

Andreas DrÄoiger

List of Publications by Year in descending order

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Version: 2024-02-01

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	The systems biology simulation core library. <i>Bioinformatics</i> , 2022, 38, 864-865.	1.8	6
2	A Computational Model of Bacterial Population Dynamics in Gastrointestinal <i>Yersinia enterocolitica</i> Infections in Mice. <i>Biology</i> , 2022, 11, 297.	1.3	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.	1.3	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.	1.0	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.	1.4	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.	1.8	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.	0.4	9
11	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
12	SBMLWebApp: Web-Based Simulation, Steady-State Analysis, and Parameter Estimation of Systems Biology Models. <i>Processes</i> , 2021, 9, 1830.	1.3	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.	1.4	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.	6.5	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.	6.6	278
16	Computational Model Informs Effective Control Interventions against <i>Y. enterocolitica</i> Co-Infection. <i>Biology</i> , 2020, 9, 431.	1.3	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.	2.4	99
18	Visualizing metabolic network dynamics through time-series metabolomic data. <i>BMC Bioinformatics</i> , 2020, 21, 130.	1.2	13

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19	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
20	FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2. <i>Bioinformatics</i> , 2020, 36, i813-i821.	1.8	36
21	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartments species, version 1, release 2. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	8
22	Systems biology graphical notation markup language (SBGNML) version 0.3. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	21
23	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
24	Community standards to facilitate development and address challenges in metabolic modeling. <i>Molecular Systems Biology</i> , 2020, 16, e9235.	3.2	37
25	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	43
26	Insights into Dynamic Network States Using Metabolomic Data. <i>Methods in Molecular Biology</i> , 2019, 1978, 243-258.	0.4	3
27	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	78
28	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	3.2	52
29	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	9.4	520
30	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	13
31	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	57
32	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	6.5	65
33	A Padawan Programmer's Guide to Developing Software Libraries. <i>Cell Systems</i> , 2017, 5, 431-437.	2.9	14
34	Evaluation of rate law approximations in bottom-up kinetic models of metabolism. <i>BMC Systems Biology</i> , 2016, 10, 40.	3.0	26
35	Synthetic promoters capable of driving robust nuclear gene expression in the green alga <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2016, 15, 135-142.	2.4	75
36	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. <i>Nucleic Acids Research</i> , 2016, 44, D515-D522.	6.5	746

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37	Coordinating Role of RXR β in Downregulating Hepatic Detoxification during Inflammation Revealed by Fuzzy-Logic Modeling. <i>PLoS Computational Biology</i> , 2016, 12, e1004431.	1.5	27
38	ZBIT Bioinformatics Toolbox: A Web-Platform for Systems Biology and Expression Data Analysis. <i>PLoS ONE</i> , 2016, 11, e0149263.	1.1	25
39	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	3.2	68
40	SBMLsqueezer 2: context-sensitive creation of kinetic equations in biochemical networks. <i>BMC Systems Biology</i> , 2015, 9, 68.	3.0	27
41	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. <i>PLoS Computational Biology</i> , 2015, 11, e1004321.	1.5	344
42	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	1.8	98
43	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10810-10815.	3.3	42
44	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. <i>Bioinformatics</i> , 2015, 31, 3383-3386.	1.8	37
45	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 271.	1.0	42
46	SBMLSimulator: A Java Tool for Model Simulation and Parameter Estimation in Systems Biology. <i>Computation</i> , 2014, 2, 246-257.	1.0	12
47	Improving Collaboration by Standardization Efforts in Systems Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 61.	2.0	52
48	The systems biology simulation core algorithm. <i>BMC Systems Biology</i> , 2013, 7, 55.	3.0	27
49	Precise generation of systems biology models from KEGG pathways. <i>BMC Systems Biology</i> , 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. <i>BMC Systems Biology</i> , 2013, 7, 135.	3.0	145
51	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
52	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. <i>Bioinformatics</i> , 2013, 29, 2216-2217.	1.8	4
53	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α -synuclein. <i>BMC Neuroscience</i> , 2013, 14, 136.	0.8	16
54	TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. <i>PLoS ONE</i> , 2013, 8, e82238.	1.1	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.	1.8	20
58	CySBML: a Cytoscape plugin for SBML. Bioinformatics, 2012, 28, 2402-2403.	1.8	49
59	Inferring statin-induced gene regulatory relationships in primary human hepatocytes. Bioinformatics, 2011, 27, 2473-2477.	1.8	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.	1.8	63
63	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	3.2	246
64	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	1.8	81
65	ModuleMaster: A new tool to decipher transcriptional regulatory networks. BioSystems, 2010, 99, 79-81.	0.9	12
66	Automating Mathematical Modeling of Biochemical Reaction Networks. Systems Biology, 2010, , 159-205.	0.1	4
67	SBML2L<sc>a</sc>TEX: Conversion of SBML files into human-readable reports. Bioinformatics, 2009, 25, 1455-1456.	1.8	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.	1.8	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