

Johannes Geiselman

List of Publications by Year in descending order

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62
papers

3,615
citations

126907

33
h-index

149698

56
g-index

64
all docs

64
docs citations

64
times ranked

3254
citing authors

#	ARTICLE	IF	CITATIONS
1	Improvement of pCVD442, a suicide plasmid for gene allele exchange in bacteria. <i>Plasmid</i> , 2004, 51, 246-255.	1.4	337
2	Qualitative simulation of genetic regulatory networks using piecewise-linear models. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 301-340.	1.9	309
3	Genetic Network Analyzer: qualitative simulation of genetic regulatory networks. <i>Bioinformatics</i> , 2003, 19, 336-344.	4.1	240
4	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
5	Acetate Metabolism and the Inhibition of Bacterial Growth by Acetate. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	137
6	Shared control of gene expression in bacteria by transcription factors and global physiology of the cell. <i>Molecular Systems Biology</i> , 2013, 9, 634.	7.2	127
7	Long-Term Experimental Evolution in <i>Escherichia coli</i> . XII. DNA Topology as a Key Target of Selection. <i>Genetics</i> , 2005, 169, 523-532.	2.9	124
8	Crl, a Low Temperature-induced Protein in <i>Escherichia coli</i> That Binds Directly to the Stationary Phase λ Subunit of RNA Polymerase. <i>Journal of Biological Chemistry</i> , 2004, 279, 19540-19550.	3.4	119
9	Understanding carbon catabolite repression in <i>Escherichia coli</i> using quantitative models. <i>Trends in Microbiology</i> , 2015, 23, 99-109.	7.7	112
10	Qualitative simulation of the carbon starvation response in <i>Escherichia coli</i> . <i>BioSystems</i> , 2006, 84, 124-152.	2.0	106
11	A physical model for the translocation and helicase activities of <i>Escherichia coli</i> transcription termination protein Rho.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 7754-7758.	7.1	100
12	Parallel Changes in Global Protein Profiles During Long-Term Experimental Evolution in <i>Escherichia coli</i> . <i>Genetics</i> , 2006, 173, 1851-1869.	2.9	98
13	Physical properties of the <i>Escherichia coli</i> transcription termination factor rho. 1. Association states and geometry of the rho hexamer. <i>Biochemistry</i> , 1992, 31, 111-121.	2.5	85
14	Dynamical Allocation of Cellular Resources as an Optimal Control Problem: Novel Insights into Microbial Growth Strategies. <i>PLoS Computational Biology</i> , 2016, 12, e1004802.	3.2	84
15	Qualitative simulation of the initiation of sporulation in. <i>Bulletin of Mathematical Biology</i> , 2004, 66, 261-299.	1.9	81
16	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
17	A synthetic growth switch based on controlled expression of RNA polymerase. <i>Molecular Systems Biology</i> , 2015, 11, 840.	7.2	76
18	Protein-DNA cross-linking at the lac promoter. <i>Nucleic Acids Research</i> , 1991, 19, 833-840.	14.5	69

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19	Functional interactions of ligand cofactors with <i>Escherichia coli</i> transcription termination factor rho. I. Binding of ATP. <i>Protein Science</i> , 1992, 1, 850-860.	7.6	67
20	Physical properties of the <i>Escherichia coli</i> transcription termination factor rho. 2. Quaternary structure of the rho hexamer. <i>Biochemistry</i> , 1992, 31, 121-132.	2.5	65
21	A quantitative UV laser footprinting analysis of the interaction of IHF with specific binding sites: re-evaluation of the effective concentration of IHF in the cell. <i>Journal of Molecular Biology</i> , 1998, 284, 949-961.	4.2	55
22	The Crl-RpoS Regulon of <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 648-659.	3.8	55
23	Characterization of the <i>Escherichia coli</i> λ S core regulon by Chromatin Immunoprecipitation-sequencing (ChIP-seq) analysis. <i>Scientific Reports</i> , 2015, 5, 10469.	3.3	52
24	Repression of Flagellar Genes in Exponential Phase by CsgD and CpxR, Two Crucial Modulators of <i>Escherichia coli</i> Biofilm Formation. <i>Journal of Bacteriology</i> , 2014, 196, 707-715.	2.2	51
25	Symbolic reachability analysis of genetic regulatory networks using discrete abstractions. <i>Automatica</i> , 2008, 44, 982-989.	5.0	46
26	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
27	Mathematical modelling of microbes: metabolism, gene expression and growth. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170502.	3.4	46
28	Structural kinetics of transcription activation at the malT promoter of <i>Escherichia coli</i> by UV laser footprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 9022-9027.	7.1	44
29	Functional interactions of ligand cofactors with <i>Escherichia coli</i> transcription termination factor rho. II. Binding of RNA. <i>Protein Science</i> , 1992, 1, 861-873.	7.6	43
30	In vivo interaction of the <i>Escherichia coli</i> integration host factor with its specific binding sites. <i>Nucleic Acids Research</i> , 1995, 23, 2959-2965.	14.5	43
31	Participation of IHF and a distant UP element in the stimulation of the phage λ PL promoter. <i>Molecular Microbiology</i> , 1998, 30, 443-451.	2.5	42
32	The tRNA function of SsrA contributes to controlling repression of bacteriophage Mu prophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10220-10225.	7.1	39
33	Maximal transcriptional activation by the IHF protein of <i>Escherichia coli</i> depends on optimal DNA bending by the activator. <i>Molecular Microbiology</i> , 1998, 30, 431-441.	2.5	38
34	Inference of Quantitative Models of Bacterial Promoters from Time-Series Reporter Gene Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004028.	3.2	38
35	A sensitive reporter gene system using bacterial luciferase based on a series of plasmid cloning vectors compatible with derivatives of pBR322. <i>Gene</i> , 1997, 186, 197-200.	2.2	33
36	Hybrid Modeling and Simulation of Genetic Regulatory Networks: A Qualitative Approach. <i>Lecture Notes in Computer Science</i> , 2003, , 267-282.	1.3	32

