

Jerzy Tiuryn

List of Publications by Year in descending order

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56
papers

1,022
citations

567281

15
h-index

454955

30
g-index

58
all docs

58
docs citations

58
times ranked

1300
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimizing genomic duplication episodes. <i>Computational Biology and Chemistry</i> , 2020, 89, 107260.	2.3	3
2	The Unconstrained Diameters of the Duplication-Loss Cost and the Loss Cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	0
3	Learning signaling networks from combinatorial perturbations by exploiting siRNA off-target effects. <i>Bioinformatics</i> , 2019, 35, i605-i614.	4.1	7
4	Contribution of NtZIP1-Like to the Regulation of Zn Homeostasis. <i>Frontiers in Plant Science</i> , 2018, 9, 185.	3.6	24
5	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2017, 24, 193-199.	1.6	3
6	Romulus: robust multi-state identification of transcription factor binding sites from DNase-seq data. <i>Bioinformatics</i> , 2016, 32, 2419-2426.	4.1	18
7	Enhanceosome transcription factors preferentially dimerize with high mobility group proteins. <i>BMC Systems Biology</i> , 2015, 10, 14.	3.0	2
8	A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. <i>Plant Physiology</i> , 2015, 169, pp.00493.2015.	4.8	101
9	eCAMBer: efficient support for large-scale comparative analysis of multiple bacterial strains. <i>BMC Bioinformatics</i> , 2014, 15, 65.	2.6	21
10	SIZE DISTRIBUTION OF GENE FAMILIES IN A GENOME. <i>Mathematical Models and Methods in Applied Sciences</i> , 2014, 24, 697-717.	3.3	13
11	GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria. <i>BMC Genomics</i> , 2014, 15, S10.	2.8	22
12	Unrooted Tree Reconciliation: A Unified Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 522-536.	3.0	39
13	Bioinformatics and Computational Biology in Poland. <i>PLoS Computational Biology</i> , 2013, 9, e1003048.	3.2	2
14	A Probabilistic Model of Neutral and Selective Dynamics of Protein Network Evolution. <i>Journal of Computational Biology</i> , 2013, 20, 631-642.	1.6	1
15	Inferring Evolutionary Scenarios in the Duplication, Loss and Horizontal Gene Transfer Model. <i>Lecture Notes in Computer Science</i> , 2012, , 83-105.	1.3	4
16	An approach to identifying drug resistance associated mutations in bacterial strains. <i>BMC Genomics</i> , 2012, 13, S23.	2.8	16
17	CAMBer: an approach to support comparative analysis of multiple bacterial strains. <i>BMC Genomics</i> , 2011, 12, S6.	2.8	22
18	Rhythmic Diel Pattern of Gene Expression in Juvenile Maize Leaf. <i>PLoS ONE</i> , 2011, 6, e23628.	2.5	12

