

# 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	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
2	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
3	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
4	<scp>SBML</scp> 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	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
6	High-resolution computational modeling of immune responses in the gut. <i>GigaScience</i> , 2019, 8, .	6.4	13
7	Efficiently Encoding Complex Biochemical Models with the Multistate Model Builder (MSMB). <i>Methods in Molecular Biology</i> , 2019, 1945, 119-139.	0.9	1
8	JigCell Model Connector: building large molecular network models from components. <i>Simulation</i> , 2018, 94, 993-1008.	1.8	2
9	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
10	Agents and networks to model the dynamic interactions of intracellular transport. <i>Cellular Logistics</i> , 2017, 7, e1392401.	0.9	9
11	COPASI and its applications in biotechnology. <i>Journal of Biotechnology</i> , 2017, 261, 215-220.	3.8	78
12	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
13	Agent-Based Modeling and High Performance Computing. , 2016, , 79-111.		6
14	Computational Modeling. , 2016, , 9-29.		0
15	Use of Computational Modeling in Immunological Research. , 2016, , 31-43.		1
16	Ordinary Differential Equations (ODEs) Based Modeling. , 2016, , 63-78.		14
17	Multiscale Modeling. , 2016, , 145-173.		2
18	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

#	ARTICLE	IF	CITATIONS
19	Multiscale modeling of mucosal immune responses. BMC Bioinformatics, 2015, 16, S2.	2.6	29
20	JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations. BMC Systems Biology, 2015, 9, 95.	3.0	3
21	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 731-901.	1.5	7
22	Sensitivity Analysis of an ENteric Immunity Simulator (ENISI)-Based Model of Immune Responses to Helicobacter pylori Infection. PLoS ONE, 2015, 10, e0136139.	2.5	24
23	Modeling the Regulatory Mechanisms by Which NLRX1 Modulates Innate Immune Responses to Helicobacter pylori Infection. PLoS ONE, 2015, 10, e0137839.	2.5	32
24	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. Journal of Integrative Bioinformatics, 2015, 12, 603-659.	1.5	39
25	Supervised Learning with the Artificial Neural Networks Algorithm for Modeling Immune Cell Differentiation. , 2015, , 1-18.		2
26	ENISI multiscale modeling of mucosal immune responses driven by high performance computing. , 2015, , .		5
27	ENISI SDE: A New Web-Based Tool for Modeling Stochastic Processes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 289-297.	3.0	7
28	Supervised learning methods in modeling of CD4+ T cell heterogeneity. BioData Mining, 2015, 8, 27.	4.0	15
29	Systems Modeling of Interactions between Mucosal Immunity and the Gut Microbiome during Clostridium difficile Infection. PLoS ONE, 2015, 10, e0134849.	2.5	25
30	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2015, 12, 266.	1.5	102
31	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. Journal of Integrative Bioinformatics, 2015, 12, 268.	1.5	31
32	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 271.	1.5	42
33	Computational modeling of heterogeneity and function of CD4+ T cells. Frontiers in Cell and Developmental Biology, 2014, 2, 31.	3.7	35
34	ENISI MSM: A novel multi-scale modeling platform for computational immunology. , 2014, , .		16
35	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. BMC Systems Biology, 2014, 8, 42.	3.0	10
36	Systems Modeling of Molecular Mechanisms Controlling Cytokine-driven CD4+ T Cell Differentiation and Phenotype Plasticity. PLoS Computational Biology, 2013, 9, e1003027.	3.2	111

#	ARTICLE	IF	CITATIONS
37	Predictive Computational Modeling of the Mucosal Immune Responses during <i>Helicobacter pylori</i> Infection. PLoS ONE, 2013, 8, e73365.	2.5	53
38	ENteric Immunity Simulator: A Tool for In Silico Study of Gastroenteric Infections. IEEE Transactions on Nanobioscience, 2012, 11, 273-288.	3.3	34
39	High-Performance Interaction-Based Simulation of Gut Immunopathologies with ENteric Immunity Simulator (ENISI). , 2012, , .		12
40	ENISI Visual, an agent-based simulator for modeling gut immunity. , 2012, , .		14
41	Condor-COPASI: high-throughput computing for biochemical networks. BMC Systems Biology, 2012, 6, 91.	3.0	44
42	Hybrid modeling and simulation of stochastic effects on progression through the eukaryotic cell cycle. Journal of Chemical Physics, 2012, 136, 034105.	3.0	31
43	Modeling the Role of Peroxisome Proliferator-Activated Receptor $\hat{1}^3$ and MicroRNA-146 in Mucosal Immune Responses to <i>Clostridium difficile</i> . PLoS ONE, 2012, 7, e47525.	2.5	30
44	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
45	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
46	Computational Modeling of Biochemical Networks Using COPASI. Methods in Molecular Biology, 2009, 500, 17-59.	0.9	163
47	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. Methods in Enzymology, 2009, 467, 583-599.	1.0	23
48	A new strategy for assessing sensitivities in biochemical models. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3619-3631.	3.4	37
49	COPASI—a COMplex PATHway Simulator. Bioinformatics, 2006, 22, 3067-3074.	4.1	2,265