

Jasmin Fisher

List of Publications by Year in descending order

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Version: 2024-02-01

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 network of SARS-CoV-2-host interaction predicts drug combination treatments. <i>Npj Digital Medicine</i> , 2022, 5, 18.	10.9	5
2	Community voices: policy proposals to promote inclusion in academia through the lens of women in science. <i>Nature Communications</i> , 2022, 13, .	12.8	3
3	Rethinking drug design in the artificial intelligence era. <i>Nature Reviews Drug Discovery</i> , 2020, 19, 353-364.	46.4	394
4	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e95.	25.8	5
5	Executable cancer models: successes and challenges. <i>Nature Reviews Cancer</i> , 2020, 20, 343-354.	28.4	43
6	Prognostic hallmarks in AML. <i>Nature Biomedical Engineering</i> , 2019, 3, 847-849.	22.5	1
7	Heterogeneity of Myc expression in breast cancer exposes pharmacological vulnerabilities revealed through executable mechanistic modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22399-22408.	7.1	15
8	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. <i>Computational Biology</i> , 2019, , 133-153.	0.2	7
9	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. <i>Cell Reports</i> , 2018, 24, 3607-3618.	6.4	30
10	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. <i>BMC Systems Biology</i> , 2018, 12, 59.	3.0	58
11	Visible Machine Learning for Biomedicine. <i>Cell</i> , 2018, 173, 1562-1565.	28.9	115
12	A toolbox for discrete modelling of cell signalling dynamics. <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 370-382.	1.3	6
13	Cell-Specific Computational Modeling of the PIM Pathway in Acute Myeloid Leukemia. <i>Cancer Research</i> , 2017, 77, 827-838.	0.9	45
14	Program synthesis meets deep learning for decoding regulatory networks. <i>Current Opinion in Systems Biology</i> , 2017, 4, 64-70.	2.6	4
15	Bringing LTL Model Checking to Biologists. <i>Lecture Notes in Computer Science</i> , 2017, , 1-13.	1.3	5
16	BTR: training asynchronous Boolean models using single-cell expression data. <i>BMC Bioinformatics</i> , 2016, 17, 355.	2.6	63
17	Processing, visualising and reconstructing network models from single-cell data. <i>Immunology and Cell Biology</i> , 2016, 94, 256-265.	2.3	18
18	Emergent Stem Cell Homeostasis in the C.Âelegans Germline Is Revealed by Hybrid Modeling. <i>Biophysical Journal</i> , 2015, 109, 428-438.	0.5	12

#	ARTICLE	IF	CITATIONS
19	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , 2015, 33, 269-276.	17.5	352
20	Drug Target Optimization in Chronic Myeloid Leukemia Using Innovative Computational Platform. <i>Scientific Reports</i> , 2015, 5, 8190.	3.3	13
21	Emergent Behaviours of Stem Cells in Organogenesis Demonstrated by Hybrid Modelling. <i>Biophysical Journal</i> , 2015, 108, 365a.	0.5	0
22	Toward Synthesizing Executable Models in Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 75.	4.1	5
23	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for <i>PU.1</i> during haematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 4018-4030.	2.5	26
24	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140245.	3.4	3
25	Predicting and Retrodicting Fate Patterns in <i>C. elegans</i> Vulval Development using Logic Programming. <i>Biophysical Journal</i> , 2014, 106, 376a.	0.5	0
26	Model Checking in Biology. , 2014, , 255-279.		5
27	Transcriptional hierarchies regulating early blood cell development. <i>Blood Cells, Molecules, and Diseases</i> , 2013, 51, 239-247.	1.4	18
28	Synthesis of biological models from mutation experiments. , 2013, , .		24
29	At the interface of biology and computation. , 2013, , .		5
30	Synthesis of biological models from mutation experiments. <i>ACM SIGPLAN Notices</i> , 2013, 48, 469-482.	0.2	9
31	Cellular resolution models for even-skipped regulation in the entire <i>Drosophila</i> embryo. <i>ELife</i> , 2013, 2, e00522.	6.0	45
32	WormQTL public archive and analysis web portal for natural variation data in <i>Caenorhabditis</i> spp. <i>Nucleic Acids Research</i> , 2012, 41, D738-D743.	14.5	33
33	Static network structure can be used to model the phenotypic effects of perturbations in regulatory networks. <i>Bioinformatics</i> , 2012, 28, 2811-2818.	4.1	20
34	Cell cycle regulation of NOTCH signaling during <i>C. elegans</i> vulval development. <i>Molecular Systems Biology</i> , 2012, 8, 618.	7.2	39
35	A Dynamic Physical Model of Cell Migration, Differentiation and Apoptosis in <i>Caenorhabditis elegans</i> . <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 211-233.	1.6	5
36	Predictive Modelling of Stem Cell Differentiation and Apoptosis in <i>C. elegans</i> . <i>Lecture Notes in Computer Science</i> , 2012, , 99-104.	1.3	2

