, 2015, 1-2.	0.9	17
108	A Support Vector Machine Classification of Thyroid Bioptic Specimens Using MALDI-MSI Data. Advances in Bioinformatics, 2016, 2016, 1-7.	5.7	17

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109	GPU-powered model analysis with PySB/cupSODA. Bioinformatics, 2017, 33, 3492-3494.	1.8	17
110	Orthology Correction for Gene Tree Reconstruction: Theoretical and Experimental Results. Procedia Computer Science, 2017, 108, 1115-1124.	1.2	17
111	Pathway-based classification of breast cancer subtypes. Frontiers in Bioscience - Landmark, 2017, 22, 1697-1712.	3.0	17
112	Computational Methods for Resting-State EEG of Patients With Disorders of Consciousness. Frontiers in Neuroscience, 2019, 13, 807.	1.4	17
113	Single-cell Digital Twins for Cancer Preclinical Investigation. Methods in Molecular Biology, 2020, 2088, 331-343.	0.4	17
114	Regular splicing languages and subclasses. Theoretical Computer Science, 2005, 340, 349-363.	0.5	16
115	A Comprehensive View of Fitness Landscapes with Neutrality and Fitness Clouds. Lecture Notes in Computer Science, 2007, , 241-250.	1.0	16
116	Non-confluence in divisionless P systems with active membranes. Theoretical Computer Science, 2010, 411, 878-887.	0.5	15
117	Combination of gene expression and genome copy number alteration has a prognostic value for breast cancer. , 2013, 2013, 608-11.		15
118	Combined analysis of chromosomal instabilities and gene expression for colon cancer progression inference. Journal of Clinical Bioinformatics, 2014, 4, 2.	1.2	15
119	A Turing machine simulation by PÂsystems without charges. Journal of Membrane Computing, 2020, 2, 71-79.	1.0	15
120	Modular algebraic nets to specify concurrent systems. IEEE Transactions on Software Engineering, 1996, 22, 689-705.	4.3	14
121	Availability of MudPIT data for classification of biological samples. Journal of Clinical Bioinformatics, 2013, 3, 1.	1.2	14
122	The counting power of P systems with antimatter. Theoretical Computer Science, 2017, 701, 161-173.	0.5	14
123	Surfing on Fitness Landscapes: A Boost on Optimization by Fourier Surrogate Modeling. Entropy, 2020, 22, 285.	1.1	14
124	Elementary Active Membranes Have the Power of Counting. International Journal of Natural Computing Research, 2011, 2, 35-48.	0.5	14
125	Solving the factorization problem with P systems. Progress in Natural Science: Materials International, 2007, 17, 471-478.	1.8	13
126	Complexity aspects of polarizationless membrane systems. Natural Computing, 2009, 8, 703-717.	1.8	13

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127	A study of the neutrality of Boolean function landscapes in genetic programming. Theoretical Computer Science, 2012, 425, 34-57.	0.5	13
128	Reverse engineering of kinetic reaction networks by means of Cartesian Genetic Programming and Particle Swarm Optimization. , 2013, , .		13
129	cupSODA: A CUDA-Powered Simulator of Mass-Action Kinetics. Lecture Notes in Computer Science, 2013, , 344-357.	1.0	13
130	CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETworks. BMC Bioinformatics, 2016, 17, 64.	1.2	13
131	Efficient Simulation of Reaction Systems on Graphics Processing Units. Fundamenta Informaticae, 2017, 154, 307-321.	0.3	13
132	Coupling Mechanistic Approaches and Fuzzy Logic to Model and Simulate Complex Systems. IEEE Transactions on Fuzzy Systems, 2020, 28, 1748-1759.	6.5	13
133	GeneSyn: a tool for detecting conserved gene order across genomes. Bioinformatics, 2004, 20, 1472-1474.	1.8	12
134	Circular splicing and regularity. RAIRO - Theoretical Informatics and Applications, 2004, 38, 189-228.	0.5	12
135	An empirical comparison of parallel and distributed particle swarm optimization methods. , 2010, , .		12
136	CoGNaC: A Chaste Plugin for the Multiscale Simulation of Gene Regulatory Networks Driving the Spatial Dynamics of Tissues and Cancer. Cancer Informatics, 2015, 14s4, CIN.S19965.	0.9	12
137	Kernel Methods: Support Vector Machines. , 2019, , 503-510.		12
138	Using Subtree Crossover Distance to Investigate Genetic Programming Dynamics. Lecture Notes in Computer Science, 2006, , 238-249.	1.0	12
139	Some recursively unsolvable problems relating to isolated cutpoints in probabilistic automata. Lecture Notes in Computer Science, 1977, , 87-94.	1.0	12
140	P Systems with Gemmation of Mobile Membranes. Lecture Notes in Computer Science, 2001, , 136-153.	1.0	12
141	PÂSystems with Elementary Active Membranes: Beyond NP and coNP. Lecture Notes in Computer Science, 2010, , 338-347.	1.0	12
142	A Surveillance System for Early-Stage Diagnosis of Endogenous Diseases by Swarms of Nanobots. Advanced Science Letters, 2010, 3, 345-352.	0.2	12
143	Covering a Graph with Clubs. Journal of Graph Algorithms and Applications, 2019, 23, 271-292.	0.4	12
144	On the power of circular splicing. Discrete Applied Mathematics, 2005, 150, 51-66.	0.5	11

