James R Faeder

List of Publications by Year
in descending order

106 papers	5,347 citations	94269 37 h-index	95083 68 g-index
115 all docs	115 docs citations	115 times ranked	4526 citing authors

#	Article	IF	Citations
1	BioNetGen: software for rule-based modeling of signal transduction based on the interactions of molecular domains. Bioinformatics, 2004, 20, 3289-3291.	1.8	381
2	Rule-Based Modeling of Biochemical Systems with BioNetGen. Methods in Molecular Biology, 2009, 500, 113-167.	0.4	366
3	Efficient modeling, simulation and coarse-graining of biological complexity with NFsim. Nature Methods, 2011, 8, 177-183.	9.0	271
4	Rules for Modeling Signal-Transduction Systems. Science Signaling, 2006, 2006, re6-re6.	1.6	267
5	Mathematical and computational models of immune-receptor signalling. Nature Reviews Immunology, 2004, 4, 445-456.	10.6	210
6	BioNetGen 2.2: advances in rule-based modeling. Bioinformatics, 2016, 32, 3366-3368.	1.8	192
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	The complexity of complexes in signal transduction. Biotechnology and Bioengineering, 2003, 84, 783-794.	1.7	176
9	Investigation of Early Events in FcÎµRI-Mediated Signaling Using a Detailed Mathematical Model. Journal of Immunology, 2003, 170, 3769-3781.	0.4	172
10	Solvation Dynamics in Aqueous Reverse Micelles:â€‰ A Computer Simulation Study. Journal of Physical Chemistry B, 2001, 105, 11148-11158.	1.2	157
11	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
12	Solvation Dynamics in Reverse Micelles:Â The Role of Headgroupâ^'Solute Interactionsâ€. Journal of Physical Chemistry B, 2005, 109, 6732-6740.	1.2	112
13	Rule-based modeling of biochemical networks. Complexity, 2005, 10, 22-41.	0.9	110
14	Molecular Dynamics Simulations of the Interior of Aqueous Reverse Micelles:Â A Comparison between Sodium and Potassium Counterions. Langmuir, 2003, 19, 2514-2520.	1.6	103
15	The Duration of T Cell Stimulation Is a Critical Determinant of Cell Fate and Plasticity. Science Signaling, 2013, 6, ra97.	1.6	98
16	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
17	Toward a quantitative theory of intrinsically disordered proteins and their function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19819-19823.	3.3	92
18	Stochastic effects and bistability in T cell receptor signaling. Journal of Theoretical Biology, 2008, 254, 110-122.	0.8	86

#	ARTICLE	IF	CITATIONS
19	Kinetic Monte Carlo method for rule-based modeling of biochemical networks. Physical Review E, 2008, 78, 031910.	0.8	83
20	Translational Systems Approaches to the Biology of Inflammation and Healing. Immunopharmacology and Immunotoxicology, 2010, 32, 181-195.	1.1	78
21	Statistical Model Checking in BioLab: Applications to the Automated Analysis of T-Cell Receptor Signaling Pathway. Lecture Notes in Computer Science, 2008, , 231-250.	1.0	67
22	NF-κB Dynamics Discriminate between TNF Doses in Single Cells. Cell Systems, 2017, 5, 638-645.e5.	2.9	66
23	Translational Systems Biology: Introduction of an Engineering Approach to the Pathophysiology of the Burn Patient. Journal of Burn Care and Research, 2008, 29, 277-285.	0.2	65
24	Aggregation of Membrane Proteins by Cytosolic Cross-Linkers: Theory and Simulation of the LAT-Grb2-SOS1 System. Biophysical Journal, 2009, 96, 2604-2623.	0.2	63
25	The mitogen-activated protein kinome from Anopheles gambiae: identification, phylogeny and functional characterization of the ERK, JNK and p38 MAP kinases. BMC Genomics, 2011, 12, 574.	1.2	57
26	Modeling for (physical) biologists: an introduction to the rule-based approach. Physical Biology, 2015, 12, 045007.	0.8	57
27	RuleBender: integrated modeling, simulation and visualization for rule-based intracellular biochemistry. BMC Bioinformatics, 2012, 13, S3.	1.2	56
28	Modeling the early signaling events mediated by FcεRI. Molecular Immunology, 2002, 38, 1213-1219.	1.0	54
29	Combinatorial complexity and dynamical restriction of network flows in signal transduction. IET Systems Biology, 2005, 2, 5-15.	2.0	54
30	Simulation of large-scale rule-based models. Bioinformatics, 2009, 25, 910-917.	1.8	54
31	Detailed qualitative dynamic knowledge representation using a BioNetGen model of TLR-4 signaling and preconditioning. Mathematical Biosciences, 2009, 217, 53-63.	0.9	51
32	Modeling Multivalent Ligand-Receptor Interactions with Steric Constraints on Configurations of Cell-Surface Receptor Aggregates. Biophysical Journal, 2010, 98, 48-56.	0.2	50
33	Cutting Edge: Differential Regulation of PTEN by TCR, Akt, and FoxO1 Controls CD4+ T Cell Fate Decisions. Journal of Immunology, 2015, 194, 4615-4619.	0.4	50
34	Analysis and verification of the HMGB1 signaling pathway. BMC Bioinformatics, 2010, 11, S10.	1.2	49
35	Vibrational polarization beats in femtosecond coherent anti-Stokes Raman spectroscopy: A signature of dissociative pump–dump–pump wave packet dynamics. Journal of Chemical Physics, 2001, 115, 8440-8454.	1.2	48
36	Structure-Based Kinetic Models of Modular Signaling Protein Function: Focus on Shp2. Biophysical Journal, 2007, 92, 2290-2300.	0.2	46

