

William S Hlavacek

List of Publications by Year in descending order

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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	BioNetGen: software for rule-based modeling of signal transduction based on the interactions of molecular domains. <i>Bioinformatics</i> , 2004, 20, 3289-3291.	1.8	381
2	Rule-Based Modeling of Biochemical Systems with BioNetGen. <i>Methods in Molecular Biology</i> , 2009, 500, 113-167.	0.4	366
3	Rules for Modeling Signal-Transduction Systems. <i>Science Signaling</i> , 2006, 2006, re6-re6.	1.6	267
4	Mathematical and computational models of immune-receptor signalling. <i>Nature Reviews Immunology</i> , 2004, 4, 445-456.	10.6	210
5	Design of gene circuits: lessons from bacteria. <i>Nature Reviews Genetics</i> , 2004, 5, 34-42.	7.7	206
6	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
7	The complexity of complexes in signal transduction. <i>Biotechnology and Bioengineering</i> , 2003, 84, 783-794.	1.7	176
8	Investigation of Early Events in Fc γ RI-Mediated Signaling Using a Detailed Mathematical Model. <i>Journal of Immunology</i> , 2003, 170, 3769-3781.	0.4	172
9	A network model of early events in epidermal growth factor receptor signaling that accounts for combinatorial complexity. <i>BioSystems</i> , 2006, 83, 136-151.	0.9	141
10	Steric Effects on Multivalent Ligand-Receptor Binding: Exclusion of Ligand Sites by Bound Cell Surface Receptors. <i>Biophysical Journal</i> , 1999, 76, 3031-3043.	0.2	124
11	Rule-based modeling of biochemical networks. <i>Complexity</i> , 2005, 10, 22-41.	0.9	110
12	Rules for Coupled Expression of Regulator and Effector Genes in Inducible Circuits. <i>Journal of Molecular Biology</i> , 1996, 255, 121-139.	2.0	101
13	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
14	Mitochondrial Morphological Features Are Associated with Fission and Fusion Events. <i>PLoS ONE</i> , 2014, 9, e95265.	1.1	92
15	Stochastic effects and bistability in T cell receptor signaling. <i>Journal of Theoretical Biology</i> , 2008, 254, 110-122.	0.8	86
16	Kinetic Monte Carlo method for rule-based modeling of biochemical networks. <i>Physical Review E</i> , 2008, 78, 031910.	0.8	83
17	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.	0.9	79
18	Multiple Functions of a Feed-Forward-Loop Gene Circuit. <i>Journal of Molecular Biology</i> , 2005, 349, 501-514.	2.0	75

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19	Exploring higher-order EGFR oligomerisation and phosphorylation—a combined experimental and theoretical approach. <i>Molecular BioSystems</i> , 2013, 9, 1849.	2.9	72
20	Modeling for (physical) biologists: an introduction to the rule-based approach. <i>Physical Biology</i> , 2015, 12, 045007.	0.8	57
21	Modeling the early signaling events mediated by Fc γ RI. <i>Molecular Immunology</i> , 2002, 38, 1213-1219.	1.0	54
22	Simulation of large-scale rule-based models. <i>Bioinformatics</i> , 2009, 25, 910-917.	1.8	54
23	Phosphorylation Site Dynamics of Early T-cell Receptor Signaling. <i>PLoS ONE</i> , 2014, 9, e104240.	1.1	54
24	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. <i>Cell Systems</i> , 2018, 7, 161-179.e14.	2.9	53
25	Design Principles for Regulator Gene Expression in a Repressible Gene Circuit. <i>Journal of Molecular Biology</i> , 2003, 332, 861-876.	2.0	50
26	RuleMonkey: software for stochastic simulation of rule-based models. <i>BMC Bioinformatics</i> , 2010, 11, 404.	1.2	50
27	Modeling Multivalent Ligand-Receptor Interactions with Steric Constraints on Configurations of Cell-Surface Receptor Aggregates. <i>Biophysical Journal</i> , 2010, 98, 48-56.	0.2	50
28	The Brucella TIR-like protein TcpB interacts with the death domain of MyD88. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 299-304.	1.0	49
29	Relaxation oscillations and hierarchy of feedbacks in MAPK signaling. <i>Scientific Reports</i> , 2017, 7, 38244.	1.6	47
30	PyBioNetFit and the Biological Property Specification Language. <i>IScience</i> , 2019, 19, 1012-1036.	1.9	47
31	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.	0.4	46
32	Graph Theory for Rule-Based Modeling of Biochemical Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 89-106.	1.0	45
33	On Imposing Detailed Balance in Complex Reaction Mechanisms. <i>Biophysical Journal</i> , 2006, 91, 1136-1141.	0.2	45
34	Optimal Aggregation of Fc γ RI with a Structurally Defined Trivalent Ligand Overrides Negative Regulation Driven by Phosphatases. <i>ACS Chemical Biology</i> , 2014, 9, 1508-1519.	1.6	40
35	Computational Analysis of an Autophagy/Translation Switch Based on Mutual Inhibition of MTORC1 and ULK1. <i>PLoS ONE</i> , 2015, 10, e0116550.	1.1	38
36	Parameter estimation and uncertainty quantification for systems biology models. <i>Current Opinion in Systems Biology</i> , 2019, 18, 9-18.	1.3	38

