Jonathan R Karr

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	Building Structural Models of a Whole Mycoplasma Cell. Journal of Molecular Biology, 2022, 434, 167351.	4.2	40
2	Model Integration in Computational Biology: The Role of Reproducibility, Credibility and Utility. Frontiers in Systems Biology, 2022, 2, .	0.7	7
3	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
4	Status and Challenges of Reproducibility in Computational Systems and Synthetic Biology. , 2021, , 406-412.		0
5	Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior. Nucleic Acids Research, 2021, 49, D516-D522.	14.5	12
6	Reusability and composability in process description maps: RAS–RAF–MEK–ERK signalling. Briefings in Bioinformatics, 2021, 22, .	6.5	3
7	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
8	Editorial: Computer-Aided Biodesign Across Scales. Frontiers in Bioengineering and Biotechnology, 2021, 9, 700418.	4.1	4
9	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
10	Practical resources for enhancing the reproducibility of mechanistic modeling in systems biology. Current Opinion in Systems Biology, 2021, 27, 100350.	2.6	3
11	Centralizing data to unlock whole-cell models. Current Opinion in Systems Biology, 2021, 27, 100353.	2.6	1
12	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
13	Simulating single-cell metabolism using a stochastic flux-balance analysis algorithm. Biophysical Journal, 2021, 120, 5231-5242.	0.5	8
14	Furthering genome design using models and algorithms. Current Opinion in Systems Biology, 2020, 24, 120-126.	2.6	2
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	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
18	Organizing genome engineering for the gigabase scale. Nature Communications, 2020, 11, 689.	12.8	14

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19	<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
20	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
21	Emerging whole-cell modeling principles and methods. Current Opinion in Biotechnology, 2018, 51, 97-102.	6.6	57
22	A blueprint for human whole-cell modeling. Current Opinion in Systems Biology, 2018, 7, 8-15.	2.6	60
23	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
24	Toward Scalable Whole-Cell Modeling of Human Cells. , 2016, , .		10
25	Guidelines for Reproducibly Building and Simulating Systems Biology Models. IEEE Transactions on Biomedical Engineering, 2016, 63, 2015-2020.	4.2	29
26	The principles of whole-cell modeling. Current Opinion in Microbiology, 2015, 27, 18-24.	5.1	66
27	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. PLoS Computational Biology, 2015, 11, e1004096.	3.2	35
28	NetworkPainter: dynamic intracellular pathway animation in Cytobank. BMC Bioinformatics, 2015, 16, 172.	2.6	3
29	A combined systems and structural modeling approach repositions antibiotics for Mycoplasma genitalium. Computational Biology and Chemistry, 2015, 59, 91-97.	2.3	13
30	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	14
31	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	16
32	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
33	CAUSAL INFERENCE IN BIOLOGY NETWORKS WITH INTEGRATED BELIEF PROPAGATION. , 2014, , .		9
34	Accelerated discovery via a whole-cell model. Nature Methods, 2013, 10, 1192-1195.	19.0	59
35	WholeCellViz: data visualization for whole-cell models. BMC Bioinformatics, 2013, 14, 253.	2.6	23
36	Towards a whole-cell modeling approach for synthetic biology. Chaos, 2013, 23, 025112.	2.5	62

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37	WholeCellKB: model organism databases for comprehensive whole-cell models. Nucleic Acids Research, 2012, 41, D787-D792.	14.5	42
38	A Whole-Cell Computational Model Predicts Phenotype from Genotype. Cell, 2012, 150, 389-401.	28.9	1,177
39	Integrating metabolic, transcriptional regulatory and signal transduction models in <i>Escherichia coli</i>. Bioinformatics, 2008, 24, 2044-2050.	4.1	285