

Stefan Hoops

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,203
citations

257450

24
h-index

315739

38
g-index

51
all docs

51
docs citations

51
times ranked

5617
citing authors

#	ARTICLE	IF	CITATIONS
1	COPASI—a COMplex PATHway Simulator. <i>Bioinformatics</i> , 2006, 22, 3067-3074.	4.1	2,265
2	Controlled vocabularies and semantics in systems biology. <i>Molecular Systems Biology</i> , 2011, 7, 543.	7.2	246
3	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e91110.	7.2	178
4	Computational Modeling of Biochemical Networks Using COPASI. <i>Methods in Molecular Biology</i> , 2009, 500, 17-59.	0.9	163
5	Minimum Information About a Simulation Experiment (MIASE). <i>PLoS Computational Biology</i> , 2011, 7, e1001122.	3.2	133
6	Systems Modeling of Molecular Mechanisms Controlling Cytokine-driven CD4+ T Cell Differentiation and Phenotype Plasticity. <i>PLoS Computational Biology</i> , 2013, 9, e1003027.	3.2	111
7	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	6.5	110
8	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 266.	1.5	102
9	COPASI and its applications in biotechnology. <i>Journal of Biotechnology</i> , 2017, 261, 215-220.	3.8	78
10	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	78
11	Predictive Computational Modeling of the Mucosal Immune Responses during <i>Helicobacter pylori</i> Infection. <i>PLoS ONE</i> , 2013, 8, e73365.	2.5	53
12	Condor-COPASI: high-throughput computing for biochemical networks. <i>BMC Systems Biology</i> , 2012, 6, 91.	3.0	44
13	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 271.	1.5	42
14	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 603-659.	1.5	39
15	A new strategy for assessing sensitivities in biochemical models. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3619-3631.	3.4	37
16	Computational modeling of heterogeneity and function of CD4+ T cells. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 31.	3.7	35
17	ENteric Immunity Simulator: A Tool for In Silico Study of Gastroenteric Infections. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 273-288.	3.3	34
18	Modeling the Regulatory Mechanisms by Which NLRX1 Modulates Innate Immune Responses to <i>Helicobacter pylori</i> Infection. <i>PLoS ONE</i> , 2015, 10, e0137839.	2.5	32

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19	Hybrid modeling and simulation of stochastic effects on progression through the eukaryotic cell cycle. <i>Journal of Chemical Physics</i> , 2012, 136, 034105.	3.0	31
20	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 268.	1.5	31
21	Modeling the Role of Peroxisome Proliferator-Activated Receptor $\hat{1}$ and MicroRNA-146 in Mucosal Immune Responses to <i>Clostridium difficile</i> . <i>PLoS ONE</i> , 2012, 7, e47525.	2.5	30
22	Multiscale modeling of mucosal immune responses. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	29
23	Modeling the Mechanisms by Which HIV-Associated Immunosuppression Influences HPV Persistence at the Oral Mucosa. <i>PLoS ONE</i> , 2017, 12, e0168133.	2.5	29
24	Bistability analyses of CD4+ T follicular helper and regulatory cells during <i>Helicobacter pylori</i> infection. <i>Journal of Theoretical Biology</i> , 2016, 398, 74-84.	1.7	25
25	Systems Modeling of Interactions between Mucosal Immunity and the Gut Microbiome during <i>Clostridium difficile</i> Infection. <i>PLoS ONE</i> , 2015, 10, e0134849.	2.5	25
26	Sensitivity Analysis of an ENteric Immunity Simulator (ENISI)-Based Model of Immune Responses to <i>Helicobacter pylori</i> Infection. <i>PLoS ONE</i> , 2015, 10, e0136139.	2.5	24
27	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. <i>Methods in Enzymology</i> , 2009, 467, 583-599.	1.0	23
28	ENISI MSM: A novel multi-scale modeling platform for computational immunology. , 2014, , .		16
29	Supervised learning methods in modeling of CD4+ T cell heterogeneity. <i>BioData Mining</i> , 2015, 8, 27.	4.0	15
30	ENISI Visual, an agent-based simulator for modeling gut immunity. , 2012, , .		14
31	Ordinary Differential Equations (ODEs) Based Modeling. , 2016, , 63-78.		14
32	High-resolution computational modeling of immune responses in the gut. <i>GigaScience</i> , 2019, 8, .	6.4	13
33	High-Performance Interaction-Based Simulation of Gut Immunopathologies with ENteric Immunity Simulator (ENISI). , 2012, , .		12
34	BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> , 2022, 50, W108-W114.	14.5	11
35	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. <i>BMC Systems Biology</i> , 2014, 8, 42.	3.0	10
36	Agents and networks to model the dynamic interactions of intracellular transport. <i>Cellular Logistics</i> , 2017, 7, e1392401.	0.9	9

#	ARTICLE	IF	CITATIONS
37	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 731-901.	1.5	7
38	ENISI SDE: A New Web-Based Tool for Modeling Stochastic Processes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 289-297.	3.0	7
39	Reconstruction of endosomal organization and function by a combination of ODE and agent-based modeling strategies. <i>Biology Direct</i> , 2018, 13, 25.	4.6	7
40	Agent-Based Modeling and High Performance Computing. , 2016, , 79-111.		6
41	ENISI multiscale modeling of mucosal immune responses driven by high performance computing. , 2015, , .		5
42	JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations. <i>BMC Systems Biology</i> , 2015, 9, 95.	3.0	3
43	Supervised Learning with the Artificial Neural Networks Algorithm for Modeling Immune Cell Differentiation. , 2015, , 1-18.		2
44	Multiscale Modeling. , 2016, , 145-173.		2
45	JigCell Model Connector: building large molecular network models from components. <i>Simulation</i> , 2018, 94, 993-1008.	1.8	2
46	Use of Computational Modeling in Immunological Research. , 2016, , 31-43.		1
47	Efficiently Encoding Complex Biochemical Models with the Multistate Model Builder (MSMB). <i>Methods in Molecular Biology</i> , 2019, 1945, 119-139.	0.9	1
48	Computational Modeling. , 2016, , 9-29.		0
49	Computational Modeling of Immune System Interactions during Cytokine Release Syndrome (CRS) and Immune Effector Cell Associated Neurotoxicity Syndrome (ICANS) after Chimeric Antigen Receptor (CAR) T-Cell Therapy. <i>Transplantation and Cellular Therapy</i> , 2022, 28, S145-S146.	1.2	0