Stefan Hoops

List of Publications by Year
in descending order

49 papers	4,203 citations	257357 24 h-index	315616 38 g-index
51 all docs	51 docs citations	51 times ranked	5617 citing authors

#	Article	IF	Citations
1	COPASI--a COmplex PAthway SImulator. Bioinformatics, 2006, 22, 3067-3074.	1.8	2,265
2	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	3.2	246
3	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
4	Computational Modeling of Biochemical Networks Using COPASI. Methods in Molecular Biology, 2009, 500, 17-59.	0.4	163
5	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	1.5	133
6	Systems Modeling of Molecular Mechanisms Controlling Cytokine-driven CD4+ T Cell Differentiation and Phenotype Plasticity. PLoS Computational Biology, 2013, 9, e1003027.	1.5	111
7	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
8	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2015, 12, 266.	1.0	102
9	COPASI and its applications in biotechnology. Journal of Biotechnology, 2017, 261, 215-220.	1.9	78
10	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	78
11	Predictive Computational Modeling of the Mucosal Immune Responses during Helicobacter pylori Infection. PLoS ONE, 2013, 8, e73365.	1.1	53
12	Condor-COPASI: high-throughput computing for biochemical networks. BMC Systems Biology, 2012, 6, 91.	3.0	44
13	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 271.	1.0	42
14	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. Journal of Integrative Bioinformatics, 2015, 12, 603-659.	1.0	39
15	A new strategy for assessing sensitivities in biochemical models. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3619-3631.	1.6	37
16	Computational modeling of heterogeneity and function of CD4+ T cells. Frontiers in Cell and Developmental Biology, 2014, 2, 31.	1.8	35
17	ENteric Immunity SImulator: A Tool for In Silico Study of Gastroenteric Infections. IEEE Transactions on Nanobioscience, 2012, 11, 273-288.	2.2	34
18	Modeling the Regulatory Mechanisms by Which NLRX1 Modulates Innate Immune Responses to Helicobacter pylori Infection. PLoS ONE, 2015, 10, e0137839.	1.1	32

#	Article	IF	Citations
19	Hybrid modeling and simulation of stochastic effects on progression through the eukaryotic cell cycle. Journal of Chemical Physics, 2012, 136, 034105.	1.2	31
20	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. Journal of Integrative Bioinformatics, 2015, 12, 268.	1.0	31
21	Modeling the Role of Peroxisome Proliferator-Activated Receptor Î³ and MicroRNA-146 in Mucosal Immune Responses to Clostridium difficile. PLoS ONE, 2012, 7, e47525.	1.1	30
22	Multiscale modeling of mucosal immune responses. BMC Bioinformatics, 2015, 16, S2.	1.2	29
23	Modeling the Mechanisms by Which HIV-Associated Immunosuppression Influences HPV Persistence at the Oral Mucosa. PLoS ONE, 2017, 12, e0168133.	1.1	29
24	Bistability analyses of CD4+ T follicular helper and regulatory cells during Helicobacter pylori infection. Journal of Theoretical Biology, 2016, 398, 74-84.	0.8	25
25	Systems Modeling of Interactions between Mucosal Immunity and the Gut Microbiome during Clostridium difficile Infection. PLoS ONE, 2015, 10, e0134849.	1.1	25
26	Sensitivity Analysis of an ENteric Immunity SImulator (ENISI)-Based Model of Immune Responses to Helicobacter pylori Infection. PLoS ONE, 2015, 10, e0136139.	1.1	24
27	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. Methods in Enzymology, 2009, 467, 583-599.	0.4	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. BioData Mining, 2015, 8, 27.	2.2	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. GigaScience, 2019, 8, .	3.3	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. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
35	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. BMC Systems Biology, 2014, 8, 42.	3.0	10
36	Agents and networks to model the dynamic interactions of intracellular transport. Cellular Logistics, 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. Journal of Integrative Bioinformatics, 2015, 12, 731-901.	1.0	7
38	ENISI SDE: A New Web-Based Tool for Modeling Stochastic Processes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 289-297.	1.9	7
39	Reconstruction of endosomal organization and function by a combination of ODE and agent-based modeling strategies. Biology Direct, 2018, 13, 25.	1.9	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. BMC Systems Biology, 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. Simulation, 2018, 94, 993-1008.	1.1	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). Methods in Molecular Biology, 2019, 1945, 119-139.	0.4	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. Transplantation and Cellular Therapy, 2022, 28, S145-S146.	0.6	0