Steffen Klamt

List of Publications by Year
in descending order

107 papers	8,187 citations	61945 43 h-index	53190 85 g-index
113 all docs	113 docs citations	113 times ranked	5964 citing authors

#	Article	IF	Citations
1	Metabolic network structure determines key aspects of functionality and regulation. Nature, 2002, 420, 190-193.	13.7	712
2	Structural and functional analysis of cellular networks with CellNetAnalyzer. BMC Systems Biology, 2007, 1, 2.	3.0	454
3	Comparison of network-based pathway analysis methods. Trends in Biotechnology, 2004, 22, 400-405.	4.9	347
4	A methodology for the structural and functional analysis of signaling and regulatory networks. BMC Bioinformatics, 2006, 7, 56.	1.2	330
5	Hypergraphs and Cellular Networks. PLoS Computational Biology, 2009, 5, e1000385.	1.5	316
6	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
7	A Logical Model Provides Insights into T Cell Receptor Signaling. PLoS Computational Biology, 2007, 3, e163.	1.5	311
8	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. Molecular Systems Biology, 2009, 5, 331.	3.2	308
9	Two approaches for metabolic pathway analysis?. Trends in Biotechnology, 2003, 21, 64-69.	4.9	257
10	Minimal cut sets in biochemical reaction networks. Bioinformatics, 2004, 20, 226-234.	1.8	239
11	Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. BMC Systems Biology, 2009, 3, 98.	3.0	212
12	Computation of elementary modes: a unifying framework and the new binary approach. BMC Bioinformatics, 2004, 5, 175.	1.2	207
13	GSMN-TB: a web-based genome-scale network model of Mycobacterium tuberculosis metabolism. Genome Biology, 2007, 8, R89.	13.9	197
14	Combinatorial complexity of pathway analysis in metabolic networks. Molecular Biology Reports, 2002, 29, 233-236.	1.0	196
15	FluxAnalyzer: exploring structure, pathways, and flux distributions in metabolic networks on interactive flux maps. Bioinformatics, 2003, 19, 261-269.	1.8	187
16	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
17	The Logic of EGFR/ErbB Signaling: Theoretical Properties and Analysis of High-Throughput Data. PLoS Computational Biology, 2009, 5, e1000438.	1.5	164
18	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

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19	Model-based metabolic engineering enables high yield itaconic acid production by Escherichia coli. Metabolic Engineering, 2016, 38, 29-37.	3.6	144
20	Calculability analysis in underdetermined metabolic networks illustrated by a model of the central metabolism in purple nonsulfur bacteria. Biotechnology and Bioengineering, 2002, 77, 734-751.	1.7	112
21	Generalized concept of minimal cut sets in biochemical networks. BioSystems, 2006, 83, 233-247.	0.9	107
22	Modeling approaches for qualitative and semi-quantitative analysis of cellular signaling networks. Cell Communication and Signaling, 2013, 11, 43.	2.7	106
23	Growth-coupled overproduction is feasible for almost all metabolites in five major production organisms. Nature Communications, 2017, 8, 15956.	5.8	105
24	Computing complex metabolic intervention strategies using constrained minimal cut sets. Metabolic Engineering, 2011, 13, 204-213.	3.6	100
25	Enumeration of Smallest Intervention Strategies in Genome-Scale Metabolic Networks. PLoS Computational Biology, 2014, 10, e1003378.	1.5	97
26	Temperatureâ€dependent dynamic control of the TCA cycle increases volumetric productivity of itaconic acid production by <i>Escherichia coli</i>. Biotechnology and Bioengineering, 2018, 115, 156-164.	1.7	97
27	Metabolic network modeling of redox balancing and biohydrogen production in purple nonsulfur bacteria. BMC Systems Biology, 2011, 5, 150.	3.0	86
28	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. Molecular BioSystems, 2013, 9, 1576.	2.9	83
29	On the feasibility of growth-coupled product synthesis in microbial strains. Metabolic Engineering, 2015, 30, 166-178.	3.6	83
30	Use of CellNetAnalyzer in biotechnology and metabolic engineering. Journal of Biotechnology, 2017, 261, 221-228.	1.9	83
31	CASOP: A Computational Approach for Strain Optimization aiming at high Productivity. Journal of Biotechnology, 2010, 147, 88-101.	1.9	78
32	In silico profiling of Escherichia coli and Saccharomyces cerevisiae as terpenoid factories. Microbial Cell Factories, 2013, 12, 84.	1.9	78
33	Cyanobacterial biofuels: new insights and strain design strategies revealed by computational modeling. Microbial Cell Factories, 2014, 13, 128.	1.9	76
34	Modeling the electron transport chain of purple nonâ€sulfur bacteria. Molecular Systems Biology, 2008, 4, 156.	3.2	73
35	Automatic construction of metabolic models with enzyme constraints. BMC Bioinformatics, 2020, 21, 19.	1.2	69
36	An application programming interface for CellNetAnalyzer. BioSystems, 2011, 105, 162-168.	0.9	63

