

# Steffen Klamt

## List of Publications by Year in descending order

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Version: 2024-02-01

107  
papers

8,187  
citations

61984

43  
h-index

53230

85  
g-index

113  
all docs

113  
docs citations

113  
times ranked

5964  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-Free Multi-Enzyme Synthesis and Purification of Uridine Diphosphate Galactose. <i>ChemBioChem</i> , 2022, 23, .	2.6	7
2	Maximizing batch fermentation efficiency by constrained model-based optimization and predictive control of adenosine triphosphate turnover. <i>AIChE Journal</i> , 2022, 68, .	3.6	5
3	CNApy: a CellNetAnalyzer GUI in Python for analyzing and designing metabolic networks. <i>Bioinformatics</i> , 2022, 38, 1467-1469.	4.1	8
4	Enabling anaerobic growth of <i>Escherichia coli</i> on glycerol in defined minimal medium using acetate as redox sink. <i>Metabolic Engineering</i> , 2022, 73, 50-57.	7.0	5
5	Analyzing and Resolving Infeasibility in Flux Balance Analysis of Metabolic Networks. <i>Metabolites</i> , 2022, 12, 585.	2.9	2
6	Increasing ATP turnover boosts productivity of 2,3-butanediol synthesis in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2021, 20, 63.	4.0	14
7	Blending industrial blast furnace gas with H <sub>2</sub> enables <i>Acetobacterium woodii</i> to efficiently co-utilize CO, CO <sub>2</sub> and H <sub>2</sub> . <i>Bioresource Technology</i> , 2021, 323, 124573.	9.6	23
8	Designing microbial communities to maximize the thermodynamic driving force for the production of chemicals. <i>PLoS Computational Biology</i> , 2021, 17, e1009093.	3.2	12
9	Systematizing the different notions of growth-coupled product synthesis and a single framework for computing corresponding strain designs. <i>Biotechnology Journal</i> , 2021, 16, e2100236.	3.5	10
10	Deciphering the physiological response of <i>Escherichia coli</i> under high ATP demand. <i>Molecular Systems Biology</i> , 2021, 17, e10504.	7.2	10
11	Speeding up the core algorithm for the dual calculation of minimal cut sets in large metabolic networks. <i>BMC Bioinformatics</i> , 2020, 21, 510.	2.6	8
12	ATPase-based implementation of enforced ATP wasting in <i>Saccharomyces cerevisiae</i> for improved ethanol production. <i>Biotechnology for Biofuels</i> , 2020, 13, 185.	6.2	17
13	An extended and generalized framework for the calculation of metabolic intervention strategies based on minimal cut sets. <i>PLoS Computational Biology</i> , 2020, 16, e1008110.	3.2	24
14	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
15	MEMO: A Method for Computing Metabolic Modules for Cell-Free Production Systems. <i>ACS Synthetic Biology</i> , 2020, 9, 556-566.	3.8	8
16	Automatic construction of metabolic models with enzyme constraints. <i>BMC Bioinformatics</i> , 2020, 21, 19.	2.6	69
17	<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
18	Title is missing!. , 2020, 16, e1008110.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1008110.		0
20	Title is missing!. , 2020, 16, e1008110.		0
21	Title is missing!. , 2020, 16, e1008110.		0
22	Augmenting Biogas Process Modeling by Resolving Intracellular Metabolic Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1095.	3.5	14
23	Broadening the Scope of Enforced ATP Wasting as a Tool for Metabolic Engineering in <i>Escherichia coli</i> . <i>Biotechnology Journal</i> , 2019, 14, e1800438.	3.5	32
24	RedCom: A strategy for reduced metabolic modeling of complex microbial communities and its application for analyzing experimental datasets from anaerobic digestion. <i>PLoS Computational Biology</i> , 2019, 15, e1006759.	3.2	29
25	Characterizing and ranking computed metabolic engineering strategies. <i>Bioinformatics</i> , 2019, 35, 3063-3072.	4.1	17
26	Designing Optimal Experiments to Discriminate Interaction Graph Models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 925-935.	3.0	1
27	A mathematical framework for yield (vs. rate) optimization in constraint-based modeling and applications in metabolic engineering. <i>Metabolic Engineering</i> , 2018, 47, 153-169.	7.0	37
28	Temperature-dependent dynamic control of the TCA cycle increases volumetric productivity of itaconic acid production by <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2018, 115, 156-164.	3.3	97
29	When Do Two-Stage Processes Outperform One-Stage Processes?. <i>Biotechnology Journal</i> , 2018, 13, 1700539.	3.5	52
30	MoVE identifies metabolic valves to switch between phenotypic states. <i>Nature Communications</i> , 2018, 9, 5332.	12.8	37
31	OptMDFpathway: Identification of metabolic pathways with maximal thermodynamic driving force and its application for analyzing the endogenous CO <sub>2</sub> fixation potential of <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2018, 14, e1006492.	3.2	45
32	One-Stage vs. Two-Stage Bioprocesses: Comparative Computational and Experimental Studies and Consequences for Strain Design. <i>IFAC-PapersOnLine</i> , 2018, 51, 7.	0.9	4
33	Generalizing Diffuse Interface Methods on Graphs: Nonsmooth Potentials and Hypergraphs. <i>SIAM Journal on Applied Mathematics</i> , 2018, 78, 1350-1377.	1.8	12
34	Establishment of a five-enzyme cell-free cascade for the synthesis of uridine diphosphate N-acetylglucosamine. <i>Journal of Biotechnology</i> , 2018, 283, 120-129.	3.8	26
35	Use of CellNetAnalyzer in biotechnology and metabolic engineering. <i>Journal of Biotechnology</i> , 2017, 261, 221-228.	3.8	83
36	EColiCore2: a reference network model of the central metabolism of <i>Escherichia coli</i> and relationships to its genome-scale parent model. <i>Scientific Reports</i> , 2017, 7, 39647.	3.3	41