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37	Bma: Visual Tool for Modeling and Analyzing Biological Networks. Lecture Notes in Computer Science, 2012, , 686-692.	1.3	30
38	Cell cycle control of NOTCH signalling during <i>C. elegans</i> vulval development. Developmental Biology, 2011, 356, 186.	2.0	0
39	The role of proteasome-mediated proteolysis in modulating potentially harmful transcription factor activity in <i>Saccharomyces cerevisiae</i> . Bioinformatics, 2011, 27, i283-i287.	4.1	3
40	Biology as reactivity. Communications of the ACM, 2011, 54, 72-82.	4.5	40
41	Proving Stabilization of Biological Systems. Lecture Notes in Computer Science, 2011, , 134-149.	1.3	25
42	Dynamic Reactive Modules. Lecture Notes in Computer Science, 2011, , 404-418.	1.3	9
43	The Only Way Is Up. Lecture Notes in Computer Science, 2011, , 3-11.	1.3	2
44	Model Checking Cell Fate Decisions. Lecture Notes in Computer Science, 2011, , 1-1.	1.3	0
45	The executable pathway to biological networks. Briefings in Functional Genomics, 2010, 9, 79-92.	2.7	21
46	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
47	Computational modeling of the EGFR network elucidates control mechanisms regulating signal dynamics. BMC Systems Biology, 2009, 3, 118.	3.0	30
48	A scenario-based approach to modeling development: A prototype model of <i>C. elegans</i> vulval fate specification. Developmental Biology, 2008, 323, 1-5.	2.0	32
49	Toward Verified Biological Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 223-234.	3.0	41
50	Bounded Asynchrony: Concurrency for Modeling Cell-Cell Interactions. , 2008, , 17-32.		24
51	Predictive Modeling of Signaling Crosstalk during <i>C. elegans</i> Vulval Development. PLoS Computational Biology, 2007, 3, e92.	3.2	88
52	Executable cell biology. Nature Biotechnology, 2007, 25, 1239-1249.	17.5	470
53	Qualitative networks: a symbolic approach to analyze biological signaling networks. BMC Systems Biology, 2007, 1, 4.	3.0	70
54	Executable Biology. , 2006, , .		8

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55	Computational insights into <i>Caenorhabditis elegans</i> vulval development. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1951-1956.	7.1	86
56	Protective autoimmunity against the enemy within: fighting glutamate toxicity. Trends in Neurosciences, 2003, 26, 297-302.	8.6	132
57	Neuroprotection by T-cells depends on their subtype and activation state. Journal of Neuroimmunology, 2002, 133, 72-80.	2.3	73
58	Vaccination for Neuroprotection in the Mouse Optic Nerve: Implications for Optic Neuropathies. Journal of Neuroscience, 2001, 21, 136-142.	3.6	163
59	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