

JÃ©rÃ©mie Bourdon

List of Publications by Year in descending order

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27
papers

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1163117

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28
all docs

28
docs citations

28
times ranked

511
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian Integrative Modeling of Genome-Scale Metabolic and Regulatory Networks. Informatics, 2020, 7, 1.	3.9	3
2	Probabilistic Modeling of Microbial Metabolic Networks for Integrating Partial Quantitative Knowledge Within the Nitrogen Cycle. Frontiers in Microbiology, 2019, 9, 3298.	3.5	0
3	Computational discovery of dynamic cell line specific Boolean networks from multiplex time-course data. PLoS Computational Biology, 2018, 14, e1006538.	3.2	25
4	A Logic for Checking the Probabilistic Steady-State Properties of Reaction Networks. Journal of Computational Biology, 2017, 24, 734-745.	1.6	2
5	Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks. PLoS Computational Biology, 2017, 13, e1005276.	3.2	77
6	A multi-objective constraint-based approach for modeling genome-scale microbial ecosystems. PLoS ONE, 2017, 12, e0171744.	2.5	47
7	Computational Methods in Systems Biology. BioSystems, 2016, 149, 1-2.	2.0	0
8	Model of the delayed translation of cyclin B maternal mRNA after sea urchin fertilization. Molecular Reproduction and Development, 2016, 83, 1070-1082.	2.0	4
9	A combinatorial approach to products of Pisot substitutions. Ergodic Theory and Dynamical Systems, 2016, 36, 1757-1794.	0.6	5
10	Multivariate Normal Approximation for the Stochastic Simulation Algorithm: Limit Theorem and Applications. Electronic Notes in Theoretical Computer Science, 2015, 316, 67-82.	0.9	2
11	OPINION PAPER Evolutionary Constraint-Based Formulation Requires New Bi-level Solving Techniques. Lecture Notes in Computer Science, 2015, , 279-281.	1.3	0
12	Modelization of the regulation of protein synthesis following fertilization in sea urchin shows requirement of two processes: a destabilization of eIF4E:4E-BP complex and a great stimulation of the 4E-BP-degradation mechanism, both rapamycin-sensitive. Frontiers in Genetics, 2014, 5, 117.	2.3	7
13	Exploring metabolism flexibility in complex organisms through quantitative study of precursor sets for system outputs. BMC Systems Biology, 2014, 8, 8.	3.0	3
14	Large deviation properties for patterns. Journal of Discrete Algorithms, 2014, 24, 2-11.	0.7	2
15	Generating Discrete Planes with Substitutions. Lecture Notes in Computer Science, 2013, , 58-70.	1.3	5
16	Toward Systems Biology in Brown Algae to Explore Acclimation and Adaptation to the Shore Environment. OMICS A Journal of Integrative Biology, 2011, 15, 883-892.	2.0	15
17	Statistical properties of factor oracles. Journal of Discrete Algorithms, 2011, 9, 57-66.	0.7	1
18	Integrating Quantitative Knowledge into a Qualitative Gene Regulatory Network. PLoS Computational Biology, 2011, 7, e1002157.	3.2	8

#	ARTICLE	IF	CITATIONS
19	A PARALLEL SCHEME FOR COMPARING TRANSCRIPTION FACTOR BINDING SITES MATRICES. Journal of Bioinformatics and Computational Biology, 2010, 08, 485-502.	0.8	4
20	Temporal constraints of a gene regulatory network: Refining a qualitative simulation. BioSystems, 2009, 98, 149-159.	2.0	16
21	Statistical Properties of Factor Oracles. Lecture Notes in Computer Science, 2009, , 326-338.	1.3	0
22	Combinations of Cytochrome P450 Gene Polymorphisms Enhancing the Risk for Sporadic Colorectal Cancer Related to Red Meat Consumption. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1460-1467.	2.5	74
23	Pattern Matching Statistics on Correlated Sources. Lecture Notes in Computer Science, 2006, , 224-237.	1.3	5
24	Dynamical analysis of \hat{L} -Euclidean algorithms. Journal of Algorithms, 2002, 44, 246-285.	0.9	14
25	Generalized Pattern Matching Statistics. , 2002, , 249-265.		14
26	On the Stack-Size of General Tries. RAIRO - Theoretical Informatics and Applications, 2001, 35, 163-185.	0.5	6
27	Size and path length of Patricia tries: Dynamical sources context. Random Structures and Algorithms, 2001, 19, 289-315.	1.1	19