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37	Growth-coupled overproduction is feasible for almost all metabolites in five major production organisms. <i>Nature Communications</i> , 2017, 8, 15956.	12.8	105
38	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. <i>PLoS Computational Biology</i> , 2017, 13, e1005409.	3.2	60
39	TRaCE+: Ensemble inference of gene regulatory networks from transcriptional expression profiles of gene knock-out experiments. <i>BMC Bioinformatics</i> , 2016, 17, 252.	2.6	13
40	MUFINS: multi-formalism interaction network simulator. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16032.	3.0	18
41	Model-based metabolic engineering enables high yield itaconic acid production by <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2016, 38, 29-37.	7.0	144
42	Predicting compositions of microbial communities from stoichiometric models with applications for the biogas process. <i>Biotechnology for Biofuels</i> , 2016, 9, 17.	6.2	20
43	Exact quantification of cellular robustness in genome-scale metabolic networks. <i>Bioinformatics</i> , 2016, 32, 730-737.	4.1	15
44	Manipulation of the ATP pool as a tool for metabolic engineering. <i>Biochemical Society Transactions</i> , 2015, 43, 1140-1145.	3.4	19
45	Extended notions of sign consistency to relate experimental data to signaling and regulatory network topologies. <i>BMC Bioinformatics</i> , 2015, 16, 345.	2.6	12
46	Enforced ATP futile cycling increases specific productivity and yield of anaerobic lactate production in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2015, 112, 2195-2199.	3.3	50
47	Disentangling the Complexity of HGF Signaling by Combining Qualitative and Quantitative Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004192.	3.2	15
48	On the feasibility of growth-coupled product synthesis in microbial strains. <i>Metabolic Engineering</i> , 2015, 30, 166-178.	7.0	83
49	Genome-scale strain designs based on regulatory minimal cut sets. <i>Bioinformatics</i> , 2015, 31, 2844-2851.	4.1	26
50	Silence on the relevant literature and errors in implementation. <i>Nature Biotechnology</i> , 2015, 33, 336-339.	17.5	14
51	T160â€phosphorylated <i>CDK</i> <sup>2</sup> defines threshold for HGFâ€dependent proliferation in primary hepatocytes. <i>Molecular Systems Biology</i> , 2015, 11, 795.	7.2	19
52	Network-Based Analysis of Nutraceuticals in Human Hepatocellular Carcinomas Reveals Mechanisms of Chemopreventive Action. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 350-361.	2.5	4
53	An algorithm for the reduction of genome-scale metabolic network models to meaningful core models. <i>BMC Systems Biology</i> , 2015, 9, 48.	3.0	61
54	Enumeration of Smallest Intervention Strategies in Genome-Scale Metabolic Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003378.	3.2	97

