

Claudine Chaouiya

List of Publications by Year in descending order

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71
papers

4,399
citations

159585

30
h-index

118850

62
g-index

79
all docs

79
docs citations

79
times ranked

3296
citing authors

#	ARTICLE	IF	CITATIONS
1	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. Briefings in Bioinformatics, 2022, 23, .	6.5	10
2	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. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25
3	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	4.1	14
4	In Silico Logical Modelling to Uncover Cooperative Interactions in Cancer. International Journal of Molecular Sciences, 2021, 22, 4897.	4.1	1
5	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
6	Assessing regulatory features of the current transcriptional network of Saccharomyces cerevisiae. Scientific Reports, 2020, 10, 17744.	3.3	8
7	Hybrid Epithelialâ€”Mesenchymal Phenotypes Are Controlled by Microenvironmental Factors. Cancer Research, 2020, 80, 2407-2420.	0.9	34
8	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
9	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	78
10	Impact of changing cell-cell communication network in models of epithelial pattern formation. IFAC-PapersOnLine, 2019, 52, 38-44.	0.9	0
11	Local Negative Circuits and Cyclic Attractors in Boolean Networks with at most Five Components. SIAM Journal on Applied Dynamical Systems, 2019, 18, 68-79.	1.6	1
12	Stable States of Boolean Regulatory Networks Composed Over Hexagonal Grids. Electronic Notes in Theoretical Computer Science, 2018, 335, 113-130.	0.9	5
13	Estimating Attractor Reachability in Asynchronous Logical Models. Frontiers in Physiology, 2018, 9, 1161.	2.8	19
14	Interactions Elicited by the Contradiction Between Figure Direction Discrimination and Figure-Ground Segregation. Frontiers in Psychology, 2018, 9, 1681.	2.1	4
15	Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. Frontiers in Physiology, 2018, 9, 646.	2.8	75
16	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. Frontiers in Physiology, 2018, 9, 680.	2.8	67
17	Logical modelling uncovers developmental constraints for primary sex determination of chicken gonads. Journal of the Royal Society Interface, 2018, 15, 20180165.	3.4	10
18	EpiLog: A software for the logical modelling of epithelial dynamics. F1000Research, 2018, 7, 1145.	1.6	11

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19	EpiLog: A software for the logical modelling of epithelial dynamics. F1000Research, 2018, 7, 1145.	1.6	14
20	Logical Modeling and Dynamical Analysis of Cellular Networks. Frontiers in Genetics, 2016, 7, 94.	2.3	216
21	Primary sex determination of placental mammals: a modelling study uncovers dynamical developmental constraints in the formation of Sertoli and granulosa cells. BMC Systems Biology, 2016, 10, 37.	3.0	14
22	SBML Level 3 package: Qualitative Models, Version 1, Release 1. Journal of Integrative Bioinformatics, 2015, 12, 691-730.	1.5	15
23	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	4.1	98
24	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. Cancer Research, 2015, 75, 4042-4052.	0.9	96
25	The Systems Biology Markup Language (SBML) Level 3 Package: Qualitative Models, Version 1, Release 1. Journal of Integrative Bioinformatics, 2015, 12, 270.	1.5	21
26	A Discrete Model of Drosophila Eggshell Patterning Reveals Cell-Autonomous and Juxtacrine Effects. PLoS Computational Biology, 2014, 10, e1003527.	3.2	26
27	Model Checking Logical Regulatory Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2014, 47, 170-175.	0.4	4
28	Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2014, 9, 1285-1301.	1.5	21
29	Modelling the onset of senescence at the G1/S cell cycle checkpoint. BMC Genomics, 2014, 15, S7.	2.8	26
30	Model Checking to Assess T-Helper Cell Plasticity. Frontiers in Bioengineering and Biotechnology, 2014, 2, 86.	4.1	82
31	Logical Modelling of Regulatory Networks, Methods and Applications. Bulletin of Mathematical Biology, 2013, 75, 891-895.	1.9	11
32	Dynamical modeling and analysis of large cellular regulatory networks. Chaos, 2013, 23, 025114.	2.5	62
33	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135.	3.0	145
34	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
35	Composition and abstraction of logical regulatory modules: application to multicellular systems. Bioinformatics, 2013, 29, 749-757.	4.1	19
36	Bringing Dicyonodonts Back to Life: Paleobiology and Anatomy of a New Emydopoid Genus from the Upper Permian of Mozambique. PLoS ONE, 2013, 8, e80974.	2.5	78

