Andreas DrÃ¤ger

List of Publications by Year
in descending order

74 papers	5,132 citations	159358 30 h-index	114278 63 g-index
93 all docs	93 docs citations	93 times ranked	6379 citing authors

#	Article	IF	Citations
1	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	6.5	746
2	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	9.4	520
3	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	1.5	344
4	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
5	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. Immunity, 2020, 53, 1296-1314.e9.	6.6	278
6	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	3.2	246
7	BioJava: an open-source framework for bioinformatics. Bioinformatics, 2008, 24, 2096-2097.	1.8	200
8	<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
9	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
10	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
11	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. Nucleic Acids Research, 2020, 48, D402-D406.	6.5	130
12	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
13	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	1.8	98
14	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	1.8	81
15	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	78
16	Synthetic promoters capable of driving robust nuclear gene expression in the green alga Chlamydomonas reinhardtii. Algal Research, 2016, 15, 135-142.	2.4	75
17	Do genome‐scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
18	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	6.5	65

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19	KEGGtranslator: visualizing and converting the KEGG PATHWAY database to various formats. Bioinformatics, 2011, 27, 2314-2315.	1.8	63
20	SBMLsqueezer: A CellDesigner plug-in to generate kinetic rate equations for biochemical networks. BMC Systems Biology, 2008, 2, 39.	3.0	61
21	Modeling metabolic networks in C. glutamicum: a comparison of rate laws in combination with various parameter optimization strategies. BMC Systems Biology, 2009, 3, 5.	3.0	59
22	Precise generation of systems biology models from KEGG pathways. BMC Systems Biology, 2013, 7, 15.	3.0	58
23	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	57
24	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
25	Improving Collaboration by Standardization Efforts in Systems Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 61.	2.0	52
26	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	3.2	52
27	CySBML: a Cytoscape plugin for SBML. Bioinformatics, 2012, 28, 2402-2403.	1.8	49
28	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	43
29	BowTieBuilder: modeling signal transduction pathways. BMC Systems Biology, 2009, 3, 67.	3.0	42
30	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10810-10815.	3.3	42
31	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 271.	1.0	42
32	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	1.8	37
33	Community standards to facilitate development and address challenges in metabolic modeling. Molecular Systems Biology, 2020, 16, e9235.	3.2	37
34	FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2. Bioinformatics, 2020, 36, i813-i821.	1.8	36
35	Genome-Scale Metabolic Model of Infection with SARS-CoV-2 Mutants Confirms Guanylate Kinase as Robust Potential Antiviral Target. Genes, 2021, 12, 796.	1.0	30
36	SBML2L<scp>a</scp>TEX: Conversion of SBML files into human-readable reports. Bioinformatics, 2009, 25, 1455-1456.	1.8	29

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37	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27
38	SBMLsqueezer 2: context-sensitive creation of kinetic equations in biochemical networks. BMC Systems Biology, 2015, 9, 68.	3.0	27
39	Coordinating Role of RXRα in Downregulating Hepatic Detoxification during Inflammation Revealed by Fuzzy-Logic Modeling. PLoS Computational Biology, 2016, 12, e1004431.	1.5	27
40	Evaluation of rate law approximations in bottom-up kinetic models of metabolism. BMC Systems Biology, 2016, 10, 40.	3.0	26
41	ZBIT Bioinformatics Toolbox: A Web-Platform for Systems Biology and Expression Data Analysis. PLoS ONE, 2016, 11, e0149263.	1.1	25
42	Systems biology graphical notation markup language (SBGNML) version 0.3. Journal of Integrative Bioinformatics, 2020, 17, .	1.0	21
43	Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653.	1.8	20
44	Inferring statin-induced gene regulatory relationships in primary human hepatocytes. Bioinformatics, 2011, 27, 2473-2477.	1.8	19
45	TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. PLoS ONE, 2013, 8, e82238.	1.1	17
46	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α-synuclein. BMC Neuroscience, 2013, 14, 136.	0.8	16
47	A Padawan Programmer's Guide to Developing Software Libraries. Cell Systems, 2017, 5, 431-437.	2.9	14
48	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	13
49	Visualizing metabolic network dynamics through time-series metabolomic data. BMC Bioinformatics, 2020, 21, 130.	1.2	13
50	ModuleMaster: A new tool to decipher transcriptional regulatory networks. BioSystems, 2010, 99, 79-81.	0.9	12
51	SBMLSimulator: A Java Tool for Model Simulation and Parameter Estimation in Systems Biology. Computation, 2014, 2, 246-257.	1.0	12
52	An updated genome-scale metabolic network reconstruction of Pseudomonas aeruginosa PA14 to characterize mucin-driven shifts in bacterial metabolism. Npj Systems Biology and Applications, 2021, 7, 37.	1.4	12
53	Curating and comparing 114 strain-specific genome-scale metabolic models of Staphylococcus aureus. Npj Systems Biology and Applications, 2021, 7, 30.	1.4	10
54	Genome-Scale Metabolic Modeling of Escherichia coli and Its Chassis Design for Synthetic Biology Applications. Methods in Molecular Biology, 2021, 2189, 217-229.	0.4	9

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55	Clinical Applications of Metabolic Models in SBML Format. , 2021, , 362-371.		8
56	First Genome-Scale Metabolic Model of Dolosigranulum pigrum Confirms Multiple Auxotrophies. Metabolites, 2021, 11, 232.	1.3	8
57	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartment species, version 1, release 2. Journal of Integrative Bioinformatics, 2020, 17, .	1.0	8
58	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	1.8	6
59	The systems biology simulation core library. Bioinformatics, 2022, 38, 864-865.	1.8	6
60	The Systems Biology Graphical Notation: Current Status and Applications in Systems Medicine. , 2021, , 372-381.		6
61	Metabolic Networks. , 2013, , 1249-1251.		5
62	INFERRING GENE REGULATORY NETWORKS BY MACHINE LEARNING METHODS. , 2007, , .		4
63	Automating Mathematical Modeling of Biochemical Reaction Networks. Systems Biology, 2010, , 159-205.	0.1	4
64	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. Bioinformatics, 2013, 29, 2216-2217.	1.8	4
65	Overview: Standards for Modeling in Systems Medicine. , 2021, , 345-353.		4
66	Insights into Dynamic Network States Using Metabolomic Data. Methods in Molecular Biology, 2019, 1978, 243-258.	0.4	3
67	Computational Model Informs Effective Control Interventions against Y. enterocolitica Co-Infection. Biology, 2020, 9, 431.	1.3	3
68	Benchmarking evolutionary algorithms on convenience kinetics models of the valine and leucine biosynthesis in C. glutamicum. , 2007, , .		2
69	Comparing various evolutionary algorithms on the parameter optimization of the valine and leucine biosynthesis in corynebacterium glutamicum. , 2007, , .		2
70	Parameter Estimation, Metabolic Network Modeling. , 2013, , 1627-1631.		1
71	ProDGe: investigating protein-protein interactions at the domain level. Nature Precedings, 2011, , .	0.1	0
72	Inferring transcriptional regulators for sets of co-expressed genes by multi-objective evolutionary optimization. , 2011, , .		0

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73	SBMLWebApp: Web-Based Simulation, Steady-State Analysis, and Parameter Estimation of Systems Biology Models. Processes, 2021, 9, 1830.	1.3	0
74	A Computational Model of Bacterial Population Dynamics in Gastrointestinal Yersinia enterocolitica Infections in Mice. Biology, 2022, 11, 297.	1.3	0