William S Hlavacek

List of Publications by Year
in descending order

101 papers	5,035 citations	109137 35 h-index	106150 65 g-index
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. Bioinformatics, 2022, 38, 1770-1772.	1.8	9
2	Bayesian Inference of State-Level COVID-19 Basic Reproduction Numbers across the United States. Viruses, 2022, 14, 157.	1.5	17
3	Daily Forecasting of Regional Epidemics of Coronavirus Disease with Bayesian Uncertainty Quantification, United States. Emerging Infectious Diseases, 2021, 27, 767-778.	2.0	14
4	Multisite EGFR phosphorylation is regulated by adaptor protein abundances and dimer lifetimes. Molecular Biology of the Cell, 2020, 31, 695-708.	0.9	20
5	Bayesian inference using qualitative observations of underlying continuous variables. Bioinformatics, 2020, 36, 3177-3184.	1.8	9
6	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartment species, version 1, release 2. Journal of Integrative Bioinformatics, 2020, 17, .	1.0	8
7	<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
8	Scaling methods for accelerating kinetic Monte Carlo simulations of chemical reaction networks. Journal of Chemical Physics, 2019, 150, 244101.	1.2	5
9	Parameter estimation and uncertainty quantification for systems biology models. Current Opinion in Systems Biology, 2019, 18, 9-18.	1.3	38
10	PyBioNetFit and the Biological Property Specification Language. IScience, 2019, 19, 1012-1036.	1.9	47
11	Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. PLoS Computational Biology, 2019, 15, e1006706.	1.5	8
12	Using RuleBuilder to Graphically Define and Visualize BioNetGen-Language Patterns and Reaction Rules. Methods in Molecular Biology, 2019, 1945, 33-42.	0.4	0
13	A Step-by-Step Guide to Using BioNetFit. Methods in Molecular Biology, 2019, 1945, 391-419.	0.4	2
14	Prediction of Optimal Drug Schedules for Controlling Autophagy. Scientific Reports, 2019, 9, 1428.	1.6	17
15	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. Seminars in Cancer Biology, 2019, 54, 162-173.	4.3	16
16	Generalizing Gillespieâ€™s Direct Method to Enable Network-Free Simulations. Bulletin of Mathematical Biology, 2019, 81, 2822-2848.	0.9	15
17	Preassembled GPCR signaling complexes mediate distinct cellular responses to ultralow ligand concentrations. Science Signaling, 2018, 11, .	1.6	36
18	Using both qualitative and quantitative data in parameter identification for systems biology models. Nature Communications, 2018, 9, 3901.	5.8	20

