

Andreas DrÄøger

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

5,132
citations

159585

30
h-index

114465

63
g-index

93
all docs

93
docs citations

93
times ranked

6379
citing authors

#	ARTICLE	IF	CITATIONS
1	The systems biology simulation core library. <i>Bioinformatics</i> , 2022, 38, 864-865.	4.1	6
2	A Computational Model of Bacterial Population Dynamics in Gastrointestinal <i>Yersinia enterocolitica</i> Infections in Mice. <i>Biology</i> , 2022, 11, 297.	2.8	0
3	Overview: Standards for Modeling in Systems Medicine. , 2021, , 345-353.		4
4	Clinical Applications of Metabolic Models in SBML Format. , 2021, , 362-371.		8
5	First Genome-Scale Metabolic Model of <i>Dolosigranulum pigrum</i> Confirms Multiple Auxotrophies. <i>Metabolites</i> , 2021, 11, 232.	2.9	8
6	Genome-Scale Metabolic Model of Infection with SARS-CoV-2 Mutants Confirms Guanylate Kinase as Robust Potential Antiviral Target. <i>Genes</i> , 2021, 12, 796.	2.4	30
7	Curating and comparing 114 strain-specific genome-scale metabolic models of <i>Staphylococcus aureus</i> . <i>Npj Systems Biology and Applications</i> , 2021, 7, 30.	3.0	10
8	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. <i>Bioinformatics</i> , 2021, 37, 3702-3706.	4.1	6
9	The Systems Biology Graphical Notation: Current Status and Applications in Systems Medicine. , 2021, , 372-381.		6
10	Genome-Scale Metabolic Modeling of <i>Escherichia coli</i> and Its Chassis Design for Synthetic Biology Applications. <i>Methods in Molecular Biology</i> , 2021, 2189, 217-229.	0.9	9
11	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
12	SBMLWebApp: Web-Based Simulation, Steady-State Analysis, and Parameter Estimation of Systems Biology Models. <i>Processes</i> , 2021, 9, 1830.	2.8	0
13	An updated genome-scale metabolic network reconstruction of <i>Pseudomonas aeruginosa</i> PA14 to characterize mucin-driven shifts in bacterial metabolism. <i>Npj Systems Biology and Applications</i> , 2021, 7, 37.	3.0	12
14	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. <i>Nucleic Acids Research</i> , 2020, 48, D402-D406.	14.5	130
15	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020, 53, 1296-1314.e9.	14.3	278
16	Computational Model Informs Effective Control Interventions against <i>Y. enterocolitica</i> Co-Infection. <i>Biology</i> , 2020, 9, 431.	2.8	3
17	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	5.3	99
18	Visualizing metabolic network dynamics through time-series metabolomic data. <i>BMC Bioinformatics</i> , 2020, 21, 130.	2.6	13

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19	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
20	FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2. Bioinformatics, 2020, 36, i813-i821.	4.1	36
21	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartments species, version 1, release 2. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	8
22	Systems biology graphical notation markup language (SBGNML) version 0.3. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	21
23	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
24	Community standards to facilitate development and address challenges in metabolic modeling. Molecular Systems Biology, 2020, 16, e9235.	7.2	37
25	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	43
26	Insights into Dynamic Network States Using Metabolomic Data. Methods in Molecular Biology, 2019, 1978, 243-258.	0.9	3
27	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	78
28	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
29	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	17.5	520
30	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	13
31	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	57
32	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	14.5	65
33	A Padawan Programmer's Guide to Developing Software Libraries. Cell Systems, 2017, 5, 431-437.	6.2	14
34	Evaluation of rate law approximations in bottom-up kinetic models of metabolism. BMC Systems Biology, 2016, 10, 40.	3.0	26
35	Synthetic promoters capable of driving robust nuclear gene expression in the green alga Chlamydomonas reinhardtii. Algal Research, 2016, 15, 135-142.	4.6	75
36	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746

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37	Coordinating Role of RXR α in Downregulating Hepatic Detoxification during Inflammation Revealed by Fuzzy-Logic Modeling. PLoS Computational Biology, 2016, 12, e1004431.	3.2	27
38	ZBIT Bioinformatics Toolbox: A Web-Platform for Systems Biology and Expression Data Analysis. PLoS ONE, 2016, 11, e0149263.	2.5	25
39	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
40	SBMLsqueezer 2: context-sensitive creation of kinetic equations in biochemical networks. BMC Systems Biology, 2015, 9, 68.	3.0	27
41	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
42	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	4.1	98
43	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.	7.1	42
44	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	4.1	37
45	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 271.	1.5	42
46	SBMLSimulator: A Java Tool for Model Simulation and Parameter Estimation in Systems Biology. Computation, 2014, 2, 246-257.	2.0	12
47	Improving Collaboration by Standardization Efforts in Systems Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 61.	4.1	52
48	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27
49	Precise generation of systems biology models from KEGG pathways. BMC Systems Biology, 2013, 7, 15.	3.0	58
50	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
51	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
52	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. Bioinformatics, 2013, 29, 2216-2217.	4.1	4
53	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α -synuclein. BMC Neuroscience, 2013, 14, 136.	1.9	16
54	TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. PLoS ONE, 2013, 8, e82238.	2.5	17

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55	Parameter Estimation, Metabolic Network Modeling. , 2013, , 1627-1631.		1
56	Metabolic Networks. , 2013, , 1249-1251.		5
57	Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653.	4.1	20
58	CySBML: a Cytoscape plugin for SBML. Bioinformatics, 2012, 28, 2402-2403.	4.1	49
59	Inferring statin-induced gene regulatory relationships in primary human hepatocytes. Bioinformatics, 2011, 27, 2473-2477.	4.1	19
60	ProDGe: investigating protein-protein interactions at the domain level. Nature Precedings, 2011, , .	0.1	0
61	Inferring transcriptional regulators for sets of co-expressed genes by multi-objective evolutionary optimization. , 2011, , .		0
62	KEGGtranslator: visualizing and converting the KEGG PATHWAY database to various formats. Bioinformatics, 2011, 27, 2314-2315.	4.1	63
63	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
64	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	4.1	81
65	ModuleMaster: A new tool to decipher transcriptional regulatory networks. BioSystems, 2010, 99, 79-81.	2.0	12
66	Automating Mathematical Modeling of Biochemical Reaction Networks. Systems Biology, 2010, , 159-205.	0.1	4
67	SBML2L _{TEX} : Conversion of SBML files into human-readable reports. Bioinformatics, 2009, 25, 1455-1456.	4.1	29
68	Modeling metabolic networks in <i>C. glutamicum</i> : a comparison of rate laws in combination with various parameter optimization strategies. BMC Systems Biology, 2009, 3, 5.	3.0	59
69	BowTieBuilder: modeling signal transduction pathways. BMC Systems Biology, 2009, 3, 67.	3.0	42
70	SBMLsqueezer: A CellDesigner plug-in to generate kinetic rate equations for biochemical networks. BMC Systems Biology, 2008, 2, 39.	3.0	61
71	BioJava: an open-source framework for bioinformatics. Bioinformatics, 2008, 24, 2096-2097.	4.1	200
72	INFERRING GENE REGULATORY NETWORKS BY MACHINE LEARNING METHODS. , 2007, , .		4

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73	Benchmarking evolutionary algorithms on convenience kinetics models of the valine and leucine biosynthesis in <i>C. glutamicum</i> . , 2007, , .		2
74	Comparing various evolutionary algorithms on the parameter optimization of the valine and leucine biosynthesis in <i>corynebacterium glutamicum</i> . , 2007, , .		2