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145	Constant-Space P Systems with Active Membranes. Fundamenta Informaticae, 2014, 134, 111-128.	0.3	11
146	A survey on space complexity of P systems with active membranes. International Journal of Advances in Engineering Sciences and Applied Mathematics, 2018, 10, 221-229.	0.7	11
147	In-Silico Integration Approach to Identify a Key miRNA Regulating a Gene Network in Aggressive Prostate Cancer. International Journal of Molecular Sciences, 2018, 19, 910.	1.8	11
148	A characterization of abstract data as model-theoretic invariants. Lecture Notes in Computer Science, 1979, , 26-37.	1.0	11
149	Pattern Discovery in RNA Secondary Structure Using Affix Trees. Lecture Notes in Computer Science, 2003, , 278-294.	1.0	11
150	Decision Problems for Linear and Circular Splicing Systems. Lecture Notes in Computer Science, 2003, , 78-92.	1.0	11
151	Two Normal Forms for Rewriting P Systems. Lecture Notes in Computer Science, 2001, , 153-164.	1.0	11
152	Copyâ€"Number Alterations for Tumor Progression Inference. Lecture Notes in Computer Science, 2013, , 104-109.	1.0	11
153	Simulation of a bounded symport/antiport P system with Brane calculi. BioSystems, 2008, 91, 558-571.	0.9	10
154	Massive Exploration of Perturbed Conditions of the Blood Coagulation Cascade through GPU Parallelization. BioMed Research International, 2014, 2014, 1-20.	0.9	10
155	Gene switching rate determines response to extrinsic perturbations in the self-activation transcriptional network motif. Scientific Reports, 2016, 6, 26980.	1.6	10
156	HaraliCU: GPU-Powered Haralick Feature Extraction on Medical Images Exploiting the Full Dynamics of Gray-Scale Levels. Lecture Notes in Computer Science, 2019, , 304-318.	1.0	10
157	On the tractability of finding disjoint clubs in a network. Theoretical Computer Science, 2019, 777, 243-251.	0.5	10
158	Fuzzy modeling and global optimization to predict novel therapeutic targets in cancer cells. Bioinformatics, 2020, 36, 2181-2188.	1.8	10
159	A Low-Dose CT-Based Radiomic Model to Improve Characterization and Screening Recall Intervals of Indeterminate Prevalent Pulmonary Nodules. Diagnostics, 2021, 11, 1610.	1.3	10
160	DNA and circular splicing?. Lecture Notes in Computer Science, 2001, , 117-129.	1.0	10
161	Implementing Cellular Automata Based Models on Parallel Architectures: The CAPP Project. Lecture Notes in Computer Science, 1999, , 167-180.	1.0	10
162	An Efficient Simulation of Polynomial-Space Turing Machines by P Systems with Active Membranes. Lecture Notes in Computer Science, 2010, , 461-478.	1.0	10