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55	Cyanobacterial biofuels: new insights and strain design strategies revealed by computational modeling. <i>Microbial Cell Factories</i> , 2014, 13, 128.	4.0	76
56	The avian cell line AGE1.CR.pIX characterized by metabolic flux analysis. <i>BMC Biotechnology</i> , 2014, 14, 72.	3.3	18
57	A model integration approach linking signalling and gene-regulatory logic with kinetic metabolic models. <i>BioSystems</i> , 2014, 124, 26-38.	2.0	18
58	Stoichiometric and Constraint-Based Analysis of Biochemical Reaction Networks. <i>Modeling and Simulation in Science, Engineering and Technology</i> , 2014, , 263-316.	0.6	12
59	Modeling approaches for qualitative and semi-quantitative analysis of cellular signaling networks. <i>Cell Communication and Signaling</i> , 2013, 11, 43.	6.5	106
60	Evaluating differences of metabolic performances: Statistical methods and their application to animal cell cultivations. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2633-2642.	3.3	5
61	In silico profiling of <i>Escherichia coli</i> and <i>Saccharomyces cerevisiae</i> as terpenoid factories. <i>Microbial Cell Factories</i> , 2013, 12, 84.	4.0	78
62	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , 2013, 7, 135.	3.0	145
63	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. <i>Molecular BioSystems</i> , 2013, 9, 1576.	2.9	83
64	Host-Pathogen Interactions. , 2013, , 107-126.		1
65	Detecting and Removing Inconsistencies between Experimental Data and Signaling Network Topologies Using Integer Linear Programming on Interaction Graphs. <i>PLoS Computational Biology</i> , 2013, 9, e1003204.	3.2	40
66	Comparison and improvement of algorithms for computing minimal cut sets. <i>BMC Bioinformatics</i> , 2013, 14, 318.	2.6	22
67	Reconstruction of large-scale regulatory networks based on perturbation graphs and transitive reduction: improved methods and their evaluation. <i>BMC Systems Biology</i> , 2013, 7, 73.	3.0	9
68	Minimal cut sets in a metabolic network are elementary modes in a dual network. <i>Bioinformatics</i> , 2012, 28, 381-387.	4.1	54
69	An integrative model links multiple inputs and signaling pathways to the onset of DNA synthesis in hepatocytes. <i>FEBS Journal</i> , 2012, 279, 3290-3313.	4.7	30
70	Large-scale network models of IL-1 and IL-6 signalling and their hepatocellular specification. <i>Molecular BioSystems</i> , 2011, 7, 3253.	2.9	22
71	Metabolic network modeling of redox balancing and biohydrogen production in purple nonsulfur bacteria. <i>BMC Systems Biology</i> , 2011, 5, 150.	3.0	86
72	An application programming interface for CellNetAnalyzer. <i>BioSystems</i> , 2011, 105, 162-168.	2.0	63

