

William S Hlavacek

List of Publications by Year in descending order

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Version: 2024-02-01

101
papers

5,035
citations

109321

35
h-index

106344

65
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109
all docs

109
docs citations

109
times ranked

6627
citing authors

#	ARTICLE	IF	CITATIONS
1	Implementation of a practical Markov chain Monte Carlo sampling algorithm in PyBioNetFit. <i>Bioinformatics</i> , 2022, 38, 1770-1772.	4.1	9
2	Bayesian Inference of State-Level COVID-19 Basic Reproduction Numbers across the United States. <i>Viruses</i> , 2022, 14, 157.	3.3	17
3	Daily Forecasting of Regional Epidemics of Coronavirus Disease with Bayesian Uncertainty Quantification, United States. <i>Emerging Infectious Diseases</i> , 2021, 27, 767-778.	4.3	14
4	Multisite EGFR phosphorylation is regulated by adaptor protein abundances and dimer lifetimes. <i>Molecular Biology of the Cell</i> , 2020, 31, 695-708.	2.1	20
5	Bayesian inference using qualitative observations of underlying continuous variables. <i>Bioinformatics</i> , 2020, 36, 3177-3184.	4.1	9
6	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartment species, version 1, release 2. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.5	8
7	<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
8	Scaling methods for accelerating kinetic Monte Carlo simulations of chemical reaction networks. <i>Journal of Chemical Physics</i> , 2019, 150, 244101.	3.0	5
9	Parameter estimation and uncertainty quantification for systems biology models. <i>Current Opinion in Systems Biology</i> , 2019, 18, 9-18.	2.6	38
10	PyBioNetFit and the Biological Property Specification Language. <i>IScience</i> , 2019, 19, 1012-1036.	4.1	47
11	Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. <i>PLoS Computational Biology</i> , 2019, 15, e1006706.	3.2	8
12	Using RuleBuilder to Graphically Define and Visualize BioNetGen-Language Patterns and Reaction Rules. <i>Methods in Molecular Biology</i> , 2019, 1945, 33-42.	0.9	0
13	A Step-by-Step Guide to Using BioNetFit. <i>Methods in Molecular Biology</i> , 2019, 1945, 391-419.	0.9	2
14	Prediction of Optimal Drug Schedules for Controlling Autophagy. <i>Scientific Reports</i> , 2019, 9, 1428.	3.3	17
15	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. <i>Seminars in Cancer Biology</i> , 2019, 54, 162-173.	9.6	16
16	Generalizing Gillespie's Direct Method to Enable Network-Free Simulations. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 2822-2848.	1.9	15
17	Preassembled GPCR signaling complexes mediate distinct cellular responses to ultralow ligand concentrations. <i>Science Signaling</i> , 2018, 11, .	3.6	36
18	Using both qualitative and quantitative data in parameter identification for systems biology models. <i>Nature Communications</i> , 2018, 9, 3901.	12.8	20

