Jerzy Tiuryn

List of Publications by Year
in descending order

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	Applying dynamic Bayesian networks to perturbed gene expression data. BMC Bioinformatics, 2006, 7, 249.	2.6	133
2	DLS-trees: A model of evolutionary scenarios. Theoretical Computer Science, 2006, 359, 378-399.	0.9	115
3	A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. Plant Physiology, 2015, 169, pp.00493.2015.	4.8	101
4	Identification of functional modules from conserved ancestral protein–protein interactions. Bioinformatics, 2007, 23, i149-i158.	4.1	87
5	Discovering regulatory binding-site modules using rule-based learning. Genome Research, 2005, 15, 856-866.	5.5	41
6	Unrooted Tree Reconciliation: A Unified Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 522-536.	3.0	39
7	Inferring phylogeny from whole genomes. Bioinformatics, 2007, 23, e116-e122.	4.1	34
8	URec: a system for unrooted reconciliation. Bioinformatics, 2007, 23, 511-512.	4.1	31
9	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. Molecular Systems Biology, 2009, 5, 287.	7.2	26
10	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. BMC Bioinformatics, 2009, 10, 82.	2.6	24
11	Contribution of NtZIP1-Like to the Regulation of Zn Homeostasis. Frontiers in Plant Science, 2018, 9, 185.	3.6	24
12	CAMBer: an approach to support comparative analysis of multiple bacterial strains. BMC Genomics, 2011, 12, S6.	2.8	22
13	GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria. BMC Genomics, 2014, 15, S10.	2.8	22
14	eCAMBer: efficient support for large-scale comparative analysis of multiple bacterial strains. BMC Bioinformatics, 2014, 15, 65.	2.6	21
15	Romulus: robust multi-state identification of transcription factor binding sites from DNase-seq data. Bioinformatics, 2016, 32, 2419-2426.	4.1	18
16	On the completeness of propositional Hoare logic. Information Sciences, 2001, 139, 187-195.	6.9	17
17	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
18	An approach to identifying drug resistance associated mutations in bacterial strains. BMC Genomics, 2012, 13, S23.	2.8	16

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19	Phylogeny-guided interaction mapping in seven eukaryotes. BMC Bioinformatics, 2009, 10, 393.	2.6	15
20	MODEVO: exploring modularity and evolution of protein interaction networks. Bioinformatics, 2010, 26, 1790-1791.	4.1	15
21	SIZE DISTRIBUTION OF GENE FAMILIES IN A GENOME. Mathematical Models and Methods in Applied Sciences, 2014, 24, 697-717.	3.3	13
22	Substructural logic and partial correctness. ACM Transactions on Computational Logic, 2003, 4, 355-378.	0.9	12
23	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	2.6	12
24	A DISCRETE MODEL OF EVOLUTION OF SMALL PARALOG FAMILIES. Mathematical Models and Methods in Applied Sciences, 2007, 17, 933-955.	3.3	12
25	Rhythmic Diel Pattern of Gene Expression in Juvenile Maize Leaf. PLoS ONE, 2011, 6, e23628.	2.5	12
26	A model for the evolution of paralog families in genomes. Journal of Mathematical Biology, 2006, 53, 759-770.	1.9	11
27	Fixed-points and algebras with infinitely long expressions: Part I. Regular algebras. Fundamenta Informaticae, 1979, 2, 103-127.	0.4	11
28	The Subtyping Problem for Second-Order Types Is Undecidable. Information and Computation, 2002, 179, 1-18.	0.7	10
29	Introducing Knowledge into Differential Expression Analysis. Journal of Computational Biology, 2010, 17, 953-967.	1.6	9
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	Fixed-points and algebras with infinitely long expressions: Part II. Î¼-clones of regular algebras. Fundamenta Informaticae, 1979, 2, 317-335.	0.4	8
32	Learning signaling networks from combinatorial perturbations by exploiting siRNA off-target effects. Bioinformatics, 2019, 35, i605-i614.	4.1	7
33	Process Algebra Semantics for Queues. Fundamenta Informaticae, 1987, 10, 213-223.	0.4	7
34	Contextual alignment of biological sequences (Extended abstract). Bioinformatics, 2002, 18, S116-S127.	4.1	6
35	A Case Study of Genome Evolution: From Continuous to Discrete Time Model. Lecture Notes in Computer Science, 2004, , 1-24.	1.3	5
36	Alignment with Context Dependent Scoring Function. Journal of Computational Biology, 2006, 13, 81-101.	1.6	5

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37	Library of local descriptors models the core of proteins accurately. Proteins: Structure, Function and Bioinformatics, 2007, 69, 499-510.	2.6	5
38	A Sequent Calculus for Subtyping Polymorphic Types. Information and Computation, 2001, 164, 345-369.	0.7	4
39	Inferring Evolutionary Scenarios in the Duplication, Loss and Horizontal Gene Transfer Model. Lecture Notes in Computer Science, 2012, , 83-105.	1.3	4
40	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'AcadÃ©mie Des Sciences SÃ©rie 3, Sciences De La Vie, 1999, 322, 455-459.	0.8	3
41	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
42	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. Journal of Computational Biology, 2017, 24, 193-199.	1.6	3
43	Minimizing genomic duplication episodes. Computational Biology and Chemistry, 2020, 89, 107260.	2.3	3
44	On Genome Evolution with Innovation. Lecture Notes in Computer Science, 2006, , 801-811.	1.3	3
45	A Formal Model of Genomic Dna Multiplication and Amplification. Computational Biology, 2000, , 503-513.	0.2	3
46	Regulatory Network Reconstruction Using Stochastic Logical Networks. Lecture Notes in Computer Science, 2006, , 142-154.	1.3	3
47	CAMBerVis: visualization software to support comparative analysis of multiple bacterial strains. Bioinformatics, 2011, 27, 3313-3314.	4.1	2
48	Bioinformatics and Computational Biology in Poland. PLoS Computational Biology, 2013, 9, e1003048.	3.2	2
49	Enhanceosome transcription factors preferentially dimerize with high mobility group proteins. BMC Systems Biology, 2015, 10, 14.	3.0	2
50	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
51	A Generalization of Cookâ€™s Auxiliary-Pushdown-Automata Theorem. Fundamenta Informaticae, 1989, 12, 497-505.	0.4	2
52	Deregulation upon DNA damage revealed by joint analysis of context-specific perturbation data. BMC Bioinformatics, 2011, 12, 249.	2.6	1
53	A Probabilistic Model of Neutral and Selective Dynamics of Protein Network Evolution. Journal of Computational Biology, 2013, 20, 631-642.	1.6	1
54	CAMBer: An approach to support comparative analysis of multiple bacterial strains. , 2010, , .		0

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55	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
56	The Unconstrained Diameters of the Duplication-Loss Cost and the Loss Cost. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	0