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37	Algorithmic approaches for computing elementary modes in large biochemical reaction networks. IET Systems Biology, 2005, 152, 249.	2.0	62
38	An algorithm for the reduction of genome-scale metabolic network models to meaningful core models. BMC Systems Biology, 2015, 9, 48.	3.0	61
39	Computing Knock-Out Strategies in Metabolic Networks. Journal of Computational Biology, 2008, 15, 259-268.	0.8	60
40	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. PLoS Computational Biology, 2017, 13, e1005409.	1.5	60
41	Host-pathogen systems biology: logical modelling of hepatocyte growth factor and Helicobacter pylori induced c-Met signal transduction. BMC Systems Biology, 2008, 2, 4.	3.0	59
42	Minimal cut sets in a metabolic network are elementary modes in a dual network. Bioinformatics, 2012, 28, 381-387.	1.8	54
43	When Do Two‐Stage Processes Outperform One‐Stage Processes?. Biotechnology Journal, 2018, 13, 1700539.	1.8	52
44	Enforced ATP futile cycling increases specific productivity and yield of anaerobic lactate production in <i>Escherichia coli</i>. Biotechnology and Bioengineering, 2015, 112, 2195-2199.	1.7	50
45	OptMDFpathway: Identification of metabolic pathways with maximal thermodynamic driving force and its application for analyzing the endogenous CO2 fixation potential of Escherichia coli. PLoS Computational Biology, 2018, 14, e1006492.	1.5	45
46	Computing Combinatorial Intervention Strategies and Failure Modes in Signaling Networks. Journal of Computational Biology, 2010, 17, 39-53.	0.8	44
47	EColiCore2: a reference network model of the central metabolism of Escherichia coli and relationships to its genome-scale parent model. Scientific Reports, 2017, 7, 39647.	1.6	41
48	Detecting and Removing Inconsistencies between Experimental Data and Signaling Network Topologies Using Integer Linear Programming on Interaction Graphs. PLoS Computational Biology, 2013, 9, e1003204.	1.5	40
49	A mathematical framework for yield (vs. rate) optimization in constraint-based modeling and applications in metabolic engineering. Metabolic Engineering, 2018, 47, 153-169.	3.6	37
50	MoVE identifies metabolic valves to switch between phenotypic states. Nature Communications, 2018, 9, 5332.	5.8	37
51	Broadening the Scope of Enforced ATP Wasting as a Tool for Metabolic Engineering in <i>Escherichia coli</i>. Biotechnology Journal, 2019, 14, e1800438.	1.8	32
52	An integrative model links multiple inputs and signaling pathways to the onset of DNA synthesis in hepatocytes. FEBS Journal, 2012, 279, 3290-3313.	2.2	30
53	Computing paths and cycles in biological interaction graphs. BMC Bioinformatics, 2009, 10, 181.	1.2	29
54	RedCom: A strategy for reduced metabolic modeling of complex microbial communities and its application for analyzing experimental datasets from anaerobic digestion. PLoS Computational Biology, 2019, 15, e1006759.	1.5	29