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19	Using Equation-Free Computation to Accelerate Network-Free Stochastic Simulation of Chemical Kinetics. <i>Journal of Physical Chemistry B</i> , 2018, 122, 6351-6356.	2.6	2
20	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. <i>Cell Systems</i> , 2018, 7, 161-179.e14.	6.2	53
21	Relaxation oscillations and hierarchy of feedbacks in MAPK signaling. <i>Scientific Reports</i> , 2017, 7, 38244.	3.3	47
22	Allergen Valency, Dose, and Fc μ RI Occupancy Set Thresholds for Secretory Responses to Pen a 1 and Motivate Design of Hypoallergens. <i>Journal of Immunology</i> , 2017, 198, 1034-1046.	0.8	13
23	Differential mast cell outcomes are sensitive to Fc μ RI-Syk binding kinetics. <i>Molecular Biology of the Cell</i> , 2017, 28, 3397-3414.	2.1	32
24	SPATKIN: a simulator for rule-based modeling of biomolecular site dynamics on surfaces. <i>Bioinformatics</i> , 2017, 33, 3667-3669.	4.1	3
25	TRuML. , 2017, , .		5
26	Timescale Separation of Positive and Negative Signaling Creates History-Dependent Responses to IgE Receptor Stimulation. <i>Scientific Reports</i> , 2017, 7, 15586.	3.3	18
27	BioNetFit: a fitting tool compatible with BioNetGen, Nfsim and distributed computing environments. <i>Bioinformatics</i> , 2016, 32, 798-800.	4.1	31
28	Inside-Out Signaling of Oncogenic EGFR Mutants Promotes Ligand-Independent Dimerization. <i>Biophysical Journal</i> , 2015, 108, 351a.	0.5	3
29	The eighth q-bio conference: meeting report and special issue preface. <i>Physical Biology</i> , 2015, 12, 060401.	1.8	0
30	Computational Analysis of an Autophagy/Translation Switch Based on Mutual Inhibition of MTORC1 and ULK1. <i>PLoS ONE</i> , 2015, 10, e0116550.	2.5	38
31	Enhanced dimerization drives ligand-independent activity of mutant epidermal growth factor receptor in lung cancer. <i>Molecular Biology of the Cell</i> , 2015, 26, 4087-4099.	2.1	79
32	Use of Mechanistic Models to Integrate and Analyze Multiple Proteomic Datasets. <i>Biophysical Journal</i> , 2015, 108, 1819-1829.	0.5	21
33	Modeling for (physical) biologists: an introduction to the rule-based approach. <i>Physical Biology</i> , 2015, 12, 045007.	1.8	57
34	Mitochondrial Morphological Features Are Associated with Fission and Fusion Events. <i>PLoS ONE</i> , 2014, 9, e95265.	2.5	92
35	Phosphorylation Site Dynamics of Early T-cell Receptor Signaling. <i>PLoS ONE</i> , 2014, 9, e104240.	2.5	54
36	The Seventh q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2014, 11, 040301.	1.8	1

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37	An Interaction Library for the FcγRI Signaling Network. <i>Frontiers in Immunology</i> , 2014, 5, 172.	4.8	16
38	Modeling Biomolecular Site Dynamics in Immunoreceptor Signaling Systems. <i>Advances in Experimental Medicine and Biology</i> , 2014, 844, 245-262.	1.6	8
39	Recruitment of the Adaptor Protein Grb2 to EGFR Tetramers. <i>Biochemistry</i> , 2014, 53, 2594-2604.	2.5	36
40	Optimal Aggregation of FcγRI with a Structurally Defined Trivalent Ligand Overrides Negative Regulation Driven by Phosphatases. <i>ACS Chemical Biology</i> , 2014, 9, 1508-1519.	3.4	40
41	Rule-based modeling: a computational approach for studying biomolecular site dynamics in cell signaling systems. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 13-36.	6.6	97
42	Perspective on the q-bio Summer School and Conference: 2007–2014 and beyond. <i>Quantitative Biology</i> , 2014, 2, 54-58.	0.5	5
43	Exploring higher-order EGFR oligomerisation and phosphorylation—a combined experimental and theoretical approach. <i>Molecular BioSystems</i> , 2013, 9, 1849.	2.9	72
44	Computational model for autophagic vesicle dynamics in single cells. <i>Autophagy</i> , 2013, 9, 74-92.	9.1	37
45	Modeling the Effect of APC Truncation on Destruction Complex Function in Colorectal Cancer Cells. <i>PLoS Computational Biology</i> , 2013, 9, e1003217.	3.2	23
46	Binding of Nucleoid-Associated Protein Fis to DNA Is Regulated by DNA Breathing Dynamics. <i>PLoS Computational Biology</i> , 2013, 9, e1002881.	3.2	23
47	Special section dedicated to The Sixth q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2013, 10, 030301.	1.8	2
48	Innovations of the Rule-Based Modeling Approach. , 2013, , 273-300.		16
49	Single-Cell Measurements of IgE-Mediated FcγRI Signaling Using an Integrated Microfluidic Platform. <i>PLoS ONE</i> , 2013, 8, e60159.	2.5	23
50	Improved predictions of transcription factor binding sites using physicochemical features of DNA. <i>Nucleic Acids Research</i> , 2012, 40, e175-e175.	14.5	30
51	A Computational Model for Early Events in B Cell Antigen Receptor Signaling: Analysis of the Roles of Lyn and Fyn. <i>Journal of Immunology</i> , 2012, 189, 646-658.	0.8	46
52	The Fifth Annual q-bio Conference on Cellular Information Processing. <i>Physical Biology</i> , 2012, 9, 050201.	1.8	0
53	The Brucella TIR-like protein TcpB interacts with the death domain of MyD88. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 299-304.	2.1	49
54	Specification, annotation, visualization and simulation of a large rule-based model for ERBB receptor signaling. <i>BMC Systems Biology</i> , 2012, 6, 107.	3.0	31

