

# Laurence Calzone

## List of Publications by Year in descending order

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57  
papers

4,054  
citations

257450

24  
h-index

144013

57  
g-index

75  
all docs

75  
docs citations

75  
times ranked

4525  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
2	Integrative Analysis of Cell Cycle Control in Budding Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 3841-3862.	2.1	584
3	BIOCHAM: an environment for modeling biological systems and formalizing experimental knowledge. <i>Bioinformatics</i> , 2006, 22, 1805-1807.	4.1	201
4	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. <i>PLoS Computational Biology</i> , 2010, 6, e1000702.	3.2	179
5	Integrative Modelling of the Influence of MAPK Network on Cancer Cell Fate Decision. <i>PLoS Computational Biology</i> , 2013, 9, e1003286.	3.2	167
6	Continuous time boolean modeling for biological signaling: application of Gillespie algorithm. <i>BMC Systems Biology</i> , 2012, 6, 116.	3.0	134
7	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. <i>PLoS Computational Biology</i> , 2015, 11, e1004571.	3.2	130
8	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. <i>Oncogenesis</i> , 2015, 4, e160-e160.	4.9	129
9	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017, 33, 2226-2228.	4.1	118
10	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008, 4, 173.	7.2	113
11	Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling. <i>Cancer Cell</i> , 2018, 34, 379-395.e7.	16.8	104
12	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008, 24, 876-877.	4.1	97
13	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. <i>Cancer Research</i> , 2015, 75, 4042-4052.	0.9	96
14	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , 2019, 35, 1188-1196.	4.1	88
15	Integrative Multi-omics Module Network Inference with Lemon-Tree. <i>PLoS Computational Biology</i> , 2015, 11, e1003983.	3.2	86
16	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
17	Personalization of Logical Models With Multi-Omics Data Allows Clinical Stratification of Patients. <i>Frontiers in Physiology</i> , 2018, 9, 1965.	2.8	66
18	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53

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19	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , 2013, 7, 100.	3.0	52
20	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	4.1	52
21	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. <i>BMC Systems Biology</i> , 2013, 7, 18.	3.0	50
22	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , 2018, 4, 2.	3.0	50
23	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016, 7, 18.	2.3	44
24	Dynamical modeling of syncytial mitotic cycles in <i>Drosophila</i> embryos. <i>Molecular Systems Biology</i> , 2007, 3, 131.	7.2	41
25	Patient-specific Boolean models of signalling networks guide personalised treatments. <i>ELife</i> , 2022, 11, .	6.0	38
26	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , 2015, 43, W560-W565.	14.5	32
27	Personalized logical models to investigate cancer response to BRAF treatments in melanomas and colorectal cancers. <i>PLoS Computational Biology</i> , 2021, 17, e1007900.	3.2	30
28	On Circuit Functionality in Boolean Networks. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 906-919.	1.9	27
29	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	2.5	25
30	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
31	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 921-929.	1.3	18
32	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , 2015, 9, 46.	3.0	17
33	A comprehensive approach to the molecular determinants of lifespan using a Boolean model of geroconversion. <i>Aging Cell</i> , 2016, 15, 1018-1026.	6.7	16
34	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , 2019, 20, 1238-1249.	6.5	15
35	Modeling Regulatory Networks at Virginia Tech. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 285-299.	2.0	14
36	Integrative proteomic and phosphoproteomic profiling of prostate cell lines. <i>PLoS ONE</i> , 2019, 14, e0224148.	2.5	14

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37	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). <i>Frontiers in Physiology</i> , 2018, 9, 787.	2.8	13
38	Dynamical Boolean Modeling of Immunogenic Cell Death. <i>Frontiers in Physiology</i> , 2020, 11, 590479.	2.8	13
39	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. <i>Lecture Notes in Computer Science</i> , 2020, , 193-209.	1.3	12
40	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
41	Logical versus kinetic modeling of biological networks: applications in cancer research. <i>Current Opinion in Chemical Engineering</i> , 2018, 21, 22-31.	7.8	10
42	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	10
43	From a Biological Hypothesis to the Construction of a Mathematical Model. <i>Methods in Molecular Biology</i> , 2013, 1021, 107-125.	0.9	9
44	Modelling of Immune Checkpoint Network Explains Synergistic Effects of Combined Immune Checkpoint Inhibitor Therapy and the Impact of Cytokines in Patient Response. <i>Cancers</i> , 2020, 12, 3600.	3.7	9
45	Practical Use of BiNoM: A Biological Network Manager Software. <i>Methods in Molecular Biology</i> , 2013, 1021, 127-146.	0.9	7
46	Cell Death and Life in Cancer: Mathematical Modeling of Cell Fate Decisions. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 261-274.	1.6	6
47	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. <i>Bioinformatics</i> , 2021, 37, 3702-3706.	4.1	6
48	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 800152.	3.5	6
49	Qualitative dynamics semantics for SBGN process description. <i>BMC Systems Biology</i> , 2016, 10, 42.	3.0	5
50	Comprehensive Map of the Regulated Cell Death Signaling Network: A Powerful Analytical Tool for Studying Diseases. <i>Cancers</i> , 2020, 12, 990.	3.7	5
51	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 754444.	3.5	3
52	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 793912.	3.5	3
53	Understanding Different Types of Cell Death Using Systems Biology. , 2012, , 125-143.		2
54	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. <i>Springer Proceedings in Mathematics</i> , 2013, , 191-204.	0.5	2

#	ARTICLE	IF	CITATIONS
55	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. BMC Bioinformatics, 2020, 21, 241.	2.6	1
56	Langages formels dans la machine abstraite biochimique BIOCHAM. Techniques Et Sciences Informatiques, 2007, 26, 47-72.	0.0	0
57	Cell Cycle Transition, Detailed Regulation of Restriction Point. , 2013, , 321-326.		0