Hidde de Jong

List of Publications by Year
in descending order

73 papers	5,382 citations	159585 30 h-index	95266 68 g-index
80 all docs	80 docs citations	80 times ranked	4396 citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling and Simulation of Genetic Regulatory Systems: A Literature Review. Journal of Computational Biology, 2002, 9, 67-103.	1.6	2,250
2	Qualitative simulation of genetic regulatory networks using piecewise-linear models. Bulletin of Mathematical Biology, 2004, 66, 301-340.	1.9	309
3	Genetic Network Analyzer: qualitative simulation of genetic regulatory networks. Bioinformatics, 2003, 19, 336-344.	4.1	240
4	SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
5	Piecewise-linear Models of Genetic Regulatory Networks: Equilibria and their Stability. Journal of Mathematical Biology, 2006, 52, 27-56.	1.9	157
6	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135.	3.0	145
7	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
8	Acetate Metabolism and the Inhibition of Bacterial Growth by Acetate. Journal of Bacteriology, 2019, 201, .	2.2	137
9	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
10	Understanding carbon catabolite repression in Escherichia coli using quantitative models. Trends in Microbiology, 2015, 23, 99-109.	7.7	112
11	Qualitative simulation of the carbon starvation response in Escherichia coli. BioSystems, 2006, 84, 124-152.	2.0	106
12	Dynamical Allocation of Cellular Resources as an Optimal Control Problem: Novel Insights into Microbial Growth Strategies. PLoS Computational Biology, 2016, 12, e1004802.	3.2	84
13	Qualitative simulation of the initiation of sporulation in. Bulletin of Mathematical Biology, 2004, 66, 261-299.	1.9	81
14	Experimental and computational validation of models of fluorescent and luminescent reporter genes in bacteria. BMC Systems Biology, 2010, 4, 55.	3.0	78
15	A synthetic growth switch based on controlled expression of RNA polymerase. Molecular Systems Biology, 2015, 11, 840.	7.2	76
16	Temporal logic patterns for querying dynamic models of cellular interaction networks. Bioinformatics, 2008, 24, i227-i233.	4.1	68
17	Experiment selection for the discrimination of semi-quantitative models of dynamical systems. Artificial Intelligence, 2006, 170, 472-506.	5.8	67
18	Efficient parameter search for qualitative models of regulatory networks using symbolic model checking. Bioinformatics, 2010, 26, i603-i610.	4.1	49

#	Article	IF	Citations
19	Search for Steady States of Piecewise-Linear Differential Equation Models of Genetic Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 208-222.	3.0	47
20	Symbolic reachability analysis of genetic regulatory networks using discrete abstractions. Automatica, 2008, 44, 982-989.	5.0	46
21	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
22	Mathematical modelling of microbes: metabolism, gene expression and growth. Journal of the Royal Society Interface, 2017, 14, 20170502.	3.4	46
23	Towards multiscale plant models: integrating cellular networks. Trends in Plant Science, 2012, 17, 728-736.	8.8	44
24	The computer revolution in science: steps towards the realization of computer-supported discovery environments. Artificial Intelligence, 1997, 91, 225-256.	5.8	38
25	Inference of Quantitative Models of Bacterial Promoters from Time-Series Reporter Gene Data. PLoS Computational Biology, 2015, 11, e1004028.	3.2	38
26	Structural Identification of Piecewise-Linear Models of Genetic Regulatory Networks. Journal of Computational Biology, 2008, 15, 1365-1380.	1.6	37
27	The Switching Threshold Reconstruction Problem for Piecewise-Affine Models of Genetic Regulatory Networks. IEEE Transactions on Automatic Control, 2008, 53, 153-165.	5.7	37
28	Hybrid Modeling and Simulation of Genetic Regulatory Networks: A Qualitative Approach. Lecture Notes in Computer Science, 2003, , 267-282.	1.3	32
29	The logic layout of the TOL network of Pseudomonas putida pWW0 plasmid stems from a metabolic amplifier motif (MAM) that optimizes biodegradation of m-xylene. BMC Systems Biology, 2011, 5, 191.	3.0	32
30	Numerical simulation of piecewise-linear models of gene regulatory networks using complementarity systems. Physica D: Nonlinear Phenomena, 2014, 269, 103-119.	2.8	32
31	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
32	Control of Bacteriophage Mu Lysogenic Repression. Journal of Molecular Biology, 2005, 353, 186-195.	4.2	29
33	On the identifiability of metabolic network models. Journal of Mathematical Biology, 2013, 67, 1795-1832.	1.9	27
34	Qualitative Analysis and Verification of Hybrid Models of Genetic Regulatory Networks: Nutritional Stress Response in Escherichia coli. Lecture Notes in Computer Science, 2005, , 134-150.	1.3	25
35	Strategies for dealing with incomplete information in the modeling of molecular interaction networks. Briefings in Bioinformatics, 2006, 7, 354-363.	6.5	23
36	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

