Ion Petre

List of Publications by Year
in descending order

102 papers	990 citations	516215 16 h-index	552369 26 g-index
113 all docs	113 docs citations	113 times ranked	510 citing authors

#	Article	IF	Citations
1	Network analytics for drug repurposing in COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	16
2	Network controllability solutions for computational drug repurposing using genetic algorithms. Scientific Reports, 2022, 12, 1437.	1.6	5
3	Scalable reaction network modeling with automatic validation of consistency in Event-B. Scientific Reports, 2022, 12, 1287.	1.6	1
4	TBMT-02. APOLLO: RAMAN-BASED PATHOLOGY OF MALIGNANT GLIOMA. Neuro-Oncology Advances, 2021, 3, i20-i20.	0.4	0
5	NetControl4BioMed: a web-based platform for controllability analysis of protein–protein interaction networks. Bioinformatics, 2021, 37, 3976-3978.	1.8	3
6	Network Controllability Analysis of Three Multiple-myeloma Patient Genetic Mutation Datasets. Fundamenta Informaticae, 2020, 175, 281-299.	0.3	1
7	Controllability of reaction systems. Journal of Membrane Computing, 2020, 2, 290-302.	1.0	8
8	Network Controllability Analysis of Three Multiple-myeloma Patient Genetic Mutation Datasets. , 2020, , .		0
9	Reaction Systems and Synchronous Digital Circuits. Molecules, 2019, 24, 1961.	1.7	3
10	Refinement-based modeling of the ErbB signaling pathway. Computers in Biology and Medicine, 2019, 106, 91-96.	3.9	1
11	A Computational Model for The Access to Medical Service in a Basic Prototype of a Healthcare System. Fundamenta Informaticae, 2019, 171, 331-343.	0.3	0
12	Structural Target Controllability of Linear Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1217-1228.	1.9	19
13	WEBRSIM: A Web-Based Reaction Systems Simulator. Lecture Notes in Computer Science, 2018, , 170-181.	1.0	3
14	NetControl4BioMed: a pipeline for biomedical data acquisition and analysis of network controllability. BMC Bioinformatics, 2018, 19, 185.	1.2	5
15	A Systems Biology Approach to Identify Mechanisms of Therapy Resistance in Multiple Myeloma. Blood, 2018, 132, 3266-3266.	0.6	0
16	Systems Biology Analysis Identifies Targetable Vulnerability Networks to Proteasome Inhibitors in Multiple Myeloma. Blood, 2018, 132, 950-950.	0.6	0
17	Stepwise construction of a metabolic network in Event-B: The heat shock response. Computers in Biology and Medicine, 2017, 91, 1-12.	3.9	3
18	Tailored Approaches in Drug Development and Diagnostics: From Molecular Design to Biological Model Systems. Advanced Healthcare Materials, 2017, 6, 1700258.	3.9	38

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19	Controlling Directed Protein Interaction Networks in Cancer. Scientific Reports, 2017, 7, 10327.	1.6	55
20	Reaction Systems: A Model of Computation Inspired by the Functioning of the Living Cell. , 2017, , 1-32.		9
21	A Foundational Framework for Step-by-step Model Construction. Fundamenta Informaticae, 2017, 154, 15-24.	0.3	0
22	Multi-Stability, Limit Cycles, and Period-Doubling Bifurcation with Reaction Systems. International Journal of Foundations of Computer Science, 2017, 28, 1007-1020.	0.8	8
23	Complexity of model checking for reaction systems. Theoretical Computer Science, 2016, 623, 103-113.	0.5	27
24	Target Controllability of Linear Networks. Lecture Notes in Computer Science, 2016, , 67-81.	1.0	8
25	Complete characterization for the fit-preserving data refinement of mass-action reaction networks. Theoretical Computer Science, 2016, 641, 11-24.	0.5	4
26	From Computer Science to Biology and Back. Theoretical Computer Science, 2015, 608, 2-3.	0.5	0
27	Dependency graphs and mass conservation in reaction systems. Theoretical Computer Science, 2015, 598, 23-39.	0.5	23
28	The Structure of Elementary Strategies for Gene Assembly in Ciliates. Fundamenta Informaticae, 2015, 138, 145-158.	0.3	0
29	An Excursion Through Quantitative Model Refinement. Lecture Notes in Computer Science, 2015, , 25-47.	1.0	0
30	Reaction System Models for the Heat Shock Response. Fundamenta Informaticae, 2014, 131, 299-312.	0.3	40
31	Fit-Preserving Data Refinement of Mass-Action Reaction Networks. Lecture Notes in Computer Science, 2014, , 204-213.	1.0	6
32	On the Implementation of Quantitative Model Refinement. Lecture Notes in Computer Science, 2014, , 95-106.	1.0	2
33	ODE Analysis of Biological Systems. Lecture Notes in Computer Science, 2013, , 29-62.	1.0	10
34	The Phosphorylation of the Heat Shock Factor as a Modulator for the Heat Shock Response. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1326-1337.	1.9	6
35	Simple gene assembly as a rewriting of directed overlap-inclusion graphs. Theoretical Computer Science, 2012, 454, 30-37.	0.5	0
36	Matrix insertion–deletion systems. Theoretical Computer Science, 2012, 456, 80-88.	0.5	28