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55	Guidelines for visualizing and annotating rule-based models. <i>Molecular BioSystems</i> , 2011, 7, 2779.	2.9	36
56	Scaffold-mediated nucleation of protein signaling complexes: Elementary principles. <i>Mathematical Biosciences</i> , 2011, 232, 164-173.	1.9	27
57	Hierarchical graphs for rule-based modeling of biochemical systems. <i>BMC Bioinformatics</i> , 2011, 12, 45.	2.6	16
58	The efficiency of reactant site sampling in network-free simulation of rule-based models for biochemical systems. <i>Physical Biology</i> , 2011, 8, 055009.	1.8	18
59	Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing. <i>Physical Biology</i> , 2011, 8, 050301.	1.8	2
60	Prediction of metabolic reactions based on atomic and molecular properties of small-molecule compounds. <i>Bioinformatics</i> , 2011, 27, 1537-1545.	4.1	32
61	RuleMonkey: software for stochastic simulation of rule-based models. <i>BMC Bioinformatics</i> , 2010, 11, 404.	2.6	50
62	Using Sequence-Specific Chemical and Structural Properties of DNA to Predict Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2010, 6, e1001007.	3.2	26
63	Modeling Multivalent Ligand-Receptor Interactions with Steric Constraints on Configurations of Cell-Surface Receptor Aggregates. <i>Biophysical Journal</i> , 2010, 98, 48-56.	0.5	50
64	How to deal with large models?. <i>Molecular Systems Biology</i> , 2009, 5, 240.	7.2	27
65	Simulation of large-scale rule-based models. <i>Bioinformatics</i> , 2009, 25, 910-917.	4.1	54
66	The Complexity of Cell Signaling and the Need for a New Mechanics. <i>Science Signaling</i> , 2009, 2, pe46.	3.6	34
67	GetBonNie for building, analyzing and sharing rule-based models. <i>Bioinformatics</i> , 2009, 25, 1457-1460.	4.1	16
68	Rule-Based Modeling of Biochemical Systems with BioNetGen. <i>Methods in Molecular Biology</i> , 2009, 500, 113-167.	0.9	366
69	Stochastic effects and bistability in T cell receptor signaling. <i>Journal of Theoretical Biology</i> , 2008, 254, 110-122.	1.7	86
70	Kinetic Monte Carlo method for rule-based modeling of biochemical networks. <i>Physical Review E</i> , 2008, 78, 031910.	2.1	83
71	Kinetic Proofreading Model. <i>Advances in Experimental Medicine and Biology</i> , 2008, 640, 82-94.	1.6	16
72	Carbon-fate maps for metabolic reactions. <i>Bioinformatics</i> , 2007, 23, 3193-3199.	4.1	33