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55	TRANSWESD: inferring cellular networks with transitive reduction. Bioinformatics, 2010, 26, 2160-2168.	1.8	27
56	Genome-scale strain designs based on regulatory minimal cut sets. Bioinformatics, 2015, 31, 2844-2851.	1.8	26
57	Establishment of a five-enzyme cell-free cascade for the synthesis of uridine diphosphate N-acetylglucosamine. Journal of Biotechnology, 2018, 283, 120-129.	1.9	26
58	An extended and generalized framework for the calculation of metabolic intervention strategies based on minimal cut sets. PLoS Computational Biology, 2020, 16, e1008110.	1.5	24
59	Blending industrial blast furnace gas with H2 enables Acetobacterium woodii to efficiently co-utilize CO, CO2 and H2. Bioresource Technology, 2021, 323, 124573.	4.8	23
60	Large-scale network models of IL-1 and IL-6 signalling and their hepatocellular specification. Molecular BioSystems, 2011, 7, 3253.	2.9	22
61	Comparison and improvement of algorithms for computing minimal cut sets. BMC Bioinformatics, 2013, 14, 318.	1.2	22
62	Predicting compositions of microbial communities from stoichiometric models with applications for the biogas process. Biotechnology for Biofuels, 2016, 9, 17.	6.2	20
63	Manipulation of the ATP pool as a tool for metabolic engineering. Biochemical Society Transactions, 2015, 43, 1140-1145.	1.6	19
64	T160‐phosphorylated <scp>CDK</scp>2 defines threshold for <scp>HGF</scp>‐dependent proliferation in primary hepatocytes. Molecular Systems Biology, 2015, 11, 795.	3.2	19
65	The avian cell line AGE1.CR.pIX characterized by metabolic flux analysis. BMC Biotechnology, 2014, 14, 72.	1.7	18
66	A model integration approach linking signalling and gene-regulatory logic with kinetic metabolic models. BioSystems, 2014, 124, 26-38.	0.9	18
67	MUFINS: multi-formalism interaction network simulator. Npj Systems Biology and Applications, 2016, 2, 16032.	1.4	18
68	Stoichiometric and Constraint-based Modeling. , 2006, , 73-96.		18
69	Characterizing and ranking computed metabolic engineering strategies. Bioinformatics, 2019, 35, 3063-3072.	1.8	17
70	ATPase-based implementation of enforced ATP wasting in Saccharomyces cerevisiae for improved ethanol production. Biotechnology for Biofuels, 2020, 13, 185.	6.2	17
71	Visual setup of logical models of signaling and regulatory networks with ProMoT. BMC Bioinformatics, 2006, 7, 506.	1.2	16
72	Calculating as many fluxes as possible in underdetermined metabolic networks. Molecular Biology Reports, 2002, 29, 243-248.	1.0	15