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163	A study of parallel and distributed particle swarm optimization methods. , 2010, , .		9
164	The l-Diversity problem: Tractability and approximability. Theoretical Computer Science, 2013, 511, 159-171.	0.5	9
165	ACDC: Automated Cell Detection and Counting for Time-Lapse Fluorescence Microscopy. Applied Sciences (Switzerland), 2020, 10, 6187.	1.3	9
166	Discovering Relations Among GO-Annotated Clusters by Graph Kernel Methods. , 2007, , 158-169.		9
167	Quantum Sequential P Systems with Unit Rules and Energy Assigned to Membranes. Lecture Notes in Computer Science, 2006, , 310-325.	1.0	9
168	Gemmating P systems: collapsing hierarchies. Theoretical Computer Science, 2003, 296, 253-267.	0.5	8
169	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. BMC Bioinformatics, 2005, 6, S1.	1.2	8
170	Seasonal variance in P system models for metapopulations. Progress in Natural Science: Materials International, 2007, 17, 392-400.	1.8	8
171	The Genopolis Microarray Database. BMC Bioinformatics, 2007, 8, S21.	1.2	8
172	An application of kernel methods to gene cluster temporal meta-analysis. Computers and Operations Research, 2010, 37, 1361-1368.	2.4	8
173	A toolbox for simpler active membrane algorithms. Theoretical Computer Science, 2017, 673, 42-57.	0.5	8
174	Modeling cell proliferation in human acute myeloid leukemia xenografts. Bioinformatics, 2019, 35, 3378-3386.	1.8	8
175	Shallow laconic P systems can count. Journal of Membrane Computing, 2020, 2, 49-58.	1.0	8
176	Parallel Rewriting P Systems with Deadlock. Lecture Notes in Computer Science, 2003, , 302-314.	1.0	8
177	Fully Automatic Multispectral MR Image Segmentation of Prostate Gland Based on the Fuzzy C-Means Clustering Algorithm. Smart Innovation, Systems and Technologies, 2018, , 23-37.	0.5	8
178	m-Asynchronous Cellular Automata. Lecture Notes in Computer Science, 2012, , 653-662.	1.0	8
179	Telemedicine Home Program in Patients with Cystic Fibrosis: Results after 10 Years. Clinica Terapeutica, 2015, 166, e384-8.	0.2	8
180	Investigating local evolutions in dynamical probabilistic P systems. , 2005, , .		7

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181	BioSimWare: A Software for the Modeling, Simulation and Analysis of Biological Systems. Lecture Notes in Computer Science, 2010, , 119-143.	1.0	7
182	Mutual Information Optimization for Mass Spectra Data Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 934-939.	1.9	7
183	Recent complexity-theoretic results on P systems with active membranes. Journal of Logic and Computation, 2015, 25, 1047-1071.	0.5	7
184	MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy. Computational and Structural Biotechnology Journal, 2020, 18, 993-999.	1.9	7
185	COMBINING IMAGE PROCESSING OPERATORS AND NEURAL NETWORKS IN A FACE RECOGNITION SYSTEM. International Journal of Pattern Recognition and Artificial Intelligence, 1992, 06, 447-467.	0.7	6
186	Nine test tubes generate any RE language. Theoretical Computer Science, 2000, 231, 171-180.	0.5	6
187	MODELING DIFFUSION IN A SIGNAL TRANSDUCTION PATHWAY: THE USE OF VIRTUAL VOLUMES IN P SYSTEMS. International Journal of Foundations of Computer Science, 2011, 22, 89-96.	0.8	6
188	A study on learning robustness using asynchronous 1D cellular automata rules. Natural Computing, 2012, 11, 289-302.	1.8	6
189	G<scp>e</scp>S<scp>to</scp>D<scp>ifferent</scp>: a Cytoscape plugin for the generation and the identification of gene regulatory networks describing a stochastic cell differentiation process. Bioinformatics, 2013, 29, 513-514.	1.8	6
190	Stochastic Hybrid Automata with delayed transitions to model biochemical systems with delays. Information and Computation, 2014, 236, 19-34.	0.5	6
191	mHealth and eHealth for Obesity and Types 2 and 1 Diabetes. Journal of Diabetes Research, 2016, 2016, 1-1.	1.0	6
192	A CUDA-powered method for the feature extraction and unsupervised analysis of medical images. Journal of Supercomputing, 2021, 77, 8514-8531.	2.4	6
193	P System Models for Mechanosensitive Channels. , 2006, , 43-81.		6
194	Regular Languages Generated by Reflexive Finite Splicing Systems. Lecture Notes in Computer Science, 2003, , 134-145.	1.0	6
195	Towards Human Cell Simulation. Lecture Notes in Computer Science, 2019, , 221-249.	1.0	6
196	Clique Editing to Support Case Versus Control Discrimination. Smart Innovation, Systems and Technologies, 2016, , 27-36.	0.5	6
197	A Multi-volume Approach to Stochastic Modeling with Membrane Systems. Natural Computing Series, 2009, , 519-542.	2.2	6
198	Early-Stage Diagnosis of Endogenous Diseases by Swarms of Nanobots: An Applicative Scenario. Lecture Notes in Computer Science, 2010, , 408-415.	1.0	6

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199	Modelling Spatial Heterogeneity and Macromolecular Crowding with Membrane Systems. Lecture Notes in Computer Science, 2010, , 285-304.	1.0	6
200	Hierarchies of parallel rewriting P systems â€" A survey. New Generation Computing, 2004, 22, 331-347.	2.5	5
201	Stochastic Simulations on a Grid Framework for Parameter Sweep Applications in Biological Models. , 2009, , .		5
202	Parallel implementation of efficient search schemes for the inference of cancer progression models. , 2016, , .		5
203	Tissue P Systems with Small Cell Volume. Fundamenta Informaticae, 2017, 154, 261-275.	0.3	5
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