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37	Quantitative Model Refinement as a Solution to the Combinatorial Size Explosion of Biomodels. Electronic Notes in Theoretical Computer Science, 2012, 284, 35-53.	0.9	5
38	Quantitative Analysis of the Self-Assembly Strategies of Intermediate Filaments from Tetrameric Vimentin. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 885-898.	1.9	6
39	A Boolean Approach for Disentangling the Roles of Submodules to the Global Properties of a Biomodel. Fundamenta Informaticae, 2012, 116, 51-63.	0.3	0
40	Computational Nature of Gene Assembly in Ciliates. , 2012, , 1233-1280.		6
41	Self-assembly Models of Variable Resolution. Lecture Notes in Computer Science, 2012, , 181-203.	1.0	7
42	Directed Overlap-inclusion Graphs as Representations of Ciliate Genes. Fundamenta Informaticae, 2011, 110, 29-44.	0.3	1
43	Methods for Biochemical Model Decomposition and Quantitative Submodel Comparison. Israel Journal of Chemistry, 2011, 51, 151-164.	1.0	3
44	A simple mass-action model for the eukaryotic heat shock response and its mathematical validation. Natural Computing, 2011, 10, 595-612.	1.8	53
45	Complexity-preserving simulations among three variants of accepting networks of evolutionary processors. Natural Computing, 2011, 10, 429-445.	1.8	9
46	The phosphorylation of the heat shock factor as a modulator for the heat shock response. , 2011, , .		2
47	Extended strings and graphs for simple gene assembly. Theoretical Computer Science, 2010, 411, 730-738.	0.5	1
48	Computing the graph-based parallel complexity of gene assembly. Theoretical Computer Science, 2010, 411, 2359-2367.	0.5	2
49	Accepting splicing systems. Theoretical Computer Science, 2010, 411, 2414-2422.	0.5	13
50	A sequence-based analysis of the pointer distribution of stichotrichous ciliates. BioSystems, 2010, 101, 109-116.	0.9	2
51	Gene assembly in Ciliates. Scholarpedia Journal, 2010, 5, 9269.	0.3	2
52	The parallel complexity of signed graphs: Decidability results and an improved algorithm. Theoretical Computer Science, 2009, 410, 2308-2315.	0.5	3
53	A New Mathematical Model for the Heat Shock Response. Natural Computing Series, 2009, , 411-425.	2.2	8
54	Algebraic Systems and Pushdown Automata. Monographs in Theoretical Computer Science, 2009, , 257-289.	0.6	20

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55	Computational Heuristics for Simplifying a Biological Model. Lecture Notes in Computer Science, 2009, , 399-408.	1.0	0
56	Solutions to computational problems through gene assembly. Natural Computing, 2008, 7, 385-401.	1.8	2
57	Parallel complexity of signed graphs for gene assembly in ciliates. Soft Computing, 2008, 12, 731-737.	2.1	4
58	Patterns of simple gene assembly in ciliates. Discrete Applied Mathematics, 2008, 156, 2581-2597.	0.5	8
59	Graph theoretic approach to parallel gene assembly. Discrete Applied Mathematics, 2008, 156, 3416-3429.	0.5	3
60	Sequential vs. parallel complexity in simple gene assembly. Theoretical Computer Science, 2008, 395, 24-30.	0.5	4
61	Parikh matrices and amiable words. Theoretical Computer Science, 2008, 390, 102-109.	0.5	47
62	Decision problem for shuffled genes. Information and Computation, 2008, 206, 1346-1352.	0.5	5
63	GENE ASSEMBLY MODELS AND BOOLEAN CIRCUITS. International Journal of Foundations of Computer Science, 2008, 19, 1133-1145.	0.8	4
64	Three models for gene assembly in ciliates: a comparison. , 2008, , .		0
65	Summary of the Workshop on Natural Computing and Graph Transformations. Lecture Notes in Computer Science, 2008, , 470-472.	1.0	0
66	COMPUTATIONAL POWER OF INTRAMOLECULAR GENE ASSEMBLY. International Journal of Foundations of Computer Science, 2007, 18, 1123-1136.	0.8	11
67	Self-assembly of strings and languages. Theoretical Computer Science, 2007, 374, 74-81.	0.5	21
68	Complexity Measures for Gene Assembly. Lecture Notes in Computer Science, 2007, , 42-60.	1.0	8
69	Computing Through Gene Assembly. Lecture Notes in Computer Science, 2007, , 91-105.	1.0	2
70	A String-Based Model for Simple Gene Assembly. Lecture Notes in Computer Science, 2007, , 161-172.	1.0	6
71	Invariants of Gene-Assembly in Stichotrichous Ciliates (Invarianten der Gen-Assemblierung in Ciliaten) Tj ETQq1 1 0.784314 rgBT /Overl	0.6	2
72	Periodic and Sturmian languages. Information Processing Letters, 2006, 98, 242-246.	0.4	0