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19	Using Equation-Free Computation to Accelerate Network-Free Stochastic Simulation of Chemical Kinetics. Journal of Physical Chemistry B, 2018, 122, 6351-6356.	1.2	2
20	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. Cell Systems, 2018, 7, 161-179.e14.	2.9	53
21	Relaxation oscillations and hierarchy of feedbacks in MAPK signaling. Scientific Reports, 2017, 7, 38244.	1.6	47
22	Allergen Valency, Dose, and FcÎµRI Occupancy Set Thresholds for Secretory Responses to Pen a 1 and Motivate Design of Hypoallergens. Journal of Immunology, 2017, 198, 1034-1046.	0.4	13
23	Differential mast cell outcomes are sensitive to FcÎµRI-Syk binding kinetics. Molecular Biology of the Cell, 2017, 28, 3397-3414.	0.9	32
24	SPATKIN: a simulator for rule-based modeling of biomolecular site dynamics on surfaces. Bioinformatics, 2017, 33, 3667-3669.	1.8	3
25	TRuML. , 2017, , .		5
26	Timescale Separation of Positive and Negative Signaling Creates History-Dependent Responses to IgE Receptor Stimulation. Scientific Reports, 2017, 7, 15586.	1.6	18
27	BioNetFit: a fitting tool compatible with BioNetGen, NFsim and distributed computing environments. Bioinformatics, 2016, 32, 798-800.	1.8	31
28	Inside-Out Signaling of Oncogenic EGFR Mutants Promotes Ligand-Independent Dimerization. Biophysical Journal, 2015, 108, 351a.	0.2	3
29	The eighth q-bio conference: meeting report and special issue preface. Physical Biology, 2015, 12, 060401.	0.8	0
30	Computational Analysis of an Autophagy/Translation Switch Based on Mutual Inhibition of MTORC1 and ULK1. PLoS ONE, 2015, 10, e0116550.	1.1	38
31	Enhanced dimerization drives ligand-independent activity of mutant epidermal growth factor receptor in lung cancer. Molecular Biology of the Cell, 2015, 26, 4087-4099.	0.9	79
32	Use of Mechanistic Models to Integrate and Analyze Multiple Proteomic Datasets. Biophysical Journal, 2015, 108, 1819-1829.	0.2	21
33	Modeling for (physical) biologists: an introduction to the rule-based approach. Physical Biology, 2015, 12, 045007.	0.8	57
34	Mitochondrial Morphological Features Are Associated with Fission and Fusion Events. PLoS ONE, 2014, 9, e95265.	1.1	92
35	Phosphorylation Site Dynamics of Early T-cell Receptor Signaling. PLoS ONE, 2014, 9, e104240.	1.1	54
36	The Seventh q-bio Conference: meeting report and preface. Physical Biology, 2014, 11, 040301.	0.8	1

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37	An Interaction Library for the FcÃŽÂµRI Signaling Network. Frontiers in Immunology, 2014, 5, 172.	2.2	16
38	Modeling Biomolecular Site Dynamics in Immunoreceptor Signaling Systems. Advances in Experimental Medicine and Biology, 2014, 844, 245-262.	0.8	8
39	Recruitment of the Adaptor Protein Grb2 to EGFR Tetramers. Biochemistry, 2014, 53, 2594-2604.	1.2	36
40	Optimal Aggregation of FcÎµRI with a Structurally Defined Trivalent Ligand Overrides Negative Regulation Driven by Phosphatases. ACS Chemical Biology, 2014, 9, 1508-1519.	1.6	40
41	Ruleâ€based modeling: a computational approach for studying biomolecular site dynamics in cell signaling systems. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 13-36.	6.6	97
42	Perspective on the q-bio Summer School and Conference: 2007â€"2014 and beyond. Quantitative Biology, 2014, 2, 54-58.	0.3	5
43	Exploring higher-order EGFR oligomerisation and phosphorylationâ€"a combined experimental and theoretical approach. Molecular BioSystems, 2013, 9, 1849.	2.9	72
44	Computational model for autophagic vesicle dynamics in single cells. Autophagy, 2013, 9, 74-92.	4.3	37
45	Modeling the Effect of APC Truncation on Destruction Complex Function in Colorectal Cancer Cells. PLoS Computational Biology, 2013, 9, e1003217.	1.5	23
46	Binding of Nucleoid-Associated Protein Fis to DNA Is Regulated by DNA Breathing Dynamics. PLoS Computational Biology, 2013, 9, e1002881.	1.5	23
47	Special section dedicated to The Sixth q-bio Conference: meeting report and preface. Physical Biology, 2013, 10, 030301.	0.8	2
48	Innovations of the Rule-Based Modeling Approach. , 2013, , 273-300.		16
49	Single-Cell Measurements of IgE-Mediated FcÎµRI Signaling Using an Integrated Microfluidic Platform. PLoS ONE, 2013, 8, e60159.	1.1	23
50	Improved predictions of transcription factor binding sites using physicochemical features of DNA. Nucleic Acids Research, 2012, 40, e175-e175.	6.5	30
51	A Computational Model for Early Events in B Cell Antigen Receptor Signaling: Analysis of the Roles of Lyn and Fyn. Journal of Immunology, 2012, 189, 646-658.	0.4	46
52	The Fifth Annual q-bio Conference on Cellular Information Processing. Physical Biology, 2012, 9, 050201.	0.8	0
53	The Brucella TIR-like protein TcpB interacts with the death domain of MyD88. Biochemical and Biophysical Research Communications, 2012, 417, 299-304.	1.0	49
54	Specification, annotation, visualization and simulation of a large rule-based model for ERBB receptor signaling. BMC Systems Biology, 2012, 6, 107.	3.0	31

