Delphine Ropers

List of Publications by Year
in descending order

34 papers	1,243 citations	471509 17 h-index	501196 28 g-index
36 all docs	36 docs citations	36 times ranked	1438 citing authors

#	Article	IF	Citations
1	Validation of qualitative models of genetic regulatory networks by model checking: analysis of the nutritional stress response in Escherichia coli. Bioinformatics, 2005, 21, i19-i28.	4.1	141
2	Acetate Metabolism and the Inhibition of Bacterial Growth by Acetate. Journal of Bacteriology, 2019, 201, .	2.2	137
3	Shared control of gene expression in bacteria by transcription factors and global physiology of the cell. Molecular Systems Biology, 2013, 9, 634.	7.2	127
4	Qualitative simulation of the carbon starvation response in Escherichia coli. BioSystems, 2006, 84, 124-152.	2.0	106
5	Experimental and computational validation of models of fluorescent and luminescent reporter genes in bacteria. BMC Systems Biology, 2010, 4, 55.	3.0	78
6	A synthetic growth switch based on controlled expression of RNA polymerase. Molecular Systems Biology, 2015, 11, 840.	7.2	76
7	Temporal logic patterns for querying dynamic models of cellular interaction networks. Bioinformatics, 2008, 24, i227-i233.	4.1	68
8	Differential Effects of the SR Proteins 9G8, SC35, ASF/SF2, and SRp40 on the Utilization of the A1 to A5 Splicing Sites of HIV-1 RNA. Journal of Biological Chemistry, 2004, 279, 29963-29973.	3.4	66
9	Biochemical and NMR Study on the Competition between Proteins SC35, SRp40, and Heterogeneous Nuclear Ribonucleoprotein A1 at the HIV-1 Tat Exon 2 Splicing Site. Journal of Biological Chemistry, 2006, 281, 37159-37174.	3.4	50
10	The Carbon Assimilation Network in Escherichia coli Is Densely Connected and Largely Sign-Determined by Directions of Metabolic Fluxes. PLoS Computational Biology, 2010, 6, e1000812.	3.2	46
11	Mathematical modelling of microbes: metabolism, gene expression and growth. Journal of the Royal Society Interface, 2017, 14, 20170502.	3.4	46
12	The post‐transcriptional regulatory system CSR controls the balance of metabolic pools in upper glycolysis of <i>Escherichia coli</i>. Molecular Microbiology, 2016, 100, 686-700.	2.5	42
13	A declarative constraint-based method for analyzing discrete genetic regulatory networks. BioSystems, 2009, 98, 91-104.	2.0	37
14	Genetic Network Analyzer: A Tool for the Qualitative Modeling and Simulation of Bacterial Regulatory Networks. Methods in Molecular Biology, 2012, 804, 439-462.	0.9	31
15	Strategies for dealing with incomplete information in the modeling of molecular interaction networks. Briefings in Bioinformatics, 2006, 7, 354-363.	6.5	23
16	The Csr System Regulates <i>Escherichia coli</i> Fitness by Controlling Glycogen Accumulation and Energy Levels. MBio, 2017, 8, .	4.1	21
17	Model Reduction Using Piecewise-Linear Approximations Preserves Dynamic Properties of the Carbon Starvation Response in Escherichia coli. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 166-181.	3.0	20
18	Resource Reallocation in Bacteria by Reengineering the Gene Expression Machinery. Trends in Microbiology, 2017, 25, 480-493.	7.7	19

#	Article	IF	Citations
19	Robust reconstruction of gene expression profiles from reporter gene data using linear inversion. Bioinformatics, 2015, 31, i71-i79.	4.1	17
20	Importance of metabolic coupling for the dynamics of gene expression following a diauxic shift in Escherichia coli. Journal of Theoretical Biology, 2012, 295, 100-115.	1.7	16
21	An ensemble of mathematical models showing diauxic growth behaviour. BMC Systems Biology, 2018, 12, 82.	3.0	16
22	Estimation of time-varying growth, uptake and excretion rates from dynamic metabolomics data. Bioinformatics, 2017, 33, i301-i310.	4.1	15
23	A genome-wide screen for identifying all regulators of a target gene. Nucleic Acids Research, 2013, 41, e164-e164.	14.5	12
24	A multi-scale constraint programming model of alternative splicing regulation. Theoretical Computer Science, 2004, 325, 3-24.	0.9	7
25	Piecewise linear approximations to model the dynamics of adaptation to osmotic stress by food-borne pathogens. International Journal of Food Microbiology, 2017, 240, 63-74.	4.7	6
26	Qualitative Analysis of Genetic Regulatory Networks in Bacteria. , 2011, , 111-130.		4
27	Multiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. ACS Synthetic Biology, 2021, 10, 2910-2926.	3.8	4
28	Reduction and Stability Analysis of a Transcription–Translation Model of RNA Polymerase. Bulletin of Mathematical Biology, 2018, 80, 294-318.	1.9	3
29	Stability analysis of a reduced transcription-translation model of RNA polymerase. , 2014, , .		2
30	Principal process analysis of biological models. BMC Systems Biology, 2018, 12, 68.	3.0	2
31	Model reduction and process analysis of biological models. , 2015, , .		1
32	Reduction of a Kinetic Model of the Carbon Starvation Response in Escherichia coli. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2009, 42, 27-32.	0.4	0
33	Importance of Metabolic Coupling for the Dynamics of Gene Expression Following a Diauxic Shift in E. coli. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2011, 44, 14851-14856.	0.4	0
34	Data for the qualitative modeling of the osmotic stress response to NaCl in Escherichia coli. Data in Brief, 2016, 9, 606-612.	1.0	0