

Jasmin Fisher

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

2,150
citations

22
h-index

46
g-index

68
ext. papers

2,567
ext. citations

9
avg, IF

4.87
L-index

#	Paper	IF	Citations
59	Executable network of SARS-CoV-2-host interaction predicts drug combination treatments.. <i>Npj Digital Medicine</i> , 2022 , 5, 18	15.7	1
58	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. <i>Current Protocols in Bioinformatics</i> , 2020 , 69, e95	24.2	1
57	Executable cancer models: successes and challenges. <i>Nature Reviews Cancer</i> , 2020 , 20, 343-354	31.3	23
56	Rethinking drug design in the artificial intelligence era. <i>Nature Reviews Drug Discovery</i> , 2020 , 19, 353-364	44.1	179
55	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. <i>Computational Biology</i> , 2019 , 133-153	0.7	3
54	Prognostic hallmarks in AML. <i>Nature Biomedical Engineering</i> , 2019 , 3, 847-849	19	
53	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	11.5	8
52	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. <i>BMC Systems Biology</i> , 2018 , 12, 59	3.5	28
51	Visible Machine Learning for Biomedicine. <i>Cell</i> , 2018 , 173, 1562-1565	56.2	71
50	A toolbox for discrete modelling of cell signalling dynamics. <i>Integrative Biology (United Kingdom)</i> , 2018 , 10, 370-382	3.7	3
49	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. <i>Cell Reports</i> , 2018 , 24, 3607-3618	18.6	14
48	Cell-Specific Computational Modeling of the PIM Pathway in Acute Myeloid Leukemia. <i>Cancer Research</i> , 2017 , 77, 827-838	10.1	30
47	Program synthesis meets deep learning for decoding regulatory networks. <i>Current Opinion in Systems Biology</i> , 2017 , 4, 64-70	3.2	3
46	Bringing LTL Model Checking to Biologists. <i>Lecture Notes in Computer Science</i> , 2017 , 1-13	0.9	5
45	BTR: training asynchronous Boolean models using single-cell expression data. <i>BMC Bioinformatics</i> , 2016 , 17, 355	3.6	31
44	Processing, visualising and reconstructing network models from single-cell data. <i>Immunology and Cell Biology</i> , 2016 , 94, 256-65	5	15
43	Drug target optimization in chronic myeloid leukemia using innovative computational platform. <i>Scientific Reports</i> , 2015 , 5, 8190	4.9	9

42	Emergent stem cell homeostasis in the <i>C. elegans</i> germline is revealed by hybrid modeling. <i>Biophysical Journal</i> , 2015 , 109, 428-38	2.9	10
41	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , 2015 , 33, 269-276	44.5	268
40	Synthesising Executable Gene Regulatory Networks from Single-Cell Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2015 , 544-560	0.9	7
39	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. <i>Journal of the Royal Society Interface</i> , 2014 , 11, 20140245	4.1	3
38	Toward synthesizing executable models in biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 75	5.8	4
37	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for PU.1 during haematopoietic specification. <i>Development (Cambridge)</i> , 2014 , 141, 4018-30	6.6	20
36	Finding Instability in Biological Models. <i>Lecture Notes in Computer Science</i> , 2014 , 358-372	0.9	4
35	Model Checking in Biology 2014 , 255-279		3
34	Transcriptional hierarchies regulating early blood cell development. <i>Blood Cells, Molecules, and Diseases</i> , 2013 , 51, 239-47	2.1	17
33	Synthesis of biological models from mutation experiments 2013 ,		21
32	At the interface of biology and computation 2013 ,		5
31	WormQTL--public archive and analysis web portal for natural variation data in <i>Caenorhabditis</i> spp. <i>Nucleic Acids Research</i> , 2013 , 41, D738-43	20.1	27
30	Synthesis of biological models from mutation experiments. <i>ACM SIGPLAN Notices</i> , 2013 , 48, 469-482	0.2	8
29	Cellular resolution models for even skipped regulation in the entire <i>Drosophila</i> embryo. <i>ELife</i> , 2013 , 2, e00522	8.9	39
28	Model-Checking Signal Transduction Networks through Decreasing Reachability Sets. <i>Lecture Notes in Computer Science</i> , 2013 , 85-100	0.9	10
27	Static network structure can be used to model the phenotypic effects of perturbations in regulatory networks. <i>Bioinformatics</i> , 2012 , 28, 2811-8	7.2	16
26	Cell-cycle regulation of NOTCH signaling during <i>C. elegans</i> vulval development. <i>Molecular Systems Biology</i> , 2012 , 8, 618	12.2	28
25	Predictive Modelling of Stem Cell Differentiation and Apoptosis in <i>C. elegans</i> . <i>Lecture Notes in Computer Science</i> , 2012 , 99-104	0.9	2

