

Jörg Stelling

List of Publications by Year in descending order

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Version: 2024-02-01

106
papers

8,222
citations

87723

38
h-index

51492

86
g-index

122
all docs

122
docs citations

122
times ranked

8166
citing authors

#	ARTICLE	IF	CITATIONS
1	Robustness of Cellular Functions. <i>Cell</i> , 2004, 118, 675-685.	13.5	930
2	Metabolic network structure determines key aspects of functionality and regulation. <i>Nature</i> , 2002, 420, 190-193.	13.7	712
3	A tunable synthetic mammalian oscillator. <i>Nature</i> , 2009, 457, 309-312.	13.7	530
4	Comparison of network-based pathway analysis methods. <i>Trends in Biotechnology</i> , 2004, 22, 400-405.	4.9	347
5	Large-scale computation of elementary flux modes with bit pattern trees. <i>Bioinformatics</i> , 2008, 24, 2229-2235.	1.8	291
6	Microbial network disturbances in relapsing refractory Crohn's disease. <i>Nature Medicine</i> , 2019, 25, 323-336.	15.2	277
7	Two approaches for metabolic pathway analysis?. <i>Trends in Biotechnology</i> , 2003, 21, 64-69.	4.9	257
8	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> . <i>Metabolism. Science</i> , 2012, 335, 1099-1103.	6.0	255
9	Robustness properties of circadian clock architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13210-13215.	3.3	249
10	Self-sufficient control of urate homeostasis in mice by a synthetic circuit. <i>Nature Biotechnology</i> , 2010, 28, 355-360.	9.4	244
11	Ensemble modeling for analysis of cell signaling dynamics. <i>Nature Biotechnology</i> , 2007, 25, 1001-1006.	9.4	214
12	Combinatorial complexity of pathway analysis in metabolic networks. <i>Molecular Biology Reports</i> , 2002, 29, 233-236.	1.0	196
13	FluxAnalyzer: exploring structure, pathways, and flux distributions in metabolic networks on interactive flux maps. <i>Bioinformatics</i> , 2003, 19, 261-269.	1.8	187
14	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
15	Î ² -cell-mimetic designer cells provide closed-loop glycemic control. <i>Science</i> , 2016, 354, 1296-1301.	6.0	173
16	Accurate cell segmentation in microscopy images using membrane patterns. <i>Bioinformatics</i> , 2014, 30, 2644-2651.	1.8	170
17	Transcriptional regulation is insufficient to explain substrate-induced flux changes in <i>Bacillus subtilis</i> . <i>Molecular Systems Biology</i> , 2013, 9, 709.	3.2	149
18	Mathematical models in microbial systems biology. <i>Current Opinion in Microbiology</i> , 2004, 7, 513-518.	2.3	145

