

Tomáš Helikar

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

2,087
citations

361413

20
h-index

276875

41
g-index

68
all docs

68
docs citations

68
times ranked

1698
citing authors

#	ARTICLE	IF	CITATIONS
1	Logical Modeling and Dynamical Analysis of Cellular Networks. <i>Frontiers in Genetics</i> , 2016, 7, 94.	2.3	216
2	The Cell Collective: Toward an open and collaborative approach to systems biology. <i>BMC Systems Biology</i> , 2012, 6, 96.	3.0	199
3	Emergent decision-making in biological signal transduction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1913-1918.	7.1	183
4	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
5	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
6	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
7	ChemChains: a platform for simulation and analysis of biochemical networks aimed to laboratory scientists. <i>BMC Systems Biology</i> , 2009, 3, 58.	3.0	79
8	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
9	Automated inference of Boolean models from molecular interaction maps using CaSQ. <i>Bioinformatics</i> , 2020, 36, 4473-4482.	4.1	57
10	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
11	A Mechanistic Computational Model Reveals That Plasticity of CD4+ T Cell Differentiation Is a Function of Cytokine Composition and Dosage. <i>Frontiers in Physiology</i> , 2018, 9, 878.	2.8	46
12	Simulation of Stimulation: Cytokine Dosage and Cell Cycle Crosstalk Driving Timing-Dependent T Cell Differentiation. <i>Frontiers in Physiology</i> , 2018, 9, 879.	2.8	44
13	A Comprehensive, Multi-Scale Dynamical Model of ErbB Receptor Signal Transduction in Human Mammary Epithelial Cells. <i>PLoS ONE</i> , 2013, 8, e61757.	2.5	42
14	A Cell Simulator Platform: The Cell Collective. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 93, 393-395.	4.7	38
15	Ergodic Sets as Cell Phenotype of Budding Yeast Cell Cycle. <i>PLoS ONE</i> , 2012, 7, e45780.	2.5	32
16	Systems Perturbation Analysis of a Large-Scale Signal Transduction Model Reveals Potentially Influential Candidates for Cancer Therapeutics. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 10.	4.1	29
17	Student Understanding of DNA Structure-Function Relationships Improves from Using 3D Learning Modules with Dynamic 3D Printed Models. <i>Biochemistry and Molecular Biology Education</i> , 2019, 47, 303-317.	1.2	29
18	Boolean Modeling of Biochemical Networks. <i>Open Bioinformatics Journal</i> , 2011, 5, 16-25.	1.0	28

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19	Integrating Interactive Computational Modeling in Biology Curricula. <i>PLoS Computational Biology</i> , 2015, 11, e1004131.	3.2	27
20	Dynamics of Influenza Virus and Human Host Interactions During Infection and Replication Cycle. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 988-1011.	1.9	26
21	Two heads are better than one: current landscape of integrating QSP and machine learning. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2022, 49, 5-18.	1.8	26
22	Setting the basis of best practices and standards for curation and annotation of logical models in biology – highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
23	Recent applications of quantitative systems pharmacology and machine learning models across diseases. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2022, 49, 19-37.	1.8	22
24	The Systems Biology Markup Language (SBML) Level 3 Package: Qualitative Models, Version 1, Release 1. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 270.	1.5	21
25	Bio-Logic Builder: A Non-Technical Tool for Building Dynamical, Qualitative Models. <i>PLoS ONE</i> , 2012, 7, e46417.	2.5	20
26	Computational Systems Biology Approach for the Study of Rheumatoid Arthritis: From a Molecular Map to a Dynamical Model. <i>Genomics and Computational Biology</i> , 2017, 4, 100050.	0.7	20
27	Simulated Computational Model Lesson Improves Foundational Systems Thinking Skills and Conceptual Knowledge in Biology Students. <i>BioScience</i> , 2018, 68, 612-621.	4.9	19
28	A practical guide to mechanistic systems modeling in biology using a logic-based approach. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	19
29	Using concept maps to characterise cellular respiration knowledge in undergraduate students. <i>Journal of Biological Education</i> , 2020, 54, 33-46.	1.5	18
30	Integrative computational approach identifies drug targets in CD4+ T-cell-mediated immune disorders. <i>Npj Systems Biology and Applications</i> , 2021, 7, 4.	3.0	18
31	Identification of potential tissue-specific cancer biomarkers and development of cancer versus normal genomic classifiers. <i>Oncotarget</i> , 2017, 8, 85692-85715.	1.8	18
32	Design, Assessment, and in vivo Evaluation of a Computational Model Illustrating the Role of CAV1 in CD4+ T-lymphocytes. <i>Frontiers in Immunology</i> , 2014, 5, 599.	4.8	16
33	SBML Level 3 package: Qualitative Models, Version 1, Release 1. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 691-730.	1.5	15
34	Teaching Metabolism in Upper-Division Undergraduate Biochemistry Courses using Online Computational Systems and Dynamical Models Improves Student Performance. <i>CBE Life Sciences Education</i> , 2021, 20, ar13.	2.3	14
35	Identification of Biologically Essential Nodes via Determinative Power in Logical Models of Cellular Processes. <i>Frontiers in Physiology</i> , 2018, 9, 1185.	2.8	13
36	Visualizing the Invisible: A Guide to Designing, Printing, and Incorporating Dynamic 3D Molecular Models to Teach Structure – Function Relationships. <i>Journal of Microbiology and Biology Education</i> , 2018, 19, .	1.0	13