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37	Computational model for autophagic vesicle dynamics in single cells. <i>Autophagy</i> , 2013, 9, 74-92.	4.3	37
38	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.	2.0	36
39	Guidelines for visualizing and annotating rule-based models. <i>Molecular BioSystems</i> , 2011, 7, 2779.	2.9	36
40	Recruitment of the Adaptor Protein Grb2 to EGFR Tetramers. <i>Biochemistry</i> , 2014, 53, 2594-2604.	1.2	36
41	Preassembled GPCR signaling complexes mediate distinct cellular responses to ultralow ligand concentrations. <i>Science Signaling</i> , 2018, 11, .	1.6	36
42	Quantifying Aggregation of IgE-Fc̳RI by Multivalent Antigen. <i>Biophysical Journal</i> , 1999, 76, 2421-2431.	0.2	35
43	The Complexity of Cell Signaling and the Need for a New Mechanics. <i>Science Signaling</i> , 2009, 2, pe46.	1.6	34
44	Carbon-fate maps for metabolic reactions. <i>Bioinformatics</i> , 2007, 23, 3193-3199.	1.8	33
45	Prediction of metabolic reactions based on atomic and molecular properties of small-molecule compounds. <i>Bioinformatics</i> , 2011, 27, 1537-1545.	1.8	32
46	Differential mast cell outcomes are sensitive to Fc̳RI-Syk binding kinetics. <i>Molecular Biology of the Cell</i> , 2017, 28, 3397-3414.	0.9	32
47	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.	2.0	31
48	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
49	BioNetFit: a fitting tool compatible with BioNetGen, NFsim and distributed computing environments. <i>Bioinformatics</i> , 2016, 32, 798-800.	1.8	31
50	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.	0.9	30
51	Improved predictions of transcription factor binding sites using physicochemical features of DNA. <i>Nucleic Acids Research</i> , 2012, 40, e175-e175.	6.5	30
52	How to deal with large models?. <i>Molecular Systems Biology</i> , 2009, 5, 240.	3.2	27
53	Scaffold-mediated nucleation of protein signaling complexes: Elementary principles. <i>Mathematical Biosciences</i> , 2011, 232, 164-173.	0.9	27
54	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.	0.9	26

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55	Using Sequence-Specific Chemical and Structural Properties of DNA to Predict Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2010, 6, e1001007.	1.5	26
56	Influence of follicular dendritic cells on HIV dynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2000, 355, 1051-1058.	1.8	25
57	Graphical rule-based representation of signal-transduction networks. , 2005, , .		25
58	Modeling the Effect of APC Truncation on Destruction Complex Function in Colorectal Cancer Cells. <i>PLoS Computational Biology</i> , 2013, 9, e1003217.	1.5	23
59	Binding of Nucleoid-Associated Protein Fis to DNA Is Regulated by DNA Breathing Dynamics. <i>PLoS Computational Biology</i> , 2013, 9, e1002881.	1.5	23
60	Single-Cell Measurements of IgE-Mediated Fc μ RI Signaling Using an Integrated Microfluidic Platform. <i>PLoS ONE</i> , 2013, 8, e60159.	1.1	23
61	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.	1.8	22
62	Prediction of oxidoreductase-catalyzed reactions based on atomic properties of metabolites. <i>Bioinformatics</i> , 2006, 22, 3082-3088.	1.8	21
63	Use of Mechanistic Models to Integrate and Analyze Multiple Proteomic Datasets. <i>Biophysical Journal</i> , 2015, 108, 1819-1829.	0.2	21
64	A quantitative approach for studying IgE μ RI aggregation. <i>Molecular Immunology</i> , 2002, 38, 1221-1228.	1.0	20
65	Using both qualitative and quantitative data in parameter identification for systems biology models. <i>Nature Communications</i> , 2018, 9, 3901.	5.8	20
66	Multisite EGFR phosphorylation is regulated by adaptor protein abundances and dimer lifetimes. <i>Molecular Biology of the Cell</i> , 2020, 31, 695-708.	0.9	20
67	Dynamics of the nucleated polymerization model of prion replication. <i>Biophysical Chemistry</i> , 2007, 125, 360-367.	1.5	18
68	The efficiency of reactant site sampling in network-free simulation of rule-based models for biochemical systems. <i>Physical Biology</i> , 2011, 8, 055009.	0.8	18
69	Timescale Separation of Positive and Negative Signaling Creates History-Dependent Responses to IgE Receptor Stimulation. <i>Scientific Reports</i> , 2017, 7, 15586.	1.6	18
70	Depicting signaling cascades. <i>Nature Biotechnology</i> , 2006, 24, 137-138.	9.4	17
71	Prediction of Optimal Drug Schedules for Controlling Autophagy. <i>Scientific Reports</i> , 2019, 9, 1428.	1.6	17
72	Bayesian Inference of State-Level COVID-19 Basic Reproduction Numbers across the United States. <i>Viruses</i> , 2022, 14, 157.	1.5	17