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19	Inducible, tightly regulated and growth condition-independent transcription factor in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2014, 42, e130-e130.	6.5	140
20	A synthetic time-delay circuit in mammalian cells and mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2643-2648.	3.3	130
21	MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. <i>Bioinformatics</i> , 2013, 29, 815-816.	1.8	120
22	Genome-scale metabolic networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 285-297.	6.6	115
23	Computational design tools for synthetic biology. <i>Current Opinion in Biotechnology</i> , 2009, 20, 479-485.	3.3	101
24	Multistable and dynamic CRISPRi-based synthetic circuits. <i>Nature Communications</i> , 2020, 11, 2746.	5.8	98
25	Synthetic two-way communication between mammalian cells. <i>Nature Biotechnology</i> , 2012, 30, 991-996.	9.4	97
26	Subnetwork analysis reveals dynamic features of complex (bio)chemical networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19175-19180.	3.3	96
27	A Synthetic Multifunctional Mammalian pH Sensor and CO ₂ Transgene-Control Device. <i>Molecular Cell</i> , 2014, 55, 397-408.	4.5	96
28	A synthetic low-frequency mammalian oscillator. <i>Nucleic Acids Research</i> , 2010, 38, 2702-2711.	6.5	93
29	Automatic Design of Digital Synthetic Gene Circuits. <i>PLoS Computational Biology</i> , 2011, 7, e1001083.	1.5	85
30	Efficient characterization of high-dimensional parameter spaces for systems biology. <i>BMC Systems Biology</i> , 2011, 5, 142.	3.0	78
31	System-Level Insights into Yeast Metabolism by Thermodynamic Analysis of Elementary Flux Modes. <i>PLoS Computational Biology</i> , 2012, 8, e1002415.	1.5	61
32	Systems interface biology. <i>Journal of the Royal Society Interface</i> , 2006, 3, 603-616.	1.5	53
33	Inflammatory signals directly instruct PU.1 in HSCs via TNF. <i>Blood</i> , 2019, 133, 816-819.	0.6	53
34	Circadian Phase Resetting via Single and Multiple Control Targets. <i>PLoS Computational Biology</i> , 2008, 4, e1000104.	1.5	50
35	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. <i>Molecular Systems Biology</i> , 2015, 11, 802.	3.2	49
36	Sensitivity analysis of oscillatory (bio)chemical systems. <i>Computers and Chemical Engineering</i> , 2005, 29, 663-673.	2.0	48

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37	Automatic Generation of Predictive Dynamic Models Reveals Nuclear Phosphorylation as the Key Msn2 Control Mechanism. <i>Science Signaling</i> , 2013, 6, ra41.	1.6	44
38	Quantitative performance metrics for robustness in circadian rhythms. <i>Bioinformatics</i> , 2007, 23, 358-364.	1.8	42
39	Integrating omics data into genome-scale metabolic network models: principles and challenges. <i>Essays in Biochemistry</i> , 2018, 62, 563-574.	2.1	40
40	Predicting ligand-dependent tumors from multi-dimensional signaling features. <i>Npj Systems Biology and Applications</i> , 2017, 3, 27.	1.4	39
41	Counter-Intuitive Stochastic Behavior of Simple Gene Circuits with Negative Feedback. <i>Biophysical Journal</i> , 2010, 98, 1742-1750.	0.2	38
42	Bridging the gaps in systems biology. <i>Molecular Genetics and Genomics</i> , 2014, 289, 727-734.	1.0	38
43	Near-optimal experimental design for model selection in systems biology. <i>Bioinformatics</i> , 2013, 29, 2625-2632.	1.8	37
44	Signaling cascades as cellular devices for spatial computations. <i>Journal of Mathematical Biology</i> , 2009, 58, 35-55.	0.8	36
45	Systems analysis of cellular networks under uncertainty. <i>FEBS Letters</i> , 2009, 583, 3923-3930.	1.3	35
46	Chemical Reaction Network Theory elucidates sources of multistability in interferon signaling. <i>PLoS Computational Biology</i> , 2017, 13, e1005454.	1.5	34
47	The Galactose Switch in <i>Kluyveromyces lactis</i> Depends on Nuclear Competition between Gal4 and Gal1 for Gal80 Binding. <i>Journal of Biological Chemistry</i> , 2006, 281, 29337-29348.	1.6	31
48	Design of a biological half adder. <i>IET Synthetic Biology</i> , 2007, 1, 53-58.	0.2	30
49	Dephosphorylation activates the purified plant plasma membrane H ⁺ -ATPase . Possible function of phosphothreonine residues in a mechanism not involving the regulatory C-terminal domain of the enzyme. <i>FEBS Journal</i> , 1998, 251, 496-503.	0.2	29
50	Effect of Immunosuppression on T-Helper 2 and B-Cell Responses to Influenza Vaccination. <i>Journal of Infectious Diseases</i> , 2015, 212, 137-146.	1.9	28
51	Modular Analysis of Biological Networks. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 3-17.	0.8	27
52	Genome-scale metabolic networks in time and space. <i>Current Opinion in Systems Biology</i> , 2018, 8, 51-58.	1.3	27
53	Use of YouScope to Implement Systematic Microscopy Protocols. <i>Current Protocols in Molecular Biology</i> , 2012, 98, Unit 14.21.1-23.	2.9	25
54	Model-based integration of genomics and metabolomics reveals SNP functionality in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8494-8502.	3.3	24