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37	The glucosyl-1-phosphate transferase WchA (Cap8E) primes the capsular polysaccharide repeat unit biosynthesis of <i>Streptococcus pneumoniae</i> serotype 8. <i>Biochemical and Biophysical Research Communications</i> , 2005, 327, 857-865.	2.1	32
38	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
39	A simple polypyrimidine repeat acts as an artificial Rho-dependent terminator in vivo and in vitro. <i>Nucleic Acids Research</i> , 1998, 26, 4895-4900.	14.5	30
40	Control of Bacteriophage Mu Lysogenic Repression. <i>Journal of Molecular Biology</i> , 2005, 353, 186-195.	4.2	29
41	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
42	Crosstalk regulation among group 2-sigma factors in <i>Synechocystis</i> PCC6803. <i>BMC Microbiology</i> , 2005, 5, 18.	3.3	19
43	Inferring the connectivity of a regulatory network from mRNA quantification in <i>Synechocystis</i> PCC6803. <i>Nucleic Acids Research</i> , 2005, 33, 3381-3389.	14.5	19
44	Expression dynamics of RpoS/Crl-dependent genes in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 2013, 164, 838-847.	2.1	19
45	Resource Reallocation in Bacteria by Reengineering the Gene Expression Machinery. <i>Trends in Microbiology</i> , 2017, 25, 480-493.	7.7	19
46	Influence of the Location of the cAMP Receptor Protein Binding Site on the Geometry of a Transcriptional Activation Complex in <i>Escherichia coli</i> . <i>Biochemistry</i> , 1996, 35, 15302-15312.	2.5	17
47	Robust reconstruction of gene expression profiles from reporter gene data using linear inversion. <i>Bioinformatics</i> , 2015, 31, i71-i79.	4.1	17
48	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
49	An ensemble of mathematical models showing diauxic growth behaviour. <i>BMC Systems Biology</i> , 2018, 12, 82.	3.0	16
50	[14] Kinetic studies on promoter-RNA polymerase complexes. <i>Methods in Enzymology</i> , 1991, 208, 236-258.	1.0	15
51	WellReader: a MATLAB program for the analysis of fluorescence and luminescence reporter gene data. <i>Bioinformatics</i> , 2010, 26, 1262-1263.	4.1	12
52	A genome-wide screen for identifying all regulators of a target gene. <i>Nucleic Acids Research</i> , 2013, 41, e164-e164.	14.5	12
53	Mutual Regulation of Crl and Fur in <i>Escherichia coli</i> W3110. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 660-668.	3.8	10
54	Qualitative modelling and simulation of developmental regulatory networks. , 2003, , 109-134.		5

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55	Qualitative Analysis of Genetic Regulatory Networks in Bacteria. , 2011, , 111-130.		4
56	Multimomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. ACS Synthetic Biology, 2021, 10, 2910-2926.	3.8	4
57	Anodic deposit from respiration metabolic pathway of Escherichia coli. Electrochimica Acta, 2014, 130, 200-205.	5.2	1
58	Fluorescent Reporter Genes and the Analysis of Bacterial Regulatory Networks. Lecture Notes in Computer Science, 2015, , 27-50.	1.3	1
59	Ultraviolet-Laser Footprinting. , 2001, 148, 161-173.		0
60	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
61	Regulation of Phycobilisome Biosynthesis and Degradation in Cyanobacteria. Books in Soils, Plants, and the Environment, 2005, , .	0.1	0
62	Systems Biology and Metabolic Engineering in Bacteria. Springer Series in Biophysics, 2014, , 351-367.	0.4	0