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37	Majority Rules with Random Tie-Breaking in Boolean Gene Regulatory Networks. PLoS ONE, 2013, 8, e69626.	2.5	13
38	656 Mathematical Modeling of Bladder Tumorigenesis. European Journal of Cancer, 2012, 48, S155-S156.	2.8	0
39	Logical Modelling of Gene Regulatory Networks with GINsim. Methods in Molecular Biology, 2012, 804, 463-479.	0.9	134
40	Automatic Inference of Regulatory and Dynamical Properties from Incomplete Gene Interaction and Expression Data. Lecture Notes in Computer Science, 2012, , 25-30.	1.3	10
41	Efficient Verification for Logical Models of Regulatory Networks. Advances in Intelligent and Soft Computing, 2012, , 259-267.	0.2	6
42	Efficient Handling of Large Signalling-Regulatory Networks by Focusing on Their Core Control. Lecture Notes in Computer Science, 2012, , 288-306.	1.3	19
43	A Modular, Qualitative Modeling of Regulatory Networks Using Petri Nets. Computational Biology, 2011, , 253-279.	0.2	5
44	Petri net representation of multi-valued logical regulatory graphs. Natural Computing, 2011, 10, 727-750.	3.0	30
45	Mapping multivalued onto Boolean dynamics. Journal of Theoretical Biology, 2011, 270, 177-184.	1.7	42
46	Dynamically consistent reduction of logical regulatory graphs. Theoretical Computer Science, 2011, 412, 2207-2218.	0.9	117
47	Relating Formalisms for the Qualitative Modelling of Regulatory Networks. Advances in Intelligent and Soft Computing, 2011, , 293-302.	0.2	0
48	Diversity and Plasticity of Th Cell Types Predicted from Regulatory Network Modelling. PLoS Computational Biology, 2010, 6, e1000912.	3.2	167
49	Reduction of logical models of regulatory networks yields insight into dynamical properties. , 2010, , .		0
50	Discrete Modelling: Petri Net and Logical Approaches. Systems Biology, 2010, , 821-855.	0.1	5
51	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. BMC Systems Biology, 2009, 3, 1.	3.0	242
52	Logical modelling of regulatory networks with GINsim 2.3. BioSystems, 2009, 97, 134-139.	2.0	188
53	Modular logical modelling of the budding yeast cell cycle. Molecular BioSystems, 2009, 5, 1787.	2.9	58
54	Petri net modelling of biological regulatory networks. Journal of Discrete Algorithms, 2008, 6, 165-177.	0.7	61

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55	Qualitative modelling of biological regulatory networks combining a logical multi-valued formalism and Petri nets. , 2008, , .		2
56	Logical modelling of the role of the Hh pathway in the patterning of the <i>Drosophila</i> wing disc. Bioinformatics, 2008, 24, i234-i240.	4.1	41
57	Segmenting the fly embryo: logical analysis of the role of the Segment Polarity cross-regulatory module. International Journal of Developmental Biology, 2008, 52, 1059-1075.	0.6	85
58	Decision Diagrams for the Representation and Analysis of Logical Models of Genetic Networks. Lecture Notes in Computer Science, 2007, , 233-247.	1.3	77
59	Petri net modelling of biological networks. Briefings in Bioinformatics, 2007, 8, 210-219.	6.5	336
60	Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle. Bioinformatics, 2006, 22, e124-e131.	4.1	570
61	GINsim: A software suite for the qualitative modelling, simulation and analysis of regulatory networks. BioSystems, 2006, 84, 91-100.	2.0	165
62	Dynamical modeling of biological regulatory networks. BioSystems, 2006, 84, 77-80.	2.0	16
63	Dynamical Analysis of the Regulatory Network Defining the Dorsal-Ventral Boundary of the Drosophila Wing Imaginal Disc. Genetics, 2006, 174, 1625-1634.	2.9	23
64	Qualitative Petri Net Modelling of Genetic Networks. Lecture Notes in Computer Science, 2006, , 95-112.	1.3	21
65	From Logical Regulatory Graphs to Standard Petri Nets: Dynamical Roles and Functionality of Feedback Circuits. Lecture Notes in Computer Science, 2006, , 56-72.	1.3	25
66	From Gradients to Stripes: A Logical Analysis of Drosophila Segmentation Genetic Network. , 2006, , 379-390.		0
67	Qualitative modelling of regulated metabolic pathways: application to the tryptophan biosynthesis in E.Coli. Bioinformatics, 2005, 21, ii190-ii196.	4.1	65
68	Qualitative Modelling of Genetic Networks: From Logical Regulatory Graphs to Standard Petri Nets. Lecture Notes in Computer Science, 2004, , 137-156.	1.3	39
69	A description of dynamical graphs associated to elementary regulatory circuits. Bioinformatics, 2003, 19, ii172-ii178.	4.1	55
70	The extended kanban control system for production coordination of assembly manufacturing systems. IIE Transactions, 2000, 32, 999-1012.	2.1	37
71	The extended kanban control system for production coordination of assembly manufacturing systems. IIE Transactions, 2000, 32, 999-1012.	2.1	20