

# James R Faeder

## List of Publications by Year in descending order

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106  
papers

5,347  
citations

94433

37  
h-index

95266

68  
g-index

115  
all docs

115  
docs citations

115  
times ranked

4526  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Combination treatment optimization using a pan-cancer pathway model. <i>PLoS Computational Biology</i> , 2021, 17, e1009689.	3.2	7
3	Parallel Tempering with Lasso for model reduction in systems biology. <i>PLoS Computational Biology</i> , 2020, 16, e1007669.	3.2	22
4	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
5	<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
6	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
7	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
8	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
9	Parallel Tempering with Lasso for model reduction in systems biology. , 2020, 16, e1007669.		0
10	Harnessing Human Microphysiology Systems as Key Experimental Models for Quantitative Systems Pharmacology. <i>Handbook of Experimental Pharmacology</i> , 2019, 260, 327-367.	1.8	14
11	MCell-R: A Particle-Resolution Network-Free Spatial Modeling Framework. <i>Methods in Molecular Biology</i> , 2019, 1945, 203-229.	0.9	17
12	Shift from stochastic to spatially-ordered expression of serine-glycine synthesis enzymes in 3D microtumors. <i>Scientific Reports</i> , 2018, 8, 9388.	3.3	10
13	Evaluation of Parallel Tempering to Accelerate Bayesian Parameter Estimation in Systems Biology. , 2018, 2018, 690-697.		15
14	Heterogeneities in Axonal Structure and Transporter Distribution Lower Dopamine Reuptake Efficiency. <i>ENeuro</i> , 2018, 5, ENEURO.0298-17.2017.	1.9	10
15	Effect of Spatial Complexity on Dopaminergic Signaling Revealed from Multiscale Simulations. <i>Biophysical Journal</i> , 2017, 112, 135a.	0.5	0
16	Demystifying the cytokine network: Mathematical models point the way. <i>Cytokine</i> , 2017, 98, 115-123.	3.2	32
17	NF- $\kappa$ B Dynamics Discriminate between TNF Doses in Single Cells. <i>Cell Systems</i> , 2017, 5, 638-645.e5.	6.2	66
18	Automated visualization of rule-based models. <i>PLoS Computational Biology</i> , 2017, 13, e1005857.	3.2	12

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19	Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using a Weighted Ensemble of Trajectories. <i>PLoS Computational Biology</i> , 2016, 12, e1004611.	3.2	35
20	High-level modeling and verification of cellular signaling. , 2016, , .		4
21	Parameter estimation of rule-based models using statistical model checking. , 2016, , .		12
22	Energy-based modeling in BioNetGen. , 2016, , .		12
23	Reductionism Is Dead: Long Live Reductionism! Systems Modeling Needs Reductionist Experiments. <i>Biophysical Journal</i> , 2016, 110, 1681-1683.	0.5	5
24	Formal Modeling and Analysis of Pancreatic Cancer Microenvironment. <i>Lecture Notes in Computer Science</i> , 2016, , 289-305.	1.3	16
25	BioNetGen 2.2: advances in rule-based modeling. <i>Bioinformatics</i> , 2016, 32, 3366-3368.	4.1	192
26	The eighth q-bio conference: meeting report and special issue preface. <i>Physical Biology</i> , 2015, 12, 060401.	1.8	0
27	High-Content Analysis with Cellular and Tissue Systems Biology. , 2015, , 369-392.e7.		9
28	Cutting Edge: Differential Regulation of PTEN by TCR, Akt, and FoxO1 Controls CD4+ T Cell Fate Decisions. <i>Journal of Immunology</i> , 2015, 194, 4615-4619.	0.8	50
29	Modeling for (physical) biologists: an introduction to the rule-based approach. <i>Physical Biology</i> , 2015, 12, 045007.	1.8	57
30	Design Automation for Biological Models. , 2015, , .		2
31	Memory of Germinant Stimuli in Bacterial Spores. <i>MBio</i> , 2015, 6, e01859-15.	4.1	19
32	<i>MCell</i> . , 2015, , 1673-1676.		3
33	The Seventh q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2014, 11, 040301.	1.8	1
34	Exact Hybrid Particle/Population Simulation of Rule-Based Models of Biochemical Systems. <i>PLoS Computational Biology</i> , 2014, 10, e1003544.	3.2	33
35	MOSBIE: a tool for comparison and analysis of rule-based biochemical models. <i>BMC Bioinformatics</i> , 2014, 15, 316.	2.6	14
36	Modeling the T cell immune response: a fascinating challenge. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2014, 41, 401-413.	1.8	7