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55	Guidelines for visualizing and annotating rule-based models. Molecular BioSystems, 2011, 7, 2779.	2.9	36
56	Scaffold-mediated nucleation of protein signaling complexes: Elementary principles. Mathematical Biosciences, 2011, 232, 164-173.	0.9	27
57	Hierarchical graphs for rule-based modeling of biochemical systems. BMC Bioinformatics, 2011, 12, 45.	1.2	16
58	The efficiency of reactant site sampling in network-free simulation of rule-based models for biochemical systems. Physical Biology, 2011, 8, 055009.	0.8	18
59	Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing. Physical Biology, 2011, 8, 050301.	0.8	2
60	Prediction of metabolic reactions based on atomic and molecular properties of small-molecule compounds. Bioinformatics, 2011, 27, 1537-1545.	1.8	32
61	RuleMonkey: software for stochastic simulation of rule-based models. BMC Bioinformatics, 2010, 11, 404.	1.2	50
62	Using Sequence-Specific Chemical and Structural Properties of DNA to Predict Transcription Factor Binding Sites. PLoS Computational Biology, 2010, 6, e1001007.	1.5	26
63	Modeling Multivalent Ligand-Receptor Interactions with Steric Constraints on Configurations of Cell-Surface Receptor Aggregates. Biophysical Journal, 2010, 98, 48-56.	0.2	50
64	How to deal with large models?. Molecular Systems Biology, 2009, 5, 240.	3.2	27
65	Simulation of large-scale rule-based models. Bioinformatics, 2009, 25, 910-917.	1.8	54
66	The Complexity of Cell Signaling and the Need for a New Mechanics. Science Signaling, 2009, 2, pe46.	1.6	34
67	GetBonNie for building, analyzing and sharing rule-based models. Bioinformatics, 2009, 25, 1457-1460.	1.8	16
68	Rule-Based Modeling of Biochemical Systems with BioNetGen. Methods in Molecular Biology, 2009, 500, 113-167.	0.4	366
69	Stochastic effects and bistability in T cell receptor signaling. Journal of Theoretical Biology, 2008, 254, 110-122.	0.8	86
70	Kinetic Monte Carlo method for rule-based modeling of biochemical networks. Physical Review E, 2008, 78, 031910.	0.8	83
71	Kinetic Proofreading Model. Advances in Experimental Medicine and Biology, 2008, 640, 82-94.	0.8	16
72	Carbon-fate maps for metabolic reactions. Bioinformatics, 2007, 23, 3193-3199.	1.8	33

