Jasmin Fisher

List of Publications by Year
in descending order

59 papers	2,877 citations	257450 24 h-index	182427 51 g-index
68 all docs	68 docs citations	68 times ranked	3731 citing authors

#	Article	IF	Citations
1	Executable cell biology. Nature Biotechnology, 2007, 25, 1239-1249.	17.5	470
2	Rethinking drug design in the artificial intelligence era. Nature Reviews Drug Discovery, 2020, 19, 353-364.	46.4	394
3	Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nature Biotechnology, 2015, 33, 269-276.	17.5	352
4	Vaccination for Neuroprotection in the Mouse Optic Nerve: Implications for Optic Neuropathies. Journal of Neuroscience, 2001, 21, 136-142.	3.6	163
5	Protective autoimmunity against the enemy within: fighting glutamate toxicity. Trends in Neurosciences, 2003, 26, 297-302.	8.6	132
6	Visible Machine Learning for Biomedicine. Cell, 2018, 173, 1562-1565.	28.9	115
7	Predictive Modeling of Signaling Crosstalk during C. elegans Vulval Development. PLoS Computational Biology, 2007, 3, e92.	3.2	88
8	Computational insights into Caenorhabditis elegans vulval development. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1951-1956.	7.1	86
9	Neuroprotection by T-cells depends on their subtype and activation state. Journal of Neuroimmunology, 2002, 133, 72-80.	2.3	73
10	Qualitative networks: a symbolic approach to analyze biological signaling networks. BMC Systems Biology, 2007, 1, 4.	3.0	70
11	BTR: training asynchronous Boolean models using single-cell expression data. BMC Bioinformatics, 2016, 17, 355.	2.6	63
12	Increased post-traumatic survival of neurons in IL-6-knockout mice on a background of EAE susceptibility. Journal of Neuroimmunology, 2001, 119, 1-9.	2.3	59
13	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. BMC Systems Biology, 2018, 12, 59.	3.0	58
14	Cell-Specific Computational Modeling of the PIM Pathway in Acute Myeloid Leukemia. Cancer Research, 2017, 77, 827-838.	0.9	45
15	Cellular resolution models for even skipped regulation in the entire Drosophila embryo. ELife, 2013, 2, e00522.	6.0	45
16	Executable cancer models: successes and challenges. Nature Reviews Cancer, 2020, 20, 343-354.	28.4	43
17	Toward Verified Biological Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 223-234.	3.0	41
18	Biology as reactivity. Communications of the ACM, 2011, 54, 72-82.	4.5	40

#	Article	IF	Citations
19	Cellâ€cycle regulation of NOTCH signaling during *C. elegans* vulval development. Molecular Systems Biology, 2012, 8, 618.	7.2	39
20	WormQTLâ€"public archive and analysis web portal for natural variation data in Caenorhabditis spp. Nucleic Acids Research, 2012, 41, D738-D743.	14.5	33
21	A scenario-based approach to modeling development: A prototype model of C. elegans vulval fate specification. Developmental Biology, 2008, 323, 1-5.	2.0	32
22	Computational modeling of the EGFR network elucidates control mechanisms regulating signal dynamics. BMC Systems Biology, 2009, 3, 118.	3.0	30
23	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. Cell Reports, 2018, 24, 3607-3618.	6.4	30
24	Bma: Visual Tool for Modeling and Analyzing Biological Networks. Lecture Notes in Computer Science, 2012, , 686-692.	1.3	30
25	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for *PU.1* during haematopoietic specification. Development (Cambridge), 2014, 141, 4018-4030.	2.5	26
26	Proving Stabilization of Biological Systems. Lecture Notes in Computer Science, 2011, , 134-149.	1.3	25
27	Synthesis of biological models from mutation experiments. , 2013, , .		24
28	Bounded Asynchrony: Concurrency for Modeling Cell-Cell Interactions. , 2008, , 17-32.		24
29	The executable pathway to biological networks. Briefings in Functional Genomics, 2010, 9, 79-92.	2.7	21
30	Static network structure can be used to model the phenotypic effects of perturbations in regulatory networks. Bioinformatics, 2012, 28, 2811-2818.	4.1	20
31	Transcriptional hierarchies regulating early blood cell development. Blood Cells, Molecules, and Diseases, 2013, 51, 239-247.	1.4	18
32	Processing, visualising and reconstructing network models from singleâ€cell data. Immunology and Cell Biology, 2016, 94, 256-265.	2.3	18
33	Heterogeneity of Myc expression in breast cancer exposes pharmacological vulnerabilities revealed through executable mechanistic modeling. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22399-22408.	7.1	15
34	Drug Target Optimization in Chronic Myeloid Leukemia Using Innovative Computational Platform. Scientific Reports, 2015, 5, 8190.	3.3	13
35	Emergent Stem Cell Homeostasis in the C.Âelegans Germline Is Revealed by Hybrid Modeling. Biophysical Journal, 2015, 109, 428-438.	0.5	12
36	Dynamic Reactive Modules. Lecture Notes in Computer Science, 2011, , 404-418.	1.3	9