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37	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
38	Dynamic behavior of cell signaling networks. , 2013, , .		8
39	In vivo, in vitro, and in silico studies suggest a conserved immune module that regulates malaria parasite transmission from mammals to mosquitoes. <i>Journal of Theoretical Biology</i> , 2013, 334, 173-186.	1.7	11
40	Studies of biological networks with statistical model checking. , 2013, , .		9
41	The Atomizer. , 2013, , .		9
42	The Duration of T Cell Stimulation Is a Critical Determinant of Cell Fate and Plasticity. <i>Science Signaling</i> , 2013, 6, ra97.	3.6	98
43	Special section dedicated to The Sixth q-bio Conference: meeting report and preface. <i>Physical Biology</i> , 2013, 10, 030301.	1.8	2
44	Efficient stochastic simulation of chemical kinetics networks using a weighted ensemble of trajectories. <i>Journal of Chemical Physics</i> , 2013, 139, 115105.	3.0	42
45	Modeling Host-Vector-Pathogen Immuno-inflammatory Interactions in Malaria. , 2013, , 265-279.		1
46	Adaptive coarse-graining for transient and quasi-equilibrium analyses of stochastic gene regulation. , 2012, , .		9
47	The Fifth Annual q-bio Conference on Cellular Information Processing. <i>Physical Biology</i> , 2012, 9, 050201.	1.8	0
48	Rule-Based Modeling of Signal Transduction: A Primer. <i>Methods in Molecular Biology</i> , 2012, 880, 139-218.	0.9	27
49	The interplay of double phosphorylation and scaffolding in MAPK pathways. <i>Journal of Theoretical Biology</i> , 2012, 295, 116-124.	1.7	31
50	RuleBender: integrated modeling, simulation and visualization for rule-based intracellular biochemistry. <i>BMC Bioinformatics</i> , 2012, 13, S3.	2.6	56
51	Computational Modeling and Verification of Signaling Pathways in Cancer. <i>Lecture Notes in Computer Science</i> , 2012, , 117-135.	1.3	12
52	Guidelines for visualizing and annotating rule-based models. <i>Molecular BioSystems</i> , 2011, 7, 2779.	2.9	36
53	RuleBender: Integrated visualization for biochemical rule-based modeling. , 2011, , .		4
54	Regulatory network analysis acceleration with reconfigurable hardware. , 2011, 2011, 149-52.		11

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55	Efficient modeling, simulation and coarse-graining of biological complexity with NFsim. Nature Methods, 2011, 8, 177-183.	19.0	271
56	Toward a comprehensive language for biological systems. BMC Biology, 2011, 9, 68.	3.8	32
57	The mitogen-activated protein kinase from <i>Anopheles gambiae</i> : identification, phylogeny and functional characterization of the ERK, JNK and p38 MAP kinases. BMC Genomics, 2011, 12, 574.	2.8	57
58	Emulation of biological networks in reconfigurable hardware. , 2011, , .		13
59	Synergism between Different Germinant Receptors in the Germination of <i>Bacillus subtilis</i> Spores. Journal of Bacteriology, 2011, 193, 4664-4671.	2.2	27
60	Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing. Physical Biology, 2011, 8, 050301.	1.8	2
61	RuleBender: a visual interface for rule-based modeling. Bioinformatics, 2011, 27, 1721-1722.	4.1	36
62	Shaping the response: the role of Fc̄μRI and Syk expression levels in mast cell signalling. IET Systems Biology, 2010, 4, 334-347.	1.5	12
63	Analysis and verification of the HMGB1 signaling pathway. BMC Bioinformatics, 2010, 11, S10.	2.6	49
64	Modeling Multivalent Ligand-Receptor Interactions with Steric Constraints on Configurations of Cell-Surface Receptor Aggregates. Biophysical Journal, 2010, 98, 48-56.	0.5	50
65	Simulations of ICl <sup>+</sup> (CO <sub>2</sub> ) <sub>n</sub> Photodissociation: Effects of Structure, Excited State Charge Flow, and Solvent Dynamics. Journal of Physical Chemistry A, 2010, 114, 1347-1356.	2.5	3
66	Translational Systems Approaches to the Biology of Inflammation and Healing. Immunopharmacology and Immunotoxicology, 2010, 32, 181-195.	2.4	78
67	Compartmental rule-based modeling of biochemical systems. , 2009, , .		20
68	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.	7.1	92
69	Simulation of large-scale rule-based models. Bioinformatics, 2009, 25, 910-917.	4.1	54
70	The Complexity of Cell Signaling and the Need for a New Mechanics. Science Signaling, 2009, 2, pe46.	3.6	34
71	A Bipolar Clamp Mechanism for Activation of Jak-Family Protein Tyrosine Kinases. PLoS Computational Biology, 2009, 5, e1000364.	3.2	17
72	GetBonNie for building, analyzing and sharing rule-based models. Bioinformatics, 2009, 25, 1457-1460.	4.1	16

