

Michel Page

List of Publications by Year in descending order

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12
papers

1,090
citations

840776

11
h-index

1281871

11
g-index

13
all docs

13
docs citations

13
times ranked

689
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Network Analyzer: A Tool for the Qualitative Modeling and Simulation of Bacterial Regulatory Networks. <i>Methods in Molecular Biology</i> , 2012, 804, 439-462.	0.9	31
2	Qualitative Analysis of Genetic Regulatory Networks in Bacteria. , 2011, , 111-130.		4
3	Efficient parameter search for qualitative models of regulatory networks using symbolic model checking. <i>Bioinformatics</i> , 2010, 26, i603-i610.	4.1	49
4	A service-oriented architecture for integrating the modeling and formal verification of genetic regulatory networks. <i>BMC Bioinformatics</i> , 2009, 10, 450.	2.6	11
5	Symbolic reachability analysis of genetic regulatory networks using discrete abstractions. <i>Automatica</i> , 2008, 44, 982-989.	5.0	46
6	Search for Steady States of Piecewise-Linear Differential Equation Models of Genetic Regulatory Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 208-222.	3.0	47
7	Qualitative simulation of the carbon starvation response in <i>Escherichia coli</i> . <i>BioSystems</i> , 2006, 84, 124-152.	2.0	106
8	Validation of qualitative models of genetic regulatory networks by model checking: analysis of the nutritional stress response in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2005, 21, i19-i28.	4.1	141
9	Qualitative Analysis and Verification of Hybrid Models of Genetic Regulatory Networks: Nutritional Stress Response in <i>Escherichia coli</i> . <i>Lecture Notes in Computer Science</i> , 2005, , 134-150.	1.3	25
10	Qualitative simulation of the initiation of sporulation in. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 261-299.	1.9	81
11	Qualitative simulation of genetic regulatory networks using piecewise-linear models. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 301-340.	1.9	309
12	Genetic Network Analyzer: qualitative simulation of genetic regulatory networks. <i>Bioinformatics</i> , 2003, 19, 336-344.	4.1	240