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73	Computing complex metabolic intervention strategies using constrained minimal cut sets. <i>Metabolic Engineering</i> , 2011, 13, 204-213.	7.0	100
74	CASOP: A Computational Approach for Strain Optimization aiming at high Productivity. <i>Journal of Biotechnology</i> , 2010, 147, 88-101.	3.8	78
75	From Binary to Multivalued to Continuous Models: The lac Operon as a Case Study. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	8
76	TRANSWESD: inferring cellular networks with transitive reduction. <i>Bioinformatics</i> , 2010, 26, 2160-2168.	4.1	27
77	Computing Combinatorial Intervention Strategies and Failure Modes in Signaling Networks. <i>Journal of Computational Biology</i> , 2010, 17, 39-53.	1.6	44
78	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. <i>Molecular Systems Biology</i> , 2009, 5, 331.	7.2	308
79	Hypergraphs and Cellular Networks. <i>PLoS Computational Biology</i> , 2009, 5, e1000385.	3.2	316
80	The Logic of EGFR/ErbB Signaling: Theoretical Properties and Analysis of High-Throughput Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000438.	3.2	164
81	Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. <i>BMC Systems Biology</i> , 2009, 3, 98.	3.0	212
82	Computing paths and cycles in biological interaction graphs. <i>BMC Bioinformatics</i> , 2009, 10, 181.	2.6	29
83	Logical network of genotoxic stress-induced NF-kappaB signal transduction predicts putative target structures for therapeutic intervention strategies. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2009, 2, 125.	2.6	3
84	Host-pathogen systems biology: logical modelling of hepatocyte growth factor and Helicobacter pylori induced c-Met signal transduction. <i>BMC Systems Biology</i> , 2008, 2, 4.	3.0	59
85	Systems-level analysis of redox signaling in <i>Rhodospirillum rubrum</i> . <i>Journal of Biotechnology</i> , 2008, 136, S108.	3.8	0
86	Computing Knock-Out Strategies in Metabolic Networks. <i>Journal of Computational Biology</i> , 2008, 15, 259-268.	1.6	60
87	Modeling the electron transport chain of purple non-sulfur bacteria. <i>Molecular Systems Biology</i> , 2008, 4, 156.	7.2	73
88	A Logical Model Provides Insights into T Cell Receptor Signaling. <i>PLoS Computational Biology</i> , 2007, 3, e163.	3.2	311
89	GSMN-TB: a web-based genome-scale network model of <i>Mycobacterium tuberculosis</i> metabolism. <i>Genome Biology</i> , 2007, 8, R89.	9.6	197
90	Structural and functional analysis of cellular networks with CellNetAnalyzer. <i>BMC Systems Biology</i> , 2007, 1, 2.	3.0	454

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91	Generalized concept of minimal cut sets in biochemical networks. <i>BioSystems</i> , 2006, 83, 233-247.	2.0	107
92	Visual setup of logical models of signaling and regulatory networks with ProMoT. <i>BMC Bioinformatics</i> , 2006, 7, 506.	2.6	16
93	A methodology for the structural and functional analysis of signaling and regulatory networks. <i>BMC Bioinformatics</i> , 2006, 7, 56.	2.6	330
94	Stoichiometric and Constraint-based Modeling. , 2006, , 73-96.		18
95	Algorithmic approaches for computing elementary modes in large biochemical reaction networks. <i>IET Systems Biology</i> , 2005, 152, 249.	2.0	62
96	A Logical Model Provides Insights into T-cell Receptor Signaling. <i>PLoS Computational Biology</i> , 2005, preprint, e163.	3.2	0
97	Minimal cut sets in biochemical reaction networks. <i>Bioinformatics</i> , 2004, 20, 226-234.	4.1	239
98	Comparison of network-based pathway analysis methods. <i>Trends in Biotechnology</i> , 2004, 22, 400-405.	9.3	347
99	Computation of elementary modes: a unifying framework and the new binary approach. <i>BMC Bioinformatics</i> , 2004, 5, 175.	2.6	207
100	Workbench zur Modellbildung, Simulation und Analyse zellulärer Systeme (Workbench for Model Set) Tj ETQq0 0 0 rgBT /Overlock 10 T 0.9 1		
101	Two approaches for metabolic pathway analysis?. <i>Trends in Biotechnology</i> , 2003, 21, 64-69.	9.3	257
102	FluxAnalyzer: exploring structure, pathways, and flux distributions in metabolic networks on interactive flux maps. <i>Bioinformatics</i> , 2003, 19, 261-269.	4.1	187
103	Applying metabolic pathway analysis to make good use of methanol. <i>Trends in Biotechnology</i> , 2002, 20, 322.	9.3	1
104	Calculability analysis in underdetermined metabolic networks illustrated by a model of the central metabolism in purple nonsulfur bacteria. <i>Biotechnology and Bioengineering</i> , 2002, 77, 734-751.	3.3	112
105	Metabolic network structure determines key aspects of functionality and regulation. <i>Nature</i> , 2002, 420, 190-193.	27.8	712
106	Combinatorial complexity of pathway analysis in metabolic networks. <i>Molecular Biology Reports</i> , 2002, 29, 233-236.	2.3	196
107	Calculating as many fluxes as possible in underdetermined metabolic networks. <i>Molecular Biology Reports</i> , 2002, 29, 243-248.	2.3	15