JÃ©rÃ©mie Bourdon

List of Publications by Year
in descending order

27 papers	358 citations	1163117 8 h-index	839539 18 g-index
28 all docs	28 docs citations	28 times ranked	511 citing authors

#	Article	IF	Citations
1	Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks. PLoS Computational Biology, 2017, 13, e1005276.	3.2	77
2	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
3	A multi-objective constraint-based approach for modeling genome-scale microbial ecosystems. PLoS ONE, 2017, 12, e0171744.	2.5	47
4	Computational discovery of dynamic cell line specific Boolean networks from multiplex time-course data. PLoS Computational Biology, 2018, 14, e1006538.	3.2	25
5	Size and path length of Patricia tries: Dynamical sources context. Random Structures and Algorithms, 2001, 19, 289-315.	1.1	19
6	Temporal constraints of a gene regulatory network: Refining a qualitative simulation. BioSystems, 2009, 98, 149-159.	2.0	16
7	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
8	Dynamical analysis of α-Euclidean algorithms. Journal of Algorithms, 2002, 44, 246-285.	0.9	14
9	Generalized Pattern Matching Statistics. , 2002, , 249-265.		14
10	Integrating Quantitative Knowledge into a Qualitative Gene Regulatory Network. PLoS Computational Biology, 2011, 7, e1002157.	3.2	8
11	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
12	On the Stack-Size of General Tries. RAIRO - Theoretical Informatics and Applications, 2001, 35, 163-185.	0.5	6
13	Pattern Matching Statistics on Correlated Sources. Lecture Notes in Computer Science, 2006, , 224-237.	1.3	5
14	Generating Discrete Planes with Substitutions. Lecture Notes in Computer Science, 2013, , 58-70.	1.3	5
15	A combinatorial approach to products of Pisot substitutions. Ergodic Theory and Dynamical Systems, 2016, 36, 1757-1794.	0.6	5
16	A PARALLEL SCHEME FOR COMPARING TRANSCRIPTION FACTOR BINDING SITES MATRICES. Journal of Bioinformatics and Computational Biology, 2010, 08, 485-502.	0.8	4
17	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
18	Exploring metabolism flexibility in complex organisms through quantitative study of precursor sets for system outputs. BMC Systems Biology, 2014, 8, 8.	3.0	3

#	Article	IF	Citations
19	Bayesian Integrative Modeling of Genome-Scale Metabolic and Regulatory Networks. Informatics, 2020, 7, 1.	3.9	3
20	Large deviation properties for patterns. Journal of Discrete Algorithms, 2014, 24, 2-11.	0.7	2
21	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
22	A Logic for Checking the Probabilistic Steady-State Properties of Reaction Networks. Journal of Computational Biology, 2017, 24, 734-745.	1.6	2
23	Statistical properties of factor oracles. Journal of Discrete Algorithms, 2011, 9, 57-66.	0.7	1
24	OPINION PAPER Evolutionary Constraint-Based Formulation Requires New Bi-level Solving Techniques. Lecture Notes in Computer Science, 2015, , 279-281.	1.3	0
25	Computational Methods in Systems Biology. BioSystems, 2016, 149, 1-2.	2.0	0
26	Probabilistic Modeling of Microbial Metabolic Networks for Integrating Partial Quantitative Knowledge Within the Nitrogen Cycle. Frontiers in Microbiology, 2019, 9, 3298.	3.5	0
27	Statistical Properties of Factor Oracles. Lecture Notes in Computer Science, 2009, , 326-338.	1.3	0