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37	Graph Theory for Rule-Based Modeling of Biochemical Networks. Lecture Notes in Computer Science, 2006, , 89-106.	1.0	45
38	Efficient stochastic simulation of chemical kinetics networks using a weighted ensemble of trajectories. Journal of Chemical Physics, 2013, 139, 115105.	1.2	42
39	Photodissociation, Recombination, and Electron Transfer in Cluster Ions:Â A Nonadiabatic Molecular Dynamics Study of I2-(CO2)n. Journal of Physical Chemistry A, 1997, 101, 8147-8151.	1.1	37
40	Guidelines for visualizing and annotating rule-based models. Molecular BioSystems, 2011, 7, 2779.	2.9	36
41	RuleBender: a visual interface for rule-based modeling. Bioinformatics, 2011, 27, 1721-1722.	1.8	36
42	Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using a Weighted Ensemble of Trajectories. PLoS Computational Biology, 2016, 12, e1004611.	1.5	35
43	The Complexity of Cell Signaling and the Need for a New Mechanics. Science Signaling, 2009, 2, pe46.	1.6	34
44	Carbon-fate maps for metabolic reactions. Bioinformatics, 2007, 23, 3193-3199.	1.8	33
45	Exact Hybrid Particle/Population Simulation of Rule-Based Models of Biochemical Systems. PLoS Computational Biology, 2014, 10, e1003544.	1.5	33
46	Toward a comprehensive language for biological systems. BMC Biology, 2011, 9, 68.	1.7	32
47	Demystifying the cytokine network: Mathematical models point the way. Cytokine, 2017, 98, 115-123.	1.4	32
48	The interplay of double phosphorylation and scaffolding in MAPK pathways. Journal of Theoretical Biology, 2012, 295, 116-124.	0.8	31
49	Synergism between Different Germinant Receptors in the Germination of Bacillus subtilis Spores. Journal of Bacteriology, 2011, 193, 4664-4671.	1.0	27
50	Rule-Based Modeling of Signal Transduction: A Primer. Methods in Molecular Biology, 2012, 880, 139-218.	0.4	27
51	Graphical rule-based representation of signal-transduction networks. , 2005, , .		25
52	Parallel Tempering with Lasso for model reduction in systems biology. PLoS Computational Biology, 2020, 16, e1007669.	1.5	22
53	Spinâ€"orbit coupling in IÂ·CO2 and IÂ·OCS van der Waals complexes: beyond the pseudo-diatomic approximation. Chemical Physics Letters, 1999, 313, 812-819.	1.2	21
54	Compartmental rule-based modeling of biochemical systems. , 2009, , .		20

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55	Memory of Germinant Stimuli in Bacterial Spores. MBio, 2015, 6, e01859-15.	1.8	19
56	Computational Models of Tandem Src Homology 2 Domain Interactions and Application to Phosphoinositide 3-Kinase. Journal of Biological Chemistry, 2008, 283, 7338-7345.	1.6	18
57	Depicting signaling cascades. Nature Biotechnology, 2006, 24, 137-138.	9.4	17
58	A Bipolar Clamp Mechanism for Activation of Jak-Family Protein Tyrosine Kinases. PLoS Computational Biology, 2009, 5, e1000364.	1.5	17
59	MCell-R: A Particle-Resolution Network-Free Spatial Modeling Framework. Methods in Molecular Biology, 2019, 1945, 203-229.	0.4	17
60	CHEMISTRY: Ultrafast Reaction Dynamics in Molecular Cluster Ions. Science, 1997, 276, 1660-1661.	6.0	16
61	'On-the-fly' or 'generate-first' modeling?. Nature Biotechnology, 2005, 23, 1344-1345.	9.4	16
62	GetBonNie for building, analyzing and sharing rule-based models. Bioinformatics, 2009, 25, 1457-1460.	1.8	16
63	Formal Modeling and Analysis of Pancreatic Cancer Microenvironment. Lecture Notes in Computer Science, 2016, , 289-305.	1.0	16
64	Kinetic Proofreading Model. Advances in Experimental Medicine and Biology, 2008, 640, 82-94.	0.8	16
65	Evaluation of Parallel Tempering to Accelerate Bayesian Parameter Estimation in Systems Biology. , 2018, 2018, 690-697.		15
66	An effective Hamiltonian for an electronically excited solute in a polarizable molecular solvent. Molecular Physics, 1998, 94, 693-706.	0.8	14
67	MOSBIE: a tool for comparison and analysis of rule-based biochemical models. BMC Bioinformatics, 2014, 15, 316.	1.2	14
68	Harnessing Human Microphysiology Systems as Key Experimental Models for Quantitative Systems Pharmacology. Handbook of Experimental Pharmacology, 2019, 260, 327-367.	0.9	14
69	Kinetic Proofreading of Ligand-FcÎµRI Interactions May Persist beyond LAT Phosphorylation. Journal of Immunology, 2007, 178, 3530-3535.	0.4	13
70	Emulation of biological networks in reconfigurable hardware. , 2011, , .		13
71	Shaping the response: the role of FcÎµRI and Syk expression levels in mast cell signalling. IET Systems Biology, 2010, 4, 334-347.	0.8	12
72	Parameter estimation of rule-based models using statistical model checking. , 2016, , .		12

