

Jörg Stelling

List of Publications by Year in descending order

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Version: 2024-02-01

106
papers

8,222
citations

87888

38
h-index

51608

86
g-index

122
all docs

122
docs citations

122
times ranked

8166
citing authors

#	ARTICLE	IF	CITATIONS
1	PolyRound: polytope rounding for random sampling in metabolic networks. <i>Bioinformatics</i> , 2022, 38, 566-567.	4.1	8
2	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.	4.0	5
3	Model-based inference of neutralizing antibody avidities against influenza virus. <i>PLoS Pathogens</i> , 2022, 18, e1010243.	4.7	3
4	Metabolic Networks, Microbial Consortia, and Analogies to Smart Grids. <i>Proceedings of the IEEE</i> , 2022, 110, 541-556.	21.8	5
5	Population Design for Synthetic Gene Circuits. <i>Lecture Notes in Computer Science</i> , 2021, , 181-197.	1.3	3
6	A rationally engineered decoder of transient intracellular signals. <i>Nature Communications</i> , 2021, 12, 1886.	12.8	11
7	Probabilistic thermodynamic analysis of metabolic networks. <i>Bioinformatics</i> , 2021, 37, 2938-2945.	4.1	16
8	Experimental analysis and modeling of single-cell time-course data. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100359.	2.6	4
9	Microbial Community Decision Making Models in Batch and Chemostat Cultures. <i>Lecture Notes in Computer Science</i> , 2021, , 141-158.	1.3	1
10	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.	4.1	10
11	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.	3.4	5
12	Multistable and dynamic CRISPRi-based synthetic circuits. <i>Nature Communications</i> , 2020, 11, 2746.	12.8	98
13	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.	7.1	24
14	TopoFilter: a MATLAB package for mechanistic model identification in systems biology. <i>BMC Bioinformatics</i> , 2020, 21, 34.	2.6	2
15	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
16	Designing genetic perturbation experiments for model selection under uncertainty. <i>IFAC-PapersOnLine</i> , 2020, 53, 15864-15869.	0.9	0
17	Microbial network disturbances in relapsing refractory Crohn's disease. <i>Nature Medicine</i> , 2019, 25, 323-336.	30.7	277
18	A Simple and Flexible Computational Framework for Inferring Sources of Heterogeneity from Single-Cell Dynamics. <i>Cell Systems</i> , 2019, 8, 15-26.e11.	6.2	19

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19	Inflammatory signals directly instruct PU.1 in HSCs via TNF. <i>Blood</i> , 2019, 133, 816-819.	1.4	53
20	Controlling cell-to-cell variability with synthetic gene circuits. <i>Biochemical Society Transactions</i> , 2019, 47, 1795-1804.	3.4	5
21	Remote control of microtubule plus-end dynamics and function from the minus-end. <i>ELife</i> , 2019, 8, .	6.0	23
22	Steady-State Differential Dose Response in Biological Systems. <i>Biophysical Journal</i> , 2018, 114, 723-736.	0.5	8
23	Bridging intracellular scales by mechanistic computational models. <i>Current Opinion in Biotechnology</i> , 2018, 52, 17-24.	6.6	7
24	Automated Planning Enables Complex Protocols on Liquid-Handling Robots. <i>ACS Synthetic Biology</i> , 2018, 7, 922-932.	3.8	18
25	Genome-scale metabolic networks in time and space. <i>Current Opinion in Systems Biology</i> , 2018, 8, 51-58.	2.6	27
26	Integrating omics data into genome-scale metabolic network models: principles and challenges. <i>Essays in Biochemistry</i> , 2018, 62, 563-574.	4.7	40
27	Predicting ligand-dependent tumors from multi-dimensional signaling features. <i>Npj Systems Biology and Applications</i> , 2017, 3, 27.	3.0	39
28	Computational design of biological circuits: putting parts into context. <i>Molecular Systems Design and Engineering</i> , 2017, 2, 410-421.	3.4	19
29	Multi-objective design of synthetic biological circuits. <i>IFAC-PapersOnLine</i> , 2017, 50, 9871-9876.	0.9	7
30	Chemical Reaction Network Theory elucidates sources of multistability in interferon signaling. <i>PLoS Computational Biology</i> , 2017, 13, e1005454.	3.2	34
31	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16011.	3.0	21
32	Efficient Reconstruction of Predictive Consensus Metabolic Network Models. <i>PLoS Computational Biology</i> , 2016, 12, e1005085.	3.2	19
33	Modular Parameter Identification of Biomolecular Networks. <i>SIAM Journal of Scientific Computing</i> , 2016, 38, B988-B1008.	2.8	8
34	Î2-cell mimetic designer cells provide closed-loop glyceimic control. <i>Science</i> , 2016, 354, 1296-1301.	12.6	173
35	An Orthogonal Permease Inducer Repressor Feedback Loop Shows Bistability. <i>ACS Synthetic Biology</i> , 2016, 5, 1098-1107.	3.8	17
36	Model Extension and Model Selection. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 213-241.	1.0	12