#	Article	IF	Citations
37	Synthesis of biological models from mutation experiments. ACM SIGPLAN Notices, 2013, 48, 469-482.	0.2	9
38	Executable Biology. , 2006, , .		8
39	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. Computational Biology, 2019, , 133-153.	0.2	7
40	A toolbox for discrete modelling of cell signalling dynamics. Integrative Biology (United Kingdom), 2018, 10, 370-382.	1.3	6
41	Mechanistic Insights into Metabolic Disturbance during Type-2 Diabetes and Obesity Using Qualitative Networks. Lecture Notes in Computer Science, 2010, , 146-162.	1.3	6
42	At the interface of biology and computation. , 2013, , .		5
43	Toward Synthesizing Executable Models in Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 75.	4.1	5
44	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. Current Protocols in Bioinformatics, 2020, 69, e95.	25.8	5
45	A Dynamic Physical Model of Cell Migration, Differentiation and Apoptosis in Caenorhabditis elegans. Advances in Experimental Medicine and Biology, 2012, 736, 211-233.	1.6	5
46	Bringing LTL Model Checking to Biologists. Lecture Notes in Computer Science, 2017, , 1-13.	1.3	5
47	Model Checking in Biology. , 2014, , 255-279.		5
48	Executable network of SARS-CoV-2-host interaction predicts drug combination treatments. Npj Digital Medicine, 2022, 5, 18.	10.9	5
49	Program synthesis meets deep learning for decoding regulatory networks. Current Opinion in Systems Biology, 2017, 4, 64-70.	2.6	4
50	The role of proteosome-mediated proteolysis in modulating potentially harmful transcription factor activity in <i>Saccharomyces cerevisiae</i>. Bioinformatics, 2011, 27, i283-i287.	4.1	3
51	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. Journal of the Royal Society Interface, 2014, 11, 20140245.	3.4	3
52	Community voices: policy proposals to promote inclusion in academia through the lens of women in science. Nature Communications, 2022, 13, .	12.8	3
53	Predictive Modelling of Stem Cell Differentiation and Apoptosis in C. elegans. Lecture Notes in Computer Science, 2012, , 99-104.	1.3	2
54	The Only Way Is Up. Lecture Notes in Computer Science, 2011, , 3-11.	1.3	2

#	Article	IF	Citations
55	Prognostic hallmarks in AML. Nature Biomedical Engineering, 2019, 3, 847-849.	22.5	1
56	Cell cycle control of NOTCH signalling during C. elegans vulval development. Developmental Biology, 2011, 356, 186.	2.0	0
57	Predicting and Retrodicting Fate Patterns in C. elegans Vulval Development using Logic Programming. Biophysical Journal, 2014, 106, 376a.	0.5	0
58	Emergent Behaviours of Stem Cells in Organogenesis Demonstrated by Hybrid Modelling. Biophysical Journal, 2015, 108, 365a.	0.5	0
59	Model Checking Cell Fate Decisions. Lecture Notes in Computer Science, 2011, , 1-1.	1.3	0