24	Bma: Visual Tool for Modeling and Analyzing Biological Networks. <i>Lecture Notes in Computer Science</i> , 2012 , 686-692	0.9	20
23	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, 211-33	3.6	5
22	The role of proteasome-mediated proteolysis in modulating potentially harmful transcription factor activity in <i>Saccharomyces cerevisiae</i> . <i>Bioinformatics</i> , 2011 , 27, i283-7	7.2	1
21	Biology as reactivity. <i>Communications of the ACM</i> , 2011 , 54, 72-82	2.5	33
20	Proving Stabilization of Biological Systems. <i>Lecture Notes in Computer Science</i> , 2011 , 134-149	0.9	22
19	Dynamic Reactive Modules. <i>Lecture Notes in Computer Science</i> , 2011 , 404-418	0.9	9
18	The Only Way Is Up. <i>Lecture Notes in Computer Science</i> , 2011 , 3-11	0.9	1
17	The executable pathway to biological networks. <i>Briefings in Functional Genomics</i> , 2010 , 9, 79-92	4.9	20
16	Mechanistic Insights into Metabolic Disturbance during Type-2 Diabetes and Obesity Using Qualitative Networks. <i>Lecture Notes in Computer Science</i> , 2010 , 146-162	0.9	4
15	Computational modeling of the EGFR network elucidates control mechanisms regulating signal dynamics. <i>BMC Systems Biology</i> , 2009 , 3, 118	3.5	26
14	A scenario-based approach to modeling development: a prototype model of <i>C. elegans</i> vulval fate specification. <i>Developmental Biology</i> , 2008 , 323, 1-5	3.1	28
13	Toward verified biological models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008 , 5, 223-34	3	33
12	Bounded Asynchrony: Concurrency for Modeling Cell-Cell Interactions 2008 , 17-32		18
11	Executable cell biology. <i>Nature Biotechnology</i> , 2007 , 25, 1239-49	44.5	411
10	Qualitative networks: a symbolic approach to analyze biological signaling networks. <i>BMC Systems Biology</i> , 2007 , 1, 4	3.5	57
9	Predictive modeling of signaling crosstalk during <i>C. elegans</i> vulval development. <i>PLoS Computational Biology</i> , 2007 , 3, e92	5	80
8	Executable Biology 2006 ,		7
7	Computational insights into <i>Caenorhabditis elegans</i> vulval development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1951-6	11.5	73

6	Protective autoimmunity against the enemy within: fighting glutamate toxicity. <i>Trends in Neurosciences</i> , 2003 , 26, 297-302	13.3	117
5	Neuroprotection by T-cells depends on their subtype and activation state. <i>Journal of Neuroimmunology</i> , 2002 , 133, 72-80	3.5	70
4	Increased post-traumatic survival of neurons in IL-6-knockout mice on a background of EAE susceptibility. <i>Journal of Neuroimmunology</i> , 2001 , 119, 1-9	3.5	50
3	Vaccination for neuroprotection in the mouse optic nerve: implications for optic neuropathies. <i>Journal of Neuroscience</i> , 2001 , 21, 136-42	6.6	146
2	Rora regulates activated T helper cells during inflammation		2
1	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data		1