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55	Mathematical Modeling of Complex Regulatory Networks. IEEE Transactions on Nanobioscience, 2004, 3, 172-179.	2.2	23
56	Remote control of microtubule plus-end dynamics and function from the minus-end. ELife, 2019, 8, .	2.8	23
57	Modular, rule-based modeling for the design of eukaryotic synthetic gene circuits. BMC Systems Biology, 2013, 7, 42.	3.0	21
58	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011.	1.4	21
59	Efficient Reconstruction of Predictive Consensus Metabolic Network Models. PLoS Computational Biology, 2016, 12, e1005085.	1.5	19
60	Computational design of biological circuits: putting parts into context. Molecular Systems Design and Engineering, 2017, 2, 410-421.	1.7	19
61	A Simple and Flexible Computational Framework for Inferring Sources of Heterogeneity from Single-Cell Dynamics. Cell Systems, 2019, 8, 15-26.e11.	2.9	19
62	Efficient Characterization of Parametric Uncertainty of Complex (Bio)chemical Networks. PLoS Computational Biology, 2015, 11, e1004457.	1.5	18
63	Automated Planning Enables Complex Protocols on Liquid-Handling Robots. ACS Synthetic Biology, 2018, 7, 922-932.	1.9	18
64	Stoichiometric and Constraint-based Modeling. , 2006, , 73-96.		18
65	Modeling the <i>Drosophila melanogaster</i> Circadian Oscillator via Phase Optimization. Journal of Biological Rhythms, 2008, 23, 525-537.	1.4	17
66	Using CellX to Quantify Intracellular Events. , 2013, Chapter 14, Unit 14.22..		17
67	An Orthogonal Permease-Inducer-Repressor Feedback Loop Shows Bistability. ACS Synthetic Biology, 2016, 5, 1098-1107.	1.9	17
68	Probabilistic thermodynamic analysis of metabolic networks. Bioinformatics, 2021, 37, 2938-2945.	1.8	16
69	A specialized ODE integrator for the efficient computation of parameter sensitivities. BMC Systems Biology, 2012, 6, 46.	3.0	15
70	Accelerating the Computation of Elementary Modes Using Pattern Trees. Lecture Notes in Computer Science, 2006, , 333-343.	1.0	13
71	Precise Regulation of Gene Expression Dynamics Favors Complex Promoter Architectures. PLoS Computational Biology, 2009, 5, e1000279.	1.5	12
72	Topological augmentation to infer hidden processes in biological systems. Bioinformatics, 2014, 30, 221-227.	1.8	12