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37	Identification of metabolic network models from incomplete high-throughput datasets. Bioinformatics, 2011, 27, i186-i195.	4.1	20
38	Optimal control of bacterial growth for the maximization of metabolite production. Journal of Mathematical Biology, 2019, 78, 985-1032.	1.9	20
39	Enhanced production of heterologous proteins by a synthetic microbial community: Conditions and trade-offs. PLoS Computational Biology, 2020, 16, e1007795.	3.2	20
40	Resource Reallocation in Bacteria by Reengineering the Gene Expression Machinery. Trends in Microbiology, 2017, 25, 480-493.	7.7	19
41	CTRL: Extension of CTL with regular expressions and fairness operators to verify genetic regulatory networks. Theoretical Computer Science, 2011, 412, 2854-2883.	0.9	18
42	Model Checking Genetic Regulatory Networks Using GNA and CADP. Lecture Notes in Computer Science, 2004, , 158-163.	1.3	18
43	Robust reconstruction of gene expression profiles from reporter gene data using linear inversion. Bioinformatics, 2015, 31, i71-i79.	4.1	17
44	Dynamical modeling of biological regulatory networks. BioSystems, 2006, 84, 77-80.	2.0	16
45	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
46	An ensemble of mathematical models showing diauxic growth behaviour. BMC Systems Biology, 2018, 12, 82.	3.0	16
47	Estimation of time-varying growth, uptake and excretion rates from dynamic metabolomics data. Bioinformatics, 2017, 33, i301-i310.	4.1	15
48	Piecewise-Linear Models of Genetic Regulatory Networks: Theory and Example. Lecture Notes in Control and Information Sciences, 2007, , 137-159.	1.0	15
49	Mass Spectrometry-based Workflow for Accurate Quantification of Escherichia coli Enzymes: How Proteomics Can Play a Key Role in Metabolic Engineering. Molecular and Cellular Proteomics, 2014, 13, 954-968.	3.8	14
50	Optimal proteome allocation and the temperature dependence of microbial growth laws. Npj Systems Biology and Applications, 2021, 7, 14.	3.0	14
51	WellReader: a MATLAB program for the analysis of fluorescence and luminescence reporter gene data. Bioinformatics, 2010, 26, 1262-1263.	4.1	12
52	A genome-wide screen for identifying all regulators of a target gene. Nucleic Acids Research, 2013, 41, e164-e164.	14.5	12
53	Qualitative simulation and related approaches for the analysis of dynamic systems. Knowledge Engineering Review, 2004, 19, 93-132.	2.6	11
54	A service-oriented architecture for integrating the modeling and formal verification of genetic regulatory networks. BMC Bioinformatics, 2009, 10, 450.	2.6	11

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55	Computation Tree Regular Logic for Genetic Regulatory Networks. Lecture Notes in Computer Science, 2008, , 48-63.	1.3	9
56	A multi-scale constraint programming model of alternative splicing regulation. Theoretical Computer Science, 2004, 325, 3-24.	0.9	7
57	WellInverter: a web application for the analysis of fluorescent reporter gene data. BMC Bioinformatics, 2019, 20, 309.	2.6	6
58	Comparative envisionment construction: A technique for the comparative analysis of dynamical systems. Artificial Intelligence, 1999, 115, 145-214.	5.8	5
59	Qualitative modelling and simulation of developmental regulatory networks. , 2003, , 109-134.		5
60	Computer-Supported Resolution of Measurement Conflicts: A Case-Study in Materials Science. Foundations of Science, 1999, 4, 427-461.	0.7	4
61	Qualitative Analysis of Genetic Regulatory Networks in Bacteria. , 2011, , 111-130.		4
62	Multiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. ACS Synthetic Biology, 2021, 10, 2910-2926.	3.8	4
63	Qualitative Modeling, Analysis and Control of Synthetic Regulatory Circuits. Methods in Molecular Biology, 2021, 2229, 1-40.	0.9	3
64	Dynamical Analysis and Optimization of a Generalized Resource Allocation Model of Microbial Growth. SIAM Journal on Applied Dynamical Systems, 2022, 21, 137-165.	1.6	3
65	Modélisation, analyse et simulationdes réseaux génétiques. Medecine/Sciences, 2002, 18, 492-502.	0.2	2
66	Identification of parameters and structure of piecewise affine models of genetic networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2009, 42, 587-592.	0.4	2
67	Structural and practical identifiability of approximate metabolic network models. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 1719-1724.	0.4	1
68	Fluorescent Reporter Genes and the Analysis of Bacterial Regulatory Networks. Lecture Notes in Computer Science, 2015, , 27-50.	1.3	1
69	Qualitative Modeling and Simulation of Bacterial Regulatory Networks. Lecture Notes in Computer Science, 2008, , 1-1.	1.3	1
70	Course 10Modeling, analysis, and simulation of genetic regulatory networks: From differential equations to logical models. Les Houches Summer School Proceedings, 2005, , 325-354.	0.2	0
71	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
72	Modeling and formal verification of biological regulatory networks: An integrative approach. , 2010, , .		0

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73	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