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73	Detailed qualitative dynamic knowledge representation using a BioNetGen model of TLR-4 signaling and preconditioning. <i>Mathematical Biosciences</i> , 2009, 217, 53-63.	1.9	51
74	Aggregation of Membrane Proteins by Cytosolic Cross-Linkers: Theory and Simulation of the LAT-Grb2-SOS1 System. <i>Biophysical Journal</i> , 2009, 96, 2604-2623.	0.5	63
75	Rule-Based Modeling of Biochemical Systems with BioNetGen. <i>Methods in Molecular Biology</i> , 2009, 500, 113-167.	0.9	366
76	Stochastic effects and bistability in T cell receptor signaling. <i>Journal of Theoretical Biology</i> , 2008, 254, 110-122.	1.7	86
77	Computational Models of Tandem Src Homology 2 Domain Interactions and Application to Phosphoinositide 3-Kinase. <i>Journal of Biological Chemistry</i> , 2008, 283, 7338-7345.	3.4	18
78	Kinetic Monte Carlo method for rule-based modeling of biochemical networks. <i>Physical Review E</i> , 2008, 78, 031910.	2.1	83
79	Translational Systems Biology: Introduction of an Engineering Approach to the Pathophysiology of the Burn Patient. <i>Journal of Burn Care and Research</i> , 2008, 29, 277-285.	0.4	65
80	Kinetic Proofreading Model. <i>Advances in Experimental Medicine and Biology</i> , 2008, 640, 82-94.	1.6	16
81	Statistical Model Checking in BioLab: Applications to the Automated Analysis of T-Cell Receptor Signaling Pathway. <i>Lecture Notes in Computer Science</i> , 2008, , 231-250.	1.3	67
82	Carbon-fate maps for metabolic reactions. <i>Bioinformatics</i> , 2007, 23, 3193-3199.	4.1	33
83	Kinetic Proofreading of Ligand-Fc $\mu$ R1 Interactions May Persist beyond LAT Phosphorylation. <i>Journal of Immunology</i> , 2007, 178, 3530-3535.	0.8	13
84	Structure-Based Kinetic Models of Modular Signaling Protein Function: Focus on Shp2. <i>Biophysical Journal</i> , 2007, 92, 2290-2300.	0.5	46
85	Rule-based modeling of signal transduction. <i>Journal of Critical Care</i> , 2007, 22, 349-350.	2.2	0
86	Rules for Modeling Signal-Transduction Systems. <i>Science Signaling</i> , 2006, 2006, re6-re6.	3.6	267
87	Graph Theory for Rule-Based Modeling of Biochemical Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 89-106.	1.3	45
88	Depicting signaling cascades. <i>Nature Biotechnology</i> , 2006, 24, 137-138.	17.5	17
89	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
90	'On-the-fly' or 'generate-first' modeling?. <i>Nature Biotechnology</i> , 2005, 23, 1344-1345.	17.5	16

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91	Rule-based modeling of biochemical networks. <i>Complexity</i> , 2005, 10, 22-41.	1.6	110
92	Graphical rule-based representation of signal-transduction networks. , 2005, , .		25
93	Combinatorial complexity and dynamical restriction of network flows in signal transduction. <i>IET Systems Biology</i> , 2005, 2, 5-15.	2.0	54
94	Solvation Dynamics in Reverse Micelles: The Role of Headgroup Solute Interactions. <i>Journal of Physical Chemistry B</i> , 2005, 109, 6732-6740.	2.6	112
95	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
96	Mathematical and computational models of immune-receptor signalling. <i>Nature Reviews Immunology</i> , 2004, 4, 445-456.	22.7	210
97	The complexity of complexes in signal transduction. <i>Biotechnology and Bioengineering</i> , 2003, 84, 783-794.	3.3	176
98	Molecular Dynamics Simulations of the Interior of Aqueous Reverse Micelles: A Comparison between Sodium and Potassium Counterions. <i>Langmuir</i> , 2003, 19, 2514-2520.	3.5	103
99	Investigation of Early Events in FcγRI-Mediated Signaling Using a Detailed Mathematical Model. <i>Journal of Immunology</i> , 2003, 170, 3769-3781.	0.8	172
100	Modeling the early signaling events mediated by FcγRI. <i>Molecular Immunology</i> , 2002, 38, 1213-1219.	2.2	54
101	Solvation Dynamics in Aqueous Reverse Micelles: A Computer Simulation Study. <i>Journal of Physical Chemistry B</i> , 2001, 105, 11148-11158.	2.6	157
102	Vibrational polarization beats in femtosecond coherent anti-Stokes Raman spectroscopy: A signature of dissociative pump-dump-pump wave packet dynamics. <i>Journal of Chemical Physics</i> , 2001, 115, 8440-8454.	3.0	48
103	Spin-orbit coupling in I-CO <sub>2</sub> and I-OCS van der Waals complexes: beyond the pseudo-diatomic approximation. <i>Chemical Physics Letters</i> , 1999, 313, 812-819.	2.6	21
104	An effective Hamiltonian for an electronically excited solute in a polarizable molecular solvent. <i>Molecular Physics</i> , 1998, 94, 693-706.	1.7	14
105	Photodissociation, Recombination, and Electron Transfer in Cluster Ions: A Nonadiabatic Molecular Dynamics Study of I <sub>2</sub> -(CO <sub>2</sub> ) <sub>n</sub> . <i>Journal of Physical Chemistry A</i> , 1997, 101, 8147-8151.	2.5	37
106	CHEMISTRY: Ultrafast Reaction Dynamics in Molecular Cluster Ions. <i>Science</i> , 1997, 276, 1660-1661.	12.6	16