#	ARTICLE	IF	CITATIONS
19	Deregulation upon DNA damage revealed by joint analysis of context-specific perturbation data. BMC Bioinformatics, 2011, 12, 249.	2.6	1
20	CAMBerVis: visualization software to support comparative analysis of multiple bacterial strains. Bioinformatics, 2011, 27, 3313-3314.	4.1	2
21	Bi-Billboard: Symmetrization and Careful Choice of Informant Species Results in Higher Accuracy of Regulatory Element Prediction. Journal of Computational Biology, 2011, 18, 809-819.	1.6	0
22	MODEVO: exploring modularity and evolution of protein interaction networks. Bioinformatics, 2010, 26, 1790-1791.	4.1	15
23	Introducing Knowledge into Differential Expression Analysis. Journal of Computational Biology, 2010, 17, 953-967.	1.6	9
24	CAMBer: An approach to support comparative analysis of multiple bacterial strains. , 2010, , .		0
25	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. Molecular Systems Biology, 2009, 5, 287.	7.2	26
26	Phylogeny-guided interaction mapping in seven eukaryotes. BMC Bioinformatics, 2009, 10, 393.	2.6	15
27	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. BMC Bioinformatics, 2009, 10, 82.	2.6	24
28	UIRec: a system for unrooted reconciliation. Bioinformatics, 2007, 23, 511-512.	4.1	31
29	Identification of functional modules from conserved ancestral protein-protein interactions. Bioinformatics, 2007, 23, i149-i158.	4.1	87
30	Evolution of Gene Families Based on Gene Duplication, Loss, Accumulated Change, and Innovation. Journal of Computational Biology, 2007, 14, 479-495.	1.6	8
31	Inferring phylogeny from whole genomes. Bioinformatics, 2007, 23, e116-e122.	4.1	34
32	A DISCRETE MODEL OF EVOLUTION OF SMALL PARALOG FAMILIES. Mathematical Models and Methods in Applied Sciences, 2007, 17, 933-955.	3.3	12
33	Automated reduction and interpretation of multidimensional mass spectra for analysis of complex peptide mixtures. International Journal of Mass Spectrometry, 2007, 260, 20-30.	1.5	16
34	Library of local descriptors models the core of proteins accurately. Proteins: Structure, Function and Bioinformatics, 2007, 69, 499-510.	2.6	5
35	A new approach to the assessment of the quality of predictions of transcription factor binding sites. Journal of Biomedical Informatics, 2007, 40, 139-149.	4.3	3
36	Reconstruction of Mammalian Cell Cycle Regulatory Network from Microarray Data Using Stochastic Logical Networks. Lecture Notes in Computer Science, 2007, , 121-135.	1.3	2

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37	DLS-trees: A model of evolutionary scenarios. Theoretical Computer Science, 2006, 359, 378-399.	0.9	115
38	A model for the evolution of paralog families in genomes. Journal of Mathematical Biology, 2006, 53, 759-770.	1.9	11
39	Applying dynamic Bayesian networks to perturbed gene expression data. BMC Bioinformatics, 2006, 7, 249.	2.6	133
40	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	2.6	12
41	Alignment with Context Dependent Scoring Function. Journal of Computational Biology, 2006, 13, 81-101.	1.6	5
42	On Genome Evolution with Innovation. Lecture Notes in Computer Science, 2006, , 801-811.	1.3	3
43	Regulatory Network Reconstruction Using Stochastic Logical Networks. Lecture Notes in Computer Science, 2006, , 142-154.	1.3	3
44	Discovering regulatory binding-site modules using rule-based learning. Genome Research, 2005, 15, 856-866.	5.5	41
45	A Case Study of Genome Evolution: From Continuous to Discrete Time Model. Lecture Notes in Computer Science, 2004, , 1-24.	1.3	5
46	Substructural logic and partial correctness. ACM Transactions on Computational Logic, 2003, 4, 355-378.	0.9	12
47	Contextual alignment of biological sequences (Extended abstract). Bioinformatics, 2002, 18, S116-S127.	4.1	6
48	The Subtyping Problem for Second-Order Types Is Undecidable. Information and Computation, 2002, 179, 1-18.	0.7	10
49	On the completeness of propositional Hoare logic. Information Sciences, 2001, 139, 187-195.	6.9	17
50	A Sequent Calculus for Subtyping Polymorphic Types. Information and Computation, 2001, 164, 345-369.	0.7	4
51	A Formal Model of Genomic Dna Multiplication and Amplification. Computational Biology, 2000, , 503-513.	0.2	3
52	Striking properties of duplicating DNA molecules. A Markov chain model demonstrates the convergence of amplified molecules to regular series of multiples of 2. Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie, 1999, 322, 455-459.	0.8	3
53	A Generalization of Cook's Auxiliary-Pushdown-Automata Theorem. Fundamenta Informaticae, 1989, 12, 497-505.	0.4	2
54	Process Algebra Semantics for Queues. Fundamenta Informaticae, 1987, 10, 213-223.	0.4	7

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55	Fixed-points and algebras with infinitely long expressions: Part I. Regular algebras. Fundamenta Informaticae, 1979, 2, 103-127.	0.4	11
56	Fixed-points and algebras with infinitely long expressions: Part II. $\hat{1}/4$ -clones of regular algebras. Fundamenta Informaticae, 1979, 2, 317-335.	0.4	8