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73	Energy-based modeling in BioNetGen. , 2016, , .		12
74	Computational Modeling and Verification of Signaling Pathways in Cancer. Lecture Notes in Computer Science, 2012, , 117-135.	1.0	12
75	Automated visualization of rule-based models. PLoS Computational Biology, 2017, 13, e1005857.	1.5	12
76	Regulatory network analysis acceleration with reconfigurable hardware. , 2011, 2011, 149-52.		11
77	In vivo, in vitro, and in silico studies suggest a conserved immune module that regulates malaria parasite transmission from mammals to mosquitoes. Journal of Theoretical Biology, 2013, 334, 173-186.	0.8	11
78	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
79	Shift from stochastic to spatially-ordered expression of serine-glycine synthesis enzymes in 3D microtumors. Scientific Reports, 2018, 8, 9388.	1.6	10
80	Heterogeneities in Axonal Structure and Transporter Distribution Lower Dopamine Reuptake Efficiency. ENeuro, 2018, 5, ENEURO.0298-17.2017.	0.9	10
81	Adaptive coarse-graining for transient and quasi-equilibrium analyses of stochastic gene regulation. , 2012, , .		9
82	Studies of biological networks with statistical model checking. , 2013, , .		9
83	The Atomizer. , 2013, , .		9
84	High-Content Analysis with Cellular and Tissue Systems Biology. , 2015, , 369-392.e7.		9
85	Dynamic behavior of cell signaling networks. , 2013, , .		8
86	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
87	Modeling the T cell immune response: a fascinating challenge. Journal of Pharmacokinetics and Pharmacodynamics, 2014, 41, 401-413.	0.8	7
88	Combination treatment optimization using a pan-cancer pathway model. PLoS Computational Biology, 2021, 17, e1009689.	1.5	7
89	Reductionism Is Dead: Long Live Reductionism! Systems Modeling Needs Reductionist Experiments. Biophysical Journal, 2016, 110, 1681-1683.	0.2	5
90	RuleBender: Integrated visualization for biochemical rule-based modeling. , 2011, , .		4

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91	High-level modeling and verification of cellular signaling. , 2016, , .		4
92	Simulations of ICl^{-}(CO$_2$)$_n$Photodissociation: Effects of Structure, Excited State Charge Flow, and Solvent Dynamics. Journal of Physical Chemistry A, 2010, 114, 1347-1356.	1.1	3
93	MCell. , 2015, , 1673-1676.		3
94	Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing. Physical Biology, 2011, 8, 050301.	0.8	2
95	Special section dedicated to The Sixth q-bio Conference: meeting report and preface. Physical Biology, 2013, 10, 030301.	0.8	2
96	Design Automation for Biological Models. , 2015, , .		2
97	The Seventh q-bio Conference: meeting report and preface. Physical Biology, 2014, 11, 040301.	0.8	1
98	Modeling Host–Vector–Pathogen Immuno-inflammatory Interactions in Malaria. , 2013, , 265-279.		1
99	Rule-based modeling of signal transduction. Journal of Critical Care, 2007, 22, 349-350.	1.0	0
100	The Fifth Annual q-bio Conference on Cellular Information Processing. Physical Biology, 2012, 9, 050201.	0.8	0
101	The eighth q-bio conference: meeting report and special issue preface. Physical Biology, 2015, 12, 060401.	0.8	0
102	Effect of Spatial Complexity on Dopaminergic Signaling Revealed from Multiscale Simulations. Biophysical Journal, 2017, 112, 135a.	0.2	0
103	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
104	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
105	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
106	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0