Jonathan R Karr

List of Publications by Year
in descending order

39	2,424	471509	361022
papers	citations	17	35
		h-index	g-index
44	44	44	3339
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Whole-Cell Computational Model Predicts Phenotype from Genotype. Cell, 2012, 150, 389-401.	28.9	1,177
2	Integrating metabolic, transcriptional regulatory and signal transduction models in *Escherichia coli*. Bioinformatics, 2008, 24, 2044-2050.	4.1	285
3	SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
4	The principles of whole-cell modeling. Current Opinion in Microbiology, 2015, 27, 18-24.	5.1	66
5	Towards a whole-cell modeling approach for synthetic biology. Chaos, 2013, 23, 025112.	2.5	62
6	A blueprint for human whole-cell modeling. Current Opinion in Systems Biology, 2018, 7, 8-15.	2.6	60
7	Accelerated discovery via a whole-cell model. Nature Methods, 2013, 10, 1192-1195.	19.0	59
8	Emerging whole-cell modeling principles and methods. Current Opinion in Biotechnology, 2018, 51, 97-102.	6.6	57
9	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
10	WholeCellKB: model organism databases for comprehensive whole-cell models. Nucleic Acids Research, 2012, 41, D787-D792.	14.5	42
11	Building Structural Models of a Whole Mycoplasma Cell. Journal of Molecular Biology, 2022, 434, 167351.	4.2	40
12	WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau095-bau095.	3.0	39
13	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. PLoS Computational Biology, 2015, 11, e1004096.	3.2	35
14	Guidelines for Reproducibly Building and Simulating Systems Biology Models. IEEE Transactions on Biomedical Engineering, 2016, 63, 2015-2020.	4.2	29
15	Computer-Aided Whole-Cell Design: Taking a Holistic Approach by Integrating Synthetic With Systems Biology. Frontiers in Bioengineering and Biotechnology, 2020, 8, 942.	4.1	25
16	Best Practices for Making Reproducible Biochemical Models. Cell Systems, 2020, 11, 109-120.	6.2	25
17	WholeCellViz: data visualization for whole-cell models. BMC Bioinformatics, 2013, 14, 253.	2.6	23
18	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	16

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19	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	14
20	Organizing genome engineering for the gigabase scale. Nature Communications, 2020, 11, 689.	12.8	14
21	A combined systems and structural modeling approach repositions antibiotics for Mycoplasma genitalium. Computational Biology and Chemistry, 2015, 59, 91-97.	2.3	13
22	RunBioSimulations: an extensible web application that simulates a wide range of computational modeling frameworks, algorithms, and formats. Nucleic Acids Research, 2021, 49, W597-W602.	14.5	13
23	Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior. Nucleic Acids Research, 2021, 49, D516-D522.	14.5	12
24	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
25	Toward Scalable Whole-Cell Modeling of Human Cells. , 2016, , .		10
26	CAUSAL INFERENCE IN BIOLOGY NETWORKS WITH INTEGRATED BELIEF PROPAGATION. , 2014, , .		9
27	BpForms and BcForms: a toolkit for concretely describing non-canonical polymers and complexes to facilitate global biochemical networks. Genome Biology, 2020, 21, 117.	8.8	8
28	The simulation experiment description markup language (SED-ML): language specification for level 1 version 4. Journal of Integrative Bioinformatics, 2021, 18, 20210021.	1.5	8
29	Simulating single-cell metabolism using a stochastic flux-balance analysis algorithm. Biophysical Journal, 2021, 120, 5231-5242.	0.5	8
30	Model Integration in Computational Biology: The Role of Reproducibility, Credibility and Utility. Frontiers in Systems Biology, 2022, 2, .	0.7	7
31	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
32	Editorial: Computer-Aided Biodesign Across Scales. Frontiers in Bioengineering and Biotechnology, 2021, 9, 700418.	4.1	4
33	NetworkPainter: dynamic intracellular pathway animation in Cytobank. BMC Bioinformatics, 2015, 16, 172.	2.6	3
34	Reusability and composability in process description maps: RAS–RAF–MEK–ERK signalling. Briefings in Bioinformatics, 2021, 22, .	6.5	3
35	Practical resources for enhancing the reproducibility of mechanistic modeling in systems biology. Current Opinion in Systems Biology, 2021, 27, 100350.	2.6	3
36	Furthering genome design using models and algorithms. Current Opinion in Systems Biology, 2020, 24, 120-126.	2.6	2

#	Article	IF	Citations
37	Centralizing data to unlock whole-cell models. Current Opinion in Systems Biology, 2021, 27, 100353.	2.6	1
38	Status and Challenges of Reproducibility in Computational Systems and Synthetic Biology. , 2021, , 406-412.		0
39	DE-Sim: an object-oriented, discrete-event simulation tool for data-intensive modeling of complex systems in Python. Journal of Open Source Software, 2020, 5, 2685.	4.6	0