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37	A multi-approach and multi-scale platform to model CD4+ T cells responding to infections. PLoS Computational Biology, 2021, 17, e1009209.	3.2	12
38	Molecular phylogeny and evolutionary dynamics of influenza A nonstructural (NS) gene. Infection, Genetics and Evolution, 2014, 22, 192-200.	2.3	11
39	Modelling activities integrating construction and simulation supported explanatory and evaluative reasoning. International Journal of Science Education, 2019, 41, 1764-1786.	1.9	11
40	CancerDiscover: an integrative pipeline for cancer biomarker and cancer class prediction from high-throughput sequencing data. Oncotarget, 2018, 9, 2565-2573.	1.8	10
41	Changes in students'™ mental models from computational modeling of gene regulatory networks. International Journal of STEM Education, 2019, 6, .	5.0	10
42	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. Briefings in Bioinformatics, 2022, 23, .	6.5	10
43	Essential role of systemic iron mobilization and redistribution for adaptive thermogenesis through HIF2-1±/hepcidin axis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2109186118.	7.1	9
44	Sensitivity analysis of biological Boolean networks using information fusion based on nonadditive set functions. BMC Systems Biology, 2014, 8, 92.	3.0	8
45	Interactive learning modules with 3D printed models improve student understanding of protein structureâ€“function relationships. Biochemistry and Molecular Biology Education, 2020, 48, 356-368.	1.2	8
46	Discovering Cellular Respiration with Computational Modeling and Simulations. CourseSource, 0, 4, .	0.0	8
47	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
48	Changes in lipid profiles of epileptic mouse model. Metabolomics, 2020, 16, 106.	3.0	7
49	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
50	Discovering Prokaryotic Gene Regulation by Building and Investigating a Computational Model of the lac Operon. CourseSource, 0, 6, .	0.0	6
51	Simulating a Computational Biological Model, Rather Than Reading, Elicits Changes in Brain Activity during Biological Reasoning. CBE Life Sciences Education, 2020, 19, ar45.	2.3	5
52	Aberrant energy metabolism and redox balance in seizure onset zones of epileptic patients. Journal of Proteomics, 2020, 223, 103812.	2.4	4
53	Integrative network analyses of transcriptomics data reveal potential drug targets for acute radiation syndrome. Scientific Reports, 2021, 11, 5585.	3.3	4
54	Programmatic access to logical models in the Cell Collective modeling environment via a REST API. BioSystems, 2016, 139, 12-16.	2.0	3

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55	Differences in Blood-Derived <i>Francisella tularensis</i> Type B Strains from Clinical Cases of Tularemia. <i>Microorganisms</i> , 2020, 8, 1515.	3.6	3
56	ccNetViz: a WebGL-based JavaScript library for visualization of large networks. <i>Bioinformatics</i> , 2020, 36, 4527-4529.	4.1	2
57	The Need for Research-Grade Systems Modeling Technologies for Life Science Education. <i>Trends in Molecular Medicine</i> , 2021, 27, 100-103.	6.7	2
58	Discovering Prokaryotic Gene Regulation with Simulations of the <i>trp</i> Operon. <i>CourseSource</i> , 0, 5, .	0.0	2
59	Decision Making in Cells. <i>Systems Biology</i> , 2010, , 295-336.	0.1	0