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73	Dynamics of the nucleated polymerization model of prion replication. Biophysical Chemistry, 2007, 125, 360-367.	1.5	18
74	Reconstruction of Metabolic Networks from High-Throughput Metabolite Profiling Data: In Silico Analysis of Red Blood Cell Metabolism. Annals of the New York Academy of Sciences, 2007, 1115, 102-115.	1.8	22
75	Rules for Modeling Signal-Transduction Systems. Science Signaling, 2006, 2006, re6-re6.	1.6	267
76	Graph Theory for Rule-Based Modeling of Biochemical Networks. Lecture Notes in Computer Science, 2006, , 89-106.	1.0	45
77	On Imposing Detailed Balance in Complex Reaction Mechanisms. Biophysical Journal, 2006, 91, 1136-1141.	0.2	45
78	Depicting signaling cascades. Nature Biotechnology, 2006, 24, 137-138.	9.4	17
79	A network model of early events in epidermal growth factor receptor signaling that accounts for combinatorial complexity. BioSystems, 2006, 83, 136-151.	0.9	141
80	Prediction of oxidoreductase-catalyzed reactions based on atomic properties of metabolites. Bioinformatics, 2006, 22, 3082-3088.	1.8	21
81	'On-the-fly' or 'generate-first' modeling?. Nature Biotechnology, 2005, 23, 1344-1345.	9.4	16
82	Rule-based modeling of biochemical networks. Complexity, 2005, 10, 22-41.	0.9	110
83	Graphical rule-based representation of signal-transduction networks. , 2005, , .		25
84	Multiple Functions of a Feed-Forward-Loop Gene Circuit. Journal of Molecular Biology, 2005, 349, 501-514.	2.0	75
85	BioNetGen: software for rule-based modeling of signal transduction based on the interactions of molecular domains. Bioinformatics, 2004, 20, 3289-3291.	1.8	381
86	Design of gene circuits: lessons from bacteria. Nature Reviews Genetics, 2004, 5, 34-42.	7.7	206
87	Mathematical and computational models of immune-receptor signalling. Nature Reviews Immunology, 2004, 4, 445-456.	10.6	210
88	Interaction of a Monoclonal IgE-Specific Antibody with Cell-Surface IgEâˆ'FcÎµRI:Â Characterization of Equilibrium Binding and Secretory Responseâ€. Biochemistry, 2004, 43, 11352-11360.	1.2	7
89	The complexity of complexes in signal transduction. Biotechnology and Bioengineering, 2003, 84, 783-794.	1.7	176
90	Design Principles for Regulator Gene Expression in a Repressible Gene Circuit. Journal of Molecular Biology, 2003, 332, 861-876.	2.0	50

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91	Investigation of Early Events in FcÎµRI-Mediated Signaling Using a Detailed Mathematical Model. Journal of Immunology, 2003, 170, 3769-3781.	0.4	172
92	Retention of antigen on follicular dendritic cells and B lymphocytes through complement-mediated multivalent ligandâ€"receptor interactions: theory and application to HIV treatment. Mathematical Biosciences, 2002, 176, 185-202.	0.9	26
93	Modeling the early signaling events mediated by FcÎµRI. Molecular Immunology, 2002, 38, 1213-1219.	1.0	54
94	A quantitative approach for studying IgEâ€"FcÎµRI aggregation. Molecular Immunology, 2002, 38, 1221-1228.	1.0	20
95	Kinetic Proofreading in Receptor-Mediated Transduction of Cellular Signals: Receptor Aggregation, Partially Activated Receptors, and Cytosolic Messengers. Bulletin of Mathematical Biology, 2002, 64, 887-911.	0.9	30
96	Influence of follicular dendritic cells on HIV dynamics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2000, 355, 1051-1058.	1.8	25
97	Quantifying Aggregation of IgE-FcÎµRI by Multivalent Antigen. Biophysical Journal, 1999, 76, 2421-2431.	0.2	35
98	Steric Effects on Multivalent Ligand-Receptor Binding: Exclusion of Ligand Sites by Bound Cell Surface Receptors. Biophysical Journal, 1999, 76, 3031-3043.	0.2	124
99	Completely uncoupled and perfectly coupled gene expression in repressible systems 1 1Edited by K. Yamamoto. Journal of Molecular Biology, 1997, 266, 538-558.	2.0	31
100	Rules for Coupled Expression of Regulator and Effector Genes in Inducible Circuits. Journal of Molecular Biology, 1996, 255, 121-139.	2.0	101
101	Subunit Structure of Regulator Proteins Influences the Design of Gene Circuitry: Analysis of Perfectly Coupled and Completely Uncoupled Circuits. Journal of Molecular Biology, 1995, 248, 739-755.	2.0	36