

Chiara Damiani

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

616
citations

687220

13
h-index

642610

23
g-index

47
all docs

47
docs citations

47
times ranked

670
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. PLoS Computational Biology, 2019, 15, e1006733.	1.5	70
2	A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect. PLoS Computational Biology, 2017, 13, e1005758.	1.5	64
3	Dynamical Properties of a Boolean Model of Gene Regulatory Network with Memory. Journal of Computational Biology, 2011, 18, 1291-1303.	0.8	56
4	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	1.3	54
5	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. Computational Biology and Chemistry, 2016, 62, 60-69.	1.1	36
6	Systems metabolomics: from metabolomic snapshots to design principles. Current Opinion in Biotechnology, 2020, 63, 190-199.	3.3	36
7	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. Bioinformatics, 2017, 33, i311-i318.	1.8	31
8	Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power. Journal of Biomedical Informatics, 2018, 87, 37-49.	2.5	28
9	INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation. PLoS Computational Biology, 2022, 18, e1009337.	1.5	24
10	Growth and Division in a Dynamic Protocell Model. Life, 2014, 4, 837-864.	1.1	23
11	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. Natural Computing, 2014, 13, 321-331.	1.8	18
12	Single-cell Digital Twins for Cancer Preclinical Investigation. Methods in Molecular Biology, 2020, 2088, 331-343.	0.4	17
13	The Diffusion of Perturbations in a Model of Coupled Random Boolean Networks. Lecture Notes in Computer Science, 2008, , 315-322.	1.0	16
14	A stochastic model of catalytic reaction networks in protocells. Natural Computing, 2014, 13, 367-377.	1.8	15
15	Parameter sensitivity analysis of stochastic models: Application to catalytic reaction networks. Computational Biology and Chemistry, 2013, 42, 5-17.	1.1	13
16	CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETWORKS. BMC Bioinformatics, 2016, 17, 64.	1.2	13
17	Dynamical regimes in non-ergodic random Boolean networks. Natural Computing, 2017, 16, 353-363.	1.8	12
18	Information Transfer among Coupled Random Boolean Networks. Lecture Notes in Computer Science, 2010, , 1-11.	1.0	12

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19	Divergent in vitro/in vivo responses to drug treatments of highly aggressive NIH-Ras cancer cells: a PET imaging and metabolomics-mass-spectrometry study. <i>Oncotarget</i> , 2016, 7, 52017-52031.	0.8	11
20	GPRuler: Metabolic gene-protein-reaction rules automatic reconstruction. <i>PLoS Computational Biology</i> , 2021, 17, e1009550.	1.5	11
21	MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 993-999.	1.9	7
22	Modeling Spatio-Temporal Dynamics of Metabolic Networks with Cellular Automata and Constraint-Based Methods. <i>Lecture Notes in Computer Science</i> , 2018, , 16-29.	1.0	6
23	PMCE: efficient inference of expressive models of cancer evolution with high prognostic power. <i>Bioinformatics</i> , 2022, 38, 754-762.	1.8	6
24	Accelerated global sensitivity analysis of genome-wide constraint-based metabolic models. <i>BMC Bioinformatics</i> , 2021, 22, 78.	1.2	5
25	On RAF Sets and Autocatalytic Cycles in Random Reaction Networks. <i>Communications in Computer and Information Science</i> , 2014, , 113-126.	0.4	5
26	Combining multi-target regression deep neural networks and kinetic modeling to predict relative fluxes in reaction systems. <i>Information and Computation</i> , 2021, 281, 104798.	0.5	3
27	Constraint-Based Modeling and Simulation of Cell Populations. <i>Communications in Computer and Information Science</i> , 2017, , 126-137.	0.4	3
28	Model Identification Using Correlation-Based Inference and Transfer Entropy Estimation. , 2011, , .		2
29	Modelling the Influence of Cell Signaling on the Dynamics of Gene Regulatory Networks. <i>Lecture Notes in Computational Vision and Biomechanics</i> , 2013, , 103-130.	0.5	2
30	Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes. <i>BMC Bioinformatics</i> , 2018, 19, 251.	1.2	2
31	Global Sensitivity Analysis of Constraint-Based Metabolic Models. <i>Lecture Notes in Computer Science</i> , 2020, , 179-186.	1.0	2
32	The role of backward reactions in a stochastic model of catalytic reaction networks. , 0, , .		2
33	Linking Alterations in Metabolic Fluxes with Shifts in Metabolite Levels by Means of Kinetic Modeling. <i>Communications in Computer and Information Science</i> , 2017, , 138-148.	0.4	1
34	COSYS: A Computational Infrastructure for Systems Biology. <i>Lecture Notes in Computer Science</i> , 2017, , 82-92.	1.0	1
35	Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System. <i>Communications in Computer and Information Science</i> , 2019, , 115-126.	0.4	1
36	Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. <i>Lecture Notes in Computer Science</i> , 2020, , 207-215.	1.0	1

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37	Constraining Mechanism Based Simulations to Identify Ensembles of Parametrizations to Characterize Metabolic Features. Lecture Notes in Computer Science, 2017, , 107-117.	1.0	0
38	The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System. Fundamenta Informaticae, 2019, 171, 279-295.	0.3	0
39	On the Use of Topological Features of Metabolic Networks for the Classification of Cancer Samples. Current Genomics, 2021, 22, 88-97.	0.7	0
40	Recent developments in research on catalytic reaction networks. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 3-13.	0.8	0
41	Investigating the Role of Network Topology and Dynamical Regimes on the Dynamics of a Cell Differentiation Model. Communications in Computer and Information Science, 2014, , 151-168.	0.4	0