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37	Efficient Characterization of Parametric Uncertainty of Complex (Bio)chemical Networks. PLoS Computational Biology, 2015, 11, e1004457.	3.2	18
38	A Coupled Stochastic Model Explains Differences in Cry Knockout Behavior. IEEE Life Sciences Letters, 2015, 1, 3-6.	1.2	6
39	Inferring causal metabolic signals that regulate the dynamic <scp>TORC</scp>1â€dependent transcriptome. Molecular Systems Biology, 2015, 11, 802.	7.2	49
40	Effect of Immunosuppression on T-Helper 2 and B-Cell Responses to Influenza Vaccination. Journal of Infectious Diseases, 2015, 212, 137-146.	4.0	28
41	Topological augmentation to infer hidden processes in biological systems. Bioinformatics, 2014, 30, 221-227.	4.1	12
42	Inducible, tightly regulated and growth condition-independent transcription factor in Saccharomyces cerevisiae. Nucleic Acids Research, 2014, 42, e130-e130.	14.5	140
43	A method for inverse bifurcation of biochemical switches: inferring parameters from dose response curves. BMC Systems Biology, 2014, 8, 114.	3.0	8
44	Predicting network functions with nested patterns. Nature Communications, 2014, 5, 3006.	12.8	11
45	Changing Face of Vaccination in Immunocompromised Hosts. Current Infectious Disease Reports, 2014, 16, 420.	3.0	8
46	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
47	A Synthetic Multifunctional Mammalian pH Sensor and CO2 Transgene-Control Device. Molecular Cell, 2014, 55, 397-408.	9.7	96
48	Accurate cell segmentation in microscopy images using membrane patterns. Bioinformatics, 2014, 30, 2644-2651.	4.1	170
49	Cutting the Wires: Modularization of Cellular Networks for Experimental Design. Biophysical Journal, 2014, 106, 321-331.	0.5	6
50	Simplified Computational Design of Digital Synthetic Gene Circuits. , 2014, , 257-271.		1
51	Modular, rule-based modeling for the design of eukaryotic synthetic gene circuits. BMC Systems Biology, 2013, 7, 42.	3.0	21
52	Using CellX to Quantify Intracellular Events. , 2013, Chapter 14, Unit 14.22..		17
53	MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. Bioinformatics, 2013, 29, 815-816.	4.1	120
54	Automatic Generation of Predictive Dynamic Models Reveals Nuclear Phosphorylation as the Key Msn2 Control Mechanism. Science Signaling, 2013, 6, ra41.	3.6	44

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55	Near-optimal experimental design for model selection in systems biology. <i>Bioinformatics</i> , 2013, 29, 2625-2632.	4.1	37
56	Transcriptional regulation is insufficient to explain substrate-induced flux changes in <i>Bacillus subtilis</i> . <i>Molecular Systems Biology</i> , 2013, 9, 709.	7.2	149
57	System-Level Insights into Yeast Metabolism by Thermodynamic Analysis of Elementary Flux Modes. <i>PLoS Computational Biology</i> , 2012, 8, e1002415.	3.2	61
58	Advances in Chemical Reaction Network Theory for the Identification of Kinetic Models. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 1713-1718.	0.4	0
59	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. <i>Science</i> , 2012, 335, 1099-1103.	12.6	255
60	Synthetic two-way communication between mammalian cells. <i>Nature Biotechnology</i> , 2012, 30, 991-996.	17.5	97
61	A specialized ODE integrator for the efficient computation of parameter sensitivities. <i>BMC Systems Biology</i> , 2012, 6, 46.	3.0	15
62	Modular Analysis of Biological Networks. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 3-17.	1.6	27
63	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
64	Autonomous Synchronization of Chemically Coupled Synthetic Oscillators. <i>Bulletin of Mathematical Biology</i> , 2011, 73, 2678-2706.	1.9	7
65	Efficient characterization of high-dimensional parameter spaces for systems biology. <i>BMC Systems Biology</i> , 2011, 5, 142.	3.0	78
66	Automatic Design of Digital Synthetic Gene Circuits. <i>PLoS Computational Biology</i> , 2011, 7, e1001083.	3.2	85
67	Challenges in synthetically designing mammalian circadian clocks. <i>Current Opinion in Biotechnology</i> , 2010, 21, 556-565.	6.6	8
68	Self-sufficient control of urate homeostasis in mice by a synthetic circuit. <i>Nature Biotechnology</i> , 2010, 28, 355-360.	17.5	244
69	A synthetic low-frequency mammalian oscillator. <i>Nucleic Acids Research</i> , 2010, 38, 2702-2711.	14.5	93
70	Counter-Intuitive Stochastic Behavior of Simple Gene Circuits with Negative Feedback. <i>Biophysical Journal</i> , 2010, 98, 1742-1750.	0.5	38
71	Precise Regulation of Gene Expression Dynamics Favors Complex Promoter Architectures. <i>PLoS Computational Biology</i> , 2009, 5, e1000279.	3.2	12
72	Systems analysis of cellular networks under uncertainty. <i>FEBS Letters</i> , 2009, 583, 3923-3930.	2.8	35