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73	Parallelism in Gene Assembly. Natural Computing, 2006, 5, 203-223.	1.8	15
74	Modelling Simple Operations for Gene Assembly. , 2006, , 361-373.		11
75	Simple Operations for Gene Assembly. Lecture Notes in Computer Science, 2006, , 96-111.	1.0	2
76	Commutation with codes. Theoretical Computer Science, 2005, 340, 322-333.	0.5	11
77	Commutation with Ternary Sets of Words. Theory of Computing Systems, 2005, 38, 161-169.	0.7	9
78	Parallelism in Gene Assembly. Lecture Notes in Computer Science, 2005, , 138-148.	1.0	8
79	Two Models for Gene Assembly in Ciliates. Lecture Notes in Computer Science, 2004, , 89-101.	1.0	5
80	Modelling Gene Assembly in Ciliates. Natural Computing Series, 2004, , 105-124.	2.2	1
81	Computation in Living Cells. Natural Computing Series, 2004, , .	2.2	66
82	GENE ASSEMBLY IN CILIATES PART I: MOLECULAR OPERATIONS. , 2004, , 527-541.		5
83	GENE ASSEMBLY IN CILIATES PART II: FORMAL FRAMEWORKS. , 2004, , 543-557.		8
84	TWO PROBLEMS ON COMMUTATION OF LANGUAGES. , 2004, , 477-493.		10
85	Patterns of Subsets of Rules. Natural Computing Series, 2004, , 131-149.	2.2	0
86	Legal Strings. Natural Computing Series, 2004, , 83-90.	2.2	0
87	Graph Pointer Reduction System. Natural Computing Series, 2004, , 109-117.	2.2	0
88	String Pointer Reduction System. Natural Computing Series, 2004, , 91-98.	2.2	0
89	The Commutation with Codes and Ternary Sets of Words. Lecture Notes in Computer Science, 2003, , 74-84.	1.0	5
90	Formal systems for gene assembly in ciliates. Theoretical Computer Science, 2003, 292, 199-219.	0.5	42

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91	Formal Properties of Gene Assembly: Equivalence Problem for Overlap Graphs. Lecture Notes in Computer Science, 2003, , 202-212.	1.0	4
92	String and graph reduction systems for gene assembly in ciliates. Mathematical Structures in Computer Science, 2002, 12, 113-134.	0.5	43
93	Characterizing the Micronuclear Gene Patterns in Ciliates. Theory of Computing Systems, 2002, 35, 501-519.	0.7	29
94	Conway's problem for three-word sets. Theoretical Computer Science, 2002, 289, 705-725.	0.5	21
95	The Branching Point Approach to Conway's Problem. Lecture Notes in Computer Science, 2002, , 69-76.	1.0	8
96	Patterns of Micronuclear Genes in Ciliates. Lecture Notes in Computer Science, 2002, , 279-289.	1.0	13
97	Tutorial on DNA Computing and Graph Transformation - Computational Nature of Gene Assembly in Ciliates. Lecture Notes in Computer Science, 2002, , 430-434.	1.0	2
98	CIRCULARITY AND OTHER INVARIANTS OF GENE ASSEMBLY IN CILIATES. , 2001, , 81-97.		23
99	Universal and Simple Operations for Gene Assembly in Ciliates. , 2001, , 329-342.		25
100	Recent results on the semilinear formal power series. Bulletin of the Belgian Mathematical Society - Simon Stevin, 2001, 8, .	0.1	0
101	On the Centralizer of a Finite Set. Lecture Notes in Computer Science, 2000, , 536-546.	1.0	15
102	Uniformly Scattered Factors. , 2000, , 187-198.		1