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73	Model Extension and Model Selection. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 213-241.	0.7	12
74	Predicting network functions with nested patterns. <i>Nature Communications</i> , 2014, 5, 3006.	5.8	11
75	A rationally engineered decoder of transient intracellular signals. <i>Nature Communications</i> , 2021, 12, 1886.	5.8	11
76	BioSwitch: a tool for the detection of bistability and multi-steady state behaviour in signalling and gene regulatory networks. <i>Bioinformatics</i> , 2020, 36, 1640-1641.	1.8	10
77	Challenges in synthetically designing mammalian circadian clocks. <i>Current Opinion in Biotechnology</i> , 2010, 21, 556-565.	3.3	8
78	A method for inverse bifurcation of biochemical switches: inferring parameters from dose response curves. <i>BMC Systems Biology</i> , 2014, 8, 114.	3.0	8
79	Changing Face of Vaccination in Immunocompromised Hosts. <i>Current Infectious Disease Reports</i> , 2014, 16, 420.	1.3	8
80	Modular Parameter Identification of Biomolecular Networks. <i>SIAM Journal of Scientific Computing</i> , 2016, 38, B988-B1008.	1.3	8
81	Steady-State Differential Dose Response in Biological Systems. <i>Biophysical Journal</i> , 2018, 114, 723-736.	0.2	8
82	PolyRound: polytope rounding for random sampling in metabolic networks. <i>Bioinformatics</i> , 2022, 38, 566-567.	1.8	8
83	Structural Sensitivity Analysis of Metabolic Networks. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2008, 41, 15879-15884.	0.4	7
84	Autonomous Synchronization of Chemically Coupled Synthetic Oscillators. <i>Bulletin of Mathematical Biology</i> , 2011, 73, 2678-2706.	0.9	7
85	Multi-objective design of synthetic biological circuits. <i>IFAC-PapersOnLine</i> , 2017, 50, 9871-9876.	0.5	7
86	Bridging intracellular scales by mechanistic computational models. <i>Current Opinion in Biotechnology</i> , 2018, 52, 17-24.	3.3	7
87	Cutting the Wires: Modularization of Cellular Networks for Experimental Design. <i>Biophysical Journal</i> , 2014, 106, 321-331.	0.2	6
88	A Coupled Stochastic Model Explains Differences in Cry Knockout Behavior. <i>IEEE Life Sciences Letters</i> , 2015, 1, 3-6.	1.2	6
89	Synthetic gene network computational design. , 2009, , .		5
90	Efficient manipulation and generation of Kirchhoff polynomials for the analysis of non-equilibrium biochemical reaction networks. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20190828.	1.5	5

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91	Association of Host Factors With Antibody Response to Seasonal Influenza Vaccination in Allogeneic Hematopoietic Stem Cell Transplant Patients. <i>Journal of Infectious Diseases</i> , 2022, 225, 1482-1493.	1.9	5
92	Controlling cell-to-cell variability with synthetic gene circuits. <i>Biochemical Society Transactions</i> , 2019, 47, 1795-1804.	1.6	5
93	Metabolic Networks, Microbial Consortia, and Analogies to Smart Grids. <i>Proceedings of the IEEE</i> , 2022, 110, 541-556.	16.4	5
94	ROBUST PERFORMANCE IN BIOPHYSICAL NETWORKS. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2005, 38, 31-36.	0.4	4
95	Elementary flux modes “ state-of-the-art implementation and scope of application. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	4
96	Experimental analysis and modeling of single-cell time-course data. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100359.	1.3	4
97	Population Design for Synthetic Gene Circuits. <i>Lecture Notes in Computer Science</i> , 2021, , 181-197.	1.0	3
98	Model-based inference of neutralizing antibody avidities against influenza virus. <i>PLoS Pathogens</i> , 2022, 18, e1010243.	2.1	3
99	TopoFilter: a MATLAB package for mechanistic model identification in systems biology. <i>BMC Bioinformatics</i> , 2020, 21, 34.	1.2	2
100	<i>Automatic Control in Systems Biology</i> . , 2009, , 1335-1360.		2
101	Microbial Community Decision Making Models in Batch and Chemostat Cultures. <i>Lecture Notes in Computer Science</i> , 2021, , 141-158.	1.0	1
102	<i>Simplified Computational Design of Digital Synthetic Gene Circuits</i> . , 2014, , 257-271.		1
103	Analysis of Degenerate Chemical Reaction Networks. <i>Lecture Notes in Control and Information Sciences</i> , 2009, , 163-171.	0.6	1
104	<i>Robustness of minimal biochemical oscillators</i> . , 2008, , .		0
105	Advances in Chemical Reaction Network Theory for the Identification of Kinetic Models. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2012, 45, 1713-1718.	0.4	0
106	Designing genetic perturbation experiments for model selection under uncertainty. <i>IFAC-PapersOnLine</i> , 2020, 53, 15864-15869.	0.5	0