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73	Signaling cascades as cellular devices for spatial computations. <i>Journal of Mathematical Biology</i> , 2009, 58, 35-55.	1.9	36
74	Genome-scale metabolic networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 285-297.	6.6	115
75	A tunable synthetic mammalian oscillator. <i>Nature</i> , 2009, 457, 309-312.	27.8	530
76	Computational design tools for synthetic biology. <i>Current Opinion in Biotechnology</i> , 2009, 20, 479-485.	6.6	101
77	Synthetic gene network computational design. , 2009, , .		5
78	Automatic Control in Systems Biology. , 2009, , 1335-1360.		2
79	Analysis of Degenerate Chemical Reaction Networks. <i>Lecture Notes in Control and Information Sciences</i> , 2009, , 163-171.	1.0	1
80	Large-scale computation of elementary flux modes with bit pattern trees. <i>Bioinformatics</i> , 2008, 24, 2229-2235.	4.1	291
81	Circadian Phase Resetting via Single and Multiple Control Targets. <i>PLoS Computational Biology</i> , 2008, 4, e1000104.	3.2	50
82	Modeling the <i>Drosophila melanogaster</i> Circadian Oscillator via Phase Optimization. <i>Journal of Biological Rhythms</i> , 2008, 23, 525-537.	2.6	17
83	Robustness of minimal biochemical oscillators. , 2008, , .		0
84	Structural Sensitivity Analysis of Metabolic Networks. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2008, 41, 15879-15884.	0.4	7
85	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.	7.1	96
86	Quantitative performance metrics for robustness in circadian rhythms. <i>Bioinformatics</i> , 2007, 23, 358-364.	4.1	42
87	Design of a biological half adder. <i>IET Synthetic Biology</i> , 2007, 1, 53-58.	0.2	30
88	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.	7.1	130
89	Ensemble modeling for analysis of cell signaling dynamics. <i>Nature Biotechnology</i> , 2007, 25, 1001-1006.	17.5	214
90	Elementary flux modes – state-of-the-art implementation and scope of application. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	4

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91	Systems interface biology. Journal of the Royal Society Interface, 2006, 3, 603-616.	3.4	53
92	The Galactose Switch in Kluyveromyces lactis Depends on Nuclear Competition between Gal4 and Gal1 for Gal80 Binding. Journal of Biological Chemistry, 2006, 281, 29337-29348.	3.4	31
93	Accelerating the Computation of Elementary Modes Using Pattern Trees. Lecture Notes in Computer Science, 2006, , 333-343.	1.3	13
94	Stoichiometric and Constraint-based Modeling. , 2006, , 73-96.		18
95	ROBUST PERFORMANCE IN BIOPHYSICAL NETWORKS. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 31-36.	0.4	4
96	Sensitivity analysis of oscillatory (bio)chemical systems. Computers and Chemical Engineering, 2005, 29, 663-673.	3.8	48
97	Robustness properties of circadian clock architectures. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13210-13215.	7.1	249
98	Comparison of network-based pathway analysis methods. Trends in Biotechnology, 2004, 22, 400-405.	9.3	347
99	Mathematical Modeling of Complex Regulatory Networks. IEEE Transactions on Nanobioscience, 2004, 3, 172-179.	3.3	23
100	Robustness of Cellular Functions. Cell, 2004, 118, 675-685.	28.9	930
101	Mathematical models in microbial systems biology. Current Opinion in Microbiology, 2004, 7, 513-518.	5.1	145
102	Two approaches for metabolic pathway analysis?. Trends in Biotechnology, 2003, 21, 64-69.	9.3	257
103	FluxAnalyzer: exploring structure, pathways, and flux distributions in metabolic networks on interactive flux maps. Bioinformatics, 2003, 19, 261-269.	4.1	187
104	Metabolic network structure determines key aspects of functionality and regulation. Nature, 2002, 420, 190-193.	27.8	712
105	Combinatorial complexity of pathway analysis in metabolic networks. Molecular Biology Reports, 2002, 29, 233-236.	2.3	196
106	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. FEBS Journal, 1998, 251, 496-503.	0.2	29