

Delphine Ropers

List of Publications by Year in descending order

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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	Multiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. ACS Synthetic Biology, 2021, 10, 2910-2926.	3.8	4
2	Acetate Metabolism and the Inhibition of Bacterial Growth by Acetate. Journal of Bacteriology, 2019, 201, .	2.2	137
3	Reduction and Stability Analysis of a Transcription-Translation Model of RNA Polymerase. Bulletin of Mathematical Biology, 2018, 80, 294-318.	1.9	3
4	An ensemble of mathematical models showing diauxic growth behaviour. BMC Systems Biology, 2018, 12, 82.	3.0	16
5	Principal process analysis of biological models. BMC Systems Biology, 2018, 12, 68.	3.0	2
6	Resource Reallocation in Bacteria by Reengineering the Gene Expression Machinery. Trends in Microbiology, 2017, 25, 480-493.	7.7	19
7	The Csr System Regulates <i>Escherichia coli</i> Fitness by Controlling Glycogen Accumulation and Energy Levels. MBio, 2017, 8, .	4.1	21
8	Mathematical modelling of microbes: metabolism, gene expression and growth. Journal of the Royal Society Interface, 2017, 14, 20170502.	3.4	46
9	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
10	Estimation of time-varying growth, uptake and excretion rates from dynamic metabolomics data. Bioinformatics, 2017, 33, i301-i310.	4.1	15
11	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
12	Data for the qualitative modeling of the osmotic stress response to NaCl in <i>Escherichia coli</i> . Data in Brief, 2016, 9, 606-612.	1.0	0
13	A synthetic growth switch based on controlled expression of RNA polymerase. Molecular Systems Biology, 2015, 11, 840.	7.2	76
14	Model reduction and process analysis of biological models. , 2015, , .		1
15	Robust reconstruction of gene expression profiles from reporter gene data using linear inversion. Bioinformatics, 2015, 31, i71-i79.	4.1	17
16	Stability analysis of a reduced transcription-translation model of RNA polymerase. , 2014, , .		2
17	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
18	A genome-wide screen for identifying all regulators of a target gene. Nucleic Acids Research, 2013, 41, e164-e164.	14.5	12

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19	Importance of metabolic coupling for the dynamics of gene expression following a diauxic shift in <i>Escherichia coli</i> . <i>Journal of Theoretical Biology</i> , 2012, 295, 100-115.	1.7	16
20	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
21	Model Reduction Using Piecewise-Linear Approximations Preserves Dynamic Properties of the Carbon Starvation Response in <i>Escherichia coli</i> . <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 166-181.	3.0	20
22	Importance of Metabolic Coupling for the Dynamics of Gene Expression Following a Diauxic Shift in <i>E. coli</i> . <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2011, 44, 14851-14856.	0.4	0
23	Qualitative Analysis of Genetic Regulatory Networks in Bacteria. , 2011, , 111-130.		4
24	Experimental and computational validation of models of fluorescent and luminescent reporter genes in bacteria. <i>BMC Systems Biology</i> , 2010, 4, 55.	3.0	78
25	The Carbon Assimilation Network in <i>Escherichia coli</i> Is Densely Connected and Largely Sign-Determined by Directions of Metabolic Fluxes. <i>PLoS Computational Biology</i> , 2010, 6, e1000812.	3.2	46
26	A declarative constraint-based method for analyzing discrete genetic regulatory networks. <i>BioSystems</i> , 2009, 98, 91-104.	2.0	37
27	Reduction of a Kinetic Model of the Carbon Starvation Response in <i>Escherichia coli</i> . <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2009, 42, 27-32.	0.4	0
28	Temporal logic patterns for querying dynamic models of cellular interaction networks. <i>Bioinformatics</i> , 2008, 24, i227-i233.	4.1	68
29	Qualitative simulation of the carbon starvation response in <i>Escherichia coli</i> . <i>BioSystems</i> , 2006, 84, 124-152.	2.0	106
30	Strategies for dealing with incomplete information in the modeling of molecular interaction networks. <i>Briefings in Bioinformatics</i> , 2006, 7, 354-363.	6.5	23
31	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. <i>Journal of Biological Chemistry</i> , 2006, 281, 37159-37174.	3.4	50
32	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
33	Differential Effects of the SR Proteins 9C8, SC35, ASF/SF2, and SRp40 on the Utilization of the A1 to A5 Splicing Sites of HIV-1 RNA. <i>Journal of Biological Chemistry</i> , 2004, 279, 29963-29973.	3.4	66
34	A multi-scale constraint programming model of alternative splicing regulation. <i>Theoretical Computer Science</i> , 2004, 325, 3-24.	0.9	7