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73	Dynamics of the nucleated polymerization model of prion replication. <i>Biophysical Chemistry</i> , 2007, 125, 360-367.	2.8	18
74	Reconstruction of Metabolic Networks from High-Throughput Metabolite Profiling Data: In Silico Analysis of Red Blood Cell Metabolism. <i>Annals of the New York Academy of Sciences</i> , 2007, 1115, 102-115.	3.8	22
75	Rules for Modeling Signal-Transduction Systems. <i>Science Signaling</i> , 2006, 2006, re6-re6.	3.6	267
76	Graph Theory for Rule-Based Modeling of Biochemical Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 89-106.	1.3	45
77	On Imposing Detailed Balance in Complex Reaction Mechanisms. <i>Biophysical Journal</i> , 2006, 91, 1136-1141.	0.5	45
78	Depicting signaling cascades. <i>Nature Biotechnology</i> , 2006, 24, 137-138.	17.5	17
79	A network model of early events in epidermal growth factor receptor signaling that accounts for combinatorial complexity. <i>BioSystems</i> , 2006, 83, 136-151.	2.0	141
80	Prediction of oxidoreductase-catalyzed reactions based on atomic properties of metabolites. <i>Bioinformatics</i> , 2006, 22, 3082-3088.	4.1	21
81	'On-the-fly' or 'generate-first' modeling?. <i>Nature Biotechnology</i> , 2005, 23, 1344-1345.	17.5	16
82	Rule-based modeling of biochemical networks. <i>Complexity</i> , 2005, 10, 22-41.	1.6	110
83	Graphical rule-based representation of signal-transduction networks. , 2005, , .		25
84	Multiple Functions of a Feed-Forward-Loop Gene Circuit. <i>Journal of Molecular Biology</i> , 2005, 349, 501-514.	4.2	75
85	BioNetGen: software for rule-based modeling of signal transduction based on the interactions of molecular domains. <i>Bioinformatics</i> , 2004, 20, 3289-3291.	4.1	381
86	Design of gene circuits: lessons from bacteria. <i>Nature Reviews Genetics</i> , 2004, 5, 34-42.	16.3	206
87	Mathematical and computational models of immune-receptor signalling. <i>Nature Reviews Immunology</i> , 2004, 4, 445-456.	22.7	210
88	Interaction of a Monoclonal IgE-Specific Antibody with Cell-Surface IgE α Fc μ RI: Characterization of Equilibrium Binding and Secretory Response. <i>Biochemistry</i> , 2004, 43, 11352-11360.	2.5	7
89	The complexity of complexes in signal transduction. <i>Biotechnology and Bioengineering</i> , 2003, 84, 783-794.	3.3	176
90	Design Principles for Regulator Gene Expression in a Repressible Gene Circuit. <i>Journal of Molecular Biology</i> , 2003, 332, 861-876.	4.2	50

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91	Investigation of Early Events in Fc γ RI-Mediated Signaling Using a Detailed Mathematical Model. <i>Journal of Immunology</i> , 2003, 170, 3769-3781.	0.8	172
92	Retention of antigen on follicular dendritic cells and B lymphocytes through complement-mediated multivalent ligand-receptor interactions: theory and application to HIV treatment. <i>Mathematical Biosciences</i> , 2002, 176, 185-202.	1.9	26
93	Modeling the early signaling events mediated by Fc γ RI. <i>Molecular Immunology</i> , 2002, 38, 1213-1219.	2.2	54
94	A quantitative approach for studying IgE-Fc γ RI aggregation. <i>Molecular Immunology</i> , 2002, 38, 1221-1228.	2.2	20
95	Kinetic Proofreading in Receptor-Mediated Transduction of Cellular Signals: Receptor Aggregation, Partially Activated Receptors, and Cytosolic Messengers. <i>Bulletin of Mathematical Biology</i> , 2002, 64, 887-911.	1.9	30
96	Influence of follicular dendritic cells on HIV dynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2000, 355, 1051-1058.	4.0	25
97	Quantifying Aggregation of IgE-Fc γ RI by Multivalent Antigen. <i>Biophysical Journal</i> , 1999, 76, 2421-2431.	0.5	35
98	Steric Effects on Multivalent Ligand-Receptor Binding: Exclusion of Ligand Sites by Bound Cell Surface Receptors. <i>Biophysical Journal</i> , 1999, 76, 3031-3043.	0.5	124
99	Completely uncoupled and perfectly coupled gene expression in repressible systems 1 Edited by K. Yamamoto. <i>Journal of Molecular Biology</i> , 1997, 266, 538-558.	4.2	31
100	Rules for Coupled Expression of Regulator and Effector Genes in Inducible Circuits. <i>Journal of Molecular Biology</i> , 1996, 255, 121-139.	4.2	101
101	Subunit Structure of Regulator Proteins Influences the Design of Gene Circuitry: Analysis of Perfectly Coupled and Completely Uncoupled Circuits. <i>Journal of Molecular Biology</i> , 1995, 248, 739-755.	4.2	36