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73	Disentangling the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. PLoS Computational Biology, 2015, 11, e1004192.	1.5	15
74	Exact quantification of cellular robustness in genome-scale metabolic networks. Bioinformatics, 2016, 32, 730-737.	1.8	15
75	Silence on the relevant literature and errors in implementation. Nature Biotechnology, 2015, 33, 336-339.	9.4	14
76	Augmenting Biogas Process Modeling by Resolving Intracellular Metabolic Activity. Frontiers in Microbiology, 2019, 10, 1095.	1.5	14
77	Increasing ATP turnover boosts productivity ofÂ2,3-butanediol synthesis inÂEscherichia coli. Microbial Cell Factories, 2021, 20, 63.	1.9	14
78	TRaCE+: Ensemble inference of gene regulatory networks from transcriptional expression profiles of gene knock-out experiments. BMC Bioinformatics, 2016, 17, 252.	1.2	13
79	Extended notions of sign consistency to relate experimental data to signaling and regulatory network topologies. BMC Bioinformatics, 2015, 16, 345.	1.2	12
80	Generalizing Diffuse Interface Methods on Graphs: Nonsmooth Potentials and Hypergraphs. SIAM Journal on Applied Mathematics, 2018, 78, 1350-1377.	0.8	12
81	Designing microbial communities to maximize the thermodynamic driving force for the production of chemicals. PLoS Computational Biology, 2021, 17, e1009093.	1.5	12
82	Stoichiometric and Constraint-Based Analysis of Biochemical Reaction Networks. Modeling and Simulation in Science, Engineering and Technology, 2014, , 263-316.	0.4	12
83	Systematizing the different notions of growthâ€coupled product synthesis and a single framework for computing corresponding strain designs. Biotechnology Journal, 2021, 16, e2100236.	1.8	10
84	Deciphering the physiological response of <i>Escherichia coli</i> under high ATP demand. Molecular Systems Biology, 2021, 17, e10504.	3.2	10
85	Reconstruction of large-scale regulatory networks based on perturbation graphs and transitive reduction: improved methods and their evaluation. BMC Systems Biology, 2013, 7, 73.	3.0	9
86	From Binary to Multivalued to Continuous Models: The lac Operon as a Case Study. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	8
87	Speeding up the core algorithm for the dual calculation of minimal cut sets in large metabolic networks. BMC Bioinformatics, 2020, 21, 510.	1.2	8
88	MEMO: A Method for Computing Metabolic Modules for Cell-Free Production Systems. ACS Synthetic Biology, 2020, 9, 556-566.	1.9	8
89	CNApy: a CellNetAnalyzer GUI in Python for analyzing and designing metabolic networks. Bioinformatics, 2022, 38, 1467-1469.	1.8	8
90	Cellâ€Free Multiâ€Enzyme Synthesis and Purification of Uridine Diphosphate Galactose. ChemBioChem, 2022, 23, .	1.3	7

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91	Evaluating differences of metabolic performances: Statistical methods and their application to animal cell cultivations. Biotechnology and Bioengineering, 2013, 110, 2633-2642.	1.7	5
92	Maximizing batch fermentation efficiency by constrained model-based optimization and predictive control of adenosine triphosphate turnover. AICHE Journal, 2022, 68, .	1.8	5
93	Enabling anaerobic growth of Escherichia coli on glycerol in defined minimal medium using acetate as redox sink. Metabolic Engineering, 2022, 73, 50-57.	3.6	5
94	Network-Based Analysis of Nutraceuticals in Human Hepatocellular Carcinomas Reveals Mechanisms of Chemopreventive Action. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 350-361.	1.3	4
95	One-Stage vs. Two-Stage Bioprocesses: Comparative Computational and Experimental Studies and Consequences for Strain Design. IFAC-PapersOnLine, 2018, 51, 7.	0.5	4
96	Logical network of genotoxic stress-induced NF-kappaB signal transduction predicts putative target structures for therapeutic intervention strategies. Advances and Applications in Bioinformatics and Chemistry, 2009, 2, 125.	1.6	3
97	Analyzing and Resolving Infeasibility in Flux Balance Analysis of Metabolic Networks. Metabolites, 2022, 12, 585.	1.3	2
98	Applying metabolic pathway analysis to make good use of methanol. Trends in Biotechnology, 2002, 20, 322.	4.9	1
99	Host–Pathogen Interactions. , 2013, , 107-126.		1
100	Designing Optimal Experiments to Discriminate Interaction Graph Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 925-935.	1.9	1
101	Workbench zur Modellbildung, Simulation und Analyse zellulärer Systeme (Workbench for Model Set) Tj ETQq1 1 0.784314 rgBT /Ov	0.6	1
102	Systems-level analysis of redox signaling in Rhodospirillum rubrum. Journal of Biotechnology, 2008, 136, S108.	1.9	0
103	A Logical Model Provides Insights into T-cell Receptor Signaling. PLoS Computational Biology, 2005, preprint, e163.	1.5	0
104	Title is missing!. , 2020, 16, e1008110.		0
105	Title is missing!. , 2020, 16, e1008110.		0
106	Title is missing!. , 2020, 16, e1008110.		0
107	Title is missing!. , 2020, 16, e1008110.		0