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73	'On-the-fly' or 'generate-first' modeling?. Nature Biotechnology, 2005, 23, 1344-1345.	9.4	16
74	GetBonNie for building, analyzing and sharing rule-based models. Bioinformatics, 2009, 25, 1457-1460.	1.8	16
75	Hierarchical graphs for rule-based modeling of biochemical systems. BMC Bioinformatics, 2011, 12, 45.	1.2	16
76	An Interaction Library for the Fc γ RI Signaling Network. Frontiers in Immunology, 2014, 5, 172.	2.2	16
77	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. Seminars in Cancer Biology, 2019, 54, 162-173.	4.3	16
78	Kinetic Proofreading Model. Advances in Experimental Medicine and Biology, 2008, 640, 82-94.	0.8	16
79	Innovations of the Rule-Based Modeling Approach. , 2013, , 273-300.		16
80	Generalizing Gillespie's Direct Method to Enable Network-Free Simulations. Bulletin of Mathematical Biology, 2019, 81, 2822-2848.	0.9	15
81	Daily Forecasting of Regional Epidemics of Coronavirus Disease with Bayesian Uncertainty Quantification, United States. Emerging Infectious Diseases, 2021, 27, 767-778.	2.0	14
82	Allergen Valency, Dose, and Fc μ RI 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
83	Bayesian inference using qualitative observations of underlying continuous variables. Bioinformatics, 2020, 36, 3177-3184.	1.8	9
84	Implementation of a practical Markov chain Monte Carlo sampling algorithm in PyBioNetFit. Bioinformatics, 2022, 38, 1770-1772.	1.8	9
85	Modeling Biomolecular Site Dynamics in Immunoreceptor Signaling Systems. Advances in Experimental Medicine and Biology, 2014, 844, 245-262.	0.8	8
86	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
87	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartments species, version 1, release 2. Journal of Integrative Bioinformatics, 2020, 17, .	1.0	8
88	Interaction of a Monoclonal IgE-Specific Antibody with Cell-Surface IgE γ Fc μ RI: A Characterization of Equilibrium Binding and Secretory Response. Biochemistry, 2004, 43, 11352-11360.	1.2	7
89	Perspective on the q-bio Summer School and Conference: 2007-2014 and beyond. Quantitative Biology, 2014, 2, 54-58.	0.3	5
90	TRuML. , 2017, .		5

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91	Scaling methods for accelerating kinetic Monte Carlo simulations of chemical reaction networks. <i>Journal of Chemical Physics</i> , 2019, 150, 244101.	1.2	5
92	Inside-Out Signaling of Oncogenic EGFR Mutants Promotes Ligand-Independent Dimerization. <i>Biophysical Journal</i> , 2015, 108, 351a.	0.2	3
93	SPATKIN: a simulator for rule-based modeling of biomolecular site dynamics on surfaces. <i>Bioinformatics</i> , 2017, 33, 3667-3669.	1.8	3
94	Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing. <i>Physical Biology</i> , 2011, 8, 050301.	0.8	2
95	Special section dedicated to The Sixth q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2013, 10, 030301.	0.8	2
96	Using Equation-Free Computation to Accelerate Network-Free Stochastic Simulation of Chemical Kinetics. <i>Journal of Physical Chemistry B</i> , 2018, 122, 6351-6356.	1.2	2
97	A Step-by-Step Guide to Using BioNetFit. <i>Methods in Molecular Biology</i> , 2019, 1945, 391-419.	0.4	2
98	The Seventh q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2014, 11, 040301.	0.8	1
99	The Fifth Annual q-bio Conference on Cellular Information Processing. <i>Physical Biology</i> , 2012, 9, 050201.	0.8	0
100	The eighth q-bio conference: meeting report and special issue preface. <i>Physical Biology</i> , 2015, 12, 060401.	0.8	0
101	Using RuleBuilder to Graphically Define and Visualize BioNetGen-Language Patterns and Reaction Rules. <i>Methods in Molecular Biology</i> , 2019, 1945, 33-42.	0.4	0