

# 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	Patient-specific Boolean models of signalling networks guide personalised treatments. <i>ELife</i> , 2022, 11, .	6.0	38
2	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 800152.	3.5	6
3	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
4	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
5	Setting the basis of best practices and standards for curation and annotation of logical models in biologyâ€”highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
6	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
7	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
8	COVID19 Disease Map, a computational knowledge repository of virusâ€™host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
9	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 754444.	3.5	3
10	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
11	Dynamical Boolean Modeling of Immunogenic Cell Death. <i>Frontiers in Physiology</i> , 2020, 11, 590479.	2.8	13
12	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
13	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. <i>BMC Bioinformatics</i> , 2020, 21, 241.	2.6	1
14	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
15	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
16	Integrative proteomic and phosphoproteomic profiling of prostate cell lines. <i>PLoS ONE</i> , 2019, 14, e0224148.	2.5	14
17	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	4.1	52
18	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , 2019, 35, 1188-1196.	4.1	88

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , 2018, 4, 2.	3.0	50
22	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
23	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
24	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
25	Personalization of Logical Models With Multi-Omics Data Allows Clinical Stratification of Patients. <i>Frontiers in Physiology</i> , 2018, 9, 1965.	2.8	66
26	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017, 33, 2226-2228.	4.1	118
27	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	2.5	25
28	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016, 7, 18.	2.3	44
29	Qualitative dynamics semantics for SBCN process description. <i>BMC Systems Biology</i> , 2016, 10, 42.	3.0	5
30	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
31	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 921-929.	1.3	18
32	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , 2015, 43, W560-W565.	14.5	32
33	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
34	Integrative Multi-omics Module Network Inference with Lemon-Tree. <i>PLoS Computational Biology</i> , 2015, 11, e1003983.	3.2	86
35	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
36	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

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37	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. PLoS Computational Biology, 2015, 11, e1004571.	3.2	130
38	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. BMC Systems Biology, 2013, 7, 18.	3.0	50
39	On Circuit Functionality in Boolean Networks. Bulletin of Mathematical Biology, 2013, 75, 906-919.	1.9	27
40	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. BMC Systems Biology, 2013, 7, 100.	3.0	52
41	Practical Use of BiNoM: A Biological Network Manager Software. Methods in Molecular Biology, 2013, 1021, 127-146.	0.9	7
42	From a Biological Hypothesis to the Construction of a Mathematical Model. Methods in Molecular Biology, 2013, 1021, 107-125.	0.9	9
43	Integrative Modelling of the Influence of MAPK Network on Cancer Cell Fate Decision. PLoS Computational Biology, 2013, 9, e1003286.	3.2	167
44	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. Springer Proceedings in Mathematics, 2013, , 191-204.	0.5	2
45	Cell Cycle Transition, Detailed Regulation of Restriction Point. , 2013, , 321-326.		0
46	Understanding Different Types of Cell Death Using Systems Biology. , 2012, , 125-143.		2
47	Continuous time boolean modeling for biological signaling: application of Gillespie algorithm. BMC Systems Biology, 2012, 6, 116.	3.0	134
48	Cell Death and Life in Cancer: Mathematical Modeling of Cell Fate Decisions. Advances in Experimental Medicine and Biology, 2012, 736, 261-274.	1.6	6
49	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. PLoS Computational Biology, 2010, 6, e1000702.	3.2	179
50	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
51	A comprehensive modular map of molecular interactions in RB/E2F pathway. Molecular Systems Biology, 2008, 4, 173.	7.2	113
52	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. Bioinformatics, 2008, 24, 876-877.	4.1	97
53	Dynamical modeling of syncytial mitotic cycles in <i>Drosophila</i> embryos. Molecular Systems Biology, 2007, 3, 131.	7.2	41
54	Langages formels dans la machine abstraite biochimique BIOCHAM. Techniques Et Sciences Informatiques, 2007, 26, 47-72.	0.0	0

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55	BIOCHAM: an environment for modeling biological systems and formalizing experimental knowledge. <i>Bioinformatics</i> , 2006, 22, 1805-1807.	4.1	201
56	Integrative Analysis of Cell Cycle Control in Budding Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 3841-3862.	2.1	584
57	Modeling Regulatory Networks at Virginia Tech. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 285-299.	2.0	14