Chiara Damiani

List of Publications by Year
in descending order

41 papers	616 citations	687363 13 h-index	642732 23 g-index
47 all docs	47 docs citations	47 times ranked	670 citing authors

#	Article	IF	Citations
1	PMCE: efficient inference of expressive models of cancer evolution with high prognostic power. Bioinformatics, 2022, 38, 754-762.	4.1	6
2	INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation. PLoS Computational Biology, 2022, 18, e1009337.	3.2	24
3	Accelerated global sensitivity analysis of genome-wide constraint-based metabolic models. BMC Bioinformatics, 2021, 22, 78.	2.6	5
4	On the Use of Topological Features of Metabolic Networks for the Classification of Cancer Samples. Current Genomics, 2021, 22, 88-97.	1.6	0
5	Combining multi-target regression deep neural networks and kinetic modeling to predict relative fluxes in reaction systems. Information and Computation, 2021, 281, 104798.	0.7	3
6	GPRuler: Metabolic gene-protein-reaction rules automatic reconstruction. PLoS Computational Biology, 2021, 17, e1009550.	3.2	11
7	MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy. Computational and Structural Biotechnology Journal, 2020, 18, 993-999.	4.1	7
8	Systems metabolomics: from metabolomic snapshots to design principles. Current Opinion in Biotechnology, 2020, 63, 190-199.	6.6	36
9	Single-cell Digital Twins for Cancer Preclinical Investigation. Methods in Molecular Biology, 2020, 2088, 331-343.	0.9	17
10	Global Sensitivity Analysis of Constraint-Based Metabolic Models. Lecture Notes in Computer Science, 2020, , 179-186.	1.3	2
11	Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. Lecture Notes in Computer Science, 2020, , 207-215.	1.3	1
12	Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System. Communications in Computer and Information Science, 2019, , 115-126.	0.5	1
13	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. PLoS Computational Biology, 2019, 15, e1006733.	3.2	70
14	The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System. Fundamenta Informaticae, 2019, 171, 279-295.	0.4	0
15	Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power. Journal of Biomedical Informatics, 2018, 87, 37-49.	4.3	28
16	Modeling Spatio-Temporal Dynamics of Metabolic Networks with Cellular Automata and Constraint-Based Methods. Lecture Notes in Computer Science, 2018, , 16-29.	1.3	6
17	Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes. BMC Bioinformatics, 2018, 19, 251.	2.6	2
18	Dynamical regimes in non-ergodic random Boolean networks. Natural Computing, 2017, 16, 353-363.	3.0	12

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19	Linking Alterations in Metabolic Fluxes with Shifts in Metabolite Levels by Means of Kinetic Modeling. Communications in Computer and Information Science, 2017, , 138-148.	0.5	1
20	Constraining Mechanism Based Simulations to Identify Ensembles of Parametrizations to Characterize Metabolic Features. Lecture Notes in Computer Science, 2017, , 107-117.	1.3	0
21	COSYS: A Computational Infrastructure for Systems Biology. Lecture Notes in Computer Science, 2017, , 82-92.	1.3	1
22	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. Bioinformatics, 2017, 33, i311-i318.	4.1	31
23	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.	3.2	64
24	Constraint-Based Modeling and Simulation of Cell Populations. Communications in Computer and Information Science, 2017, , 126-137.	0.5	3
25	CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETworks. BMC Bioinformatics, 2016, 17, 64.	2.6	13
26	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. Computational Biology and Chemistry, 2016, 62, 60-69.	2.3	36
27	Divergent in vitro/in vivo responses to drug treatments of highly aggressive NIH-Ras cancer cells: a PET imaging and metabolomics-mass-spectrometry study. Oncotarget, 2016, 7, 52017-52031.	1.8	11
28	Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087.	2.9	54
29	Growth and Division in a Dynamic Protocell Model. Life, 2014, 4, 837-864.	2.4	23
30	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. Natural Computing, 2014, 13, 321-331.	3.0	18
31	A stochastic model of catalytic reaction networks in protocells. Natural Computing, 2014, 13, 367-377.	3.0	15
32	On RAF Sets and Autocatalytic Cycles in Random Reaction Networks. Communications in Computer and Information Science, 2014, , 113-126.	0.5	5
33	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.	0.5	0
34	Parameter sensitivity analysis of stochastic models: Application to catalytic reaction networks. Computational Biology and Chemistry, 2013, 42, 5-17.	2.3	13
35	Modelling the Influence of Cell Signaling on the Dynamics of Gene Regulatory Networks. Lecture Notes in Computational Vision and Biomechanics, 2013, , 103-130.	0.5	2
36	Model Identification Using Correlation-Based Inference and Transfer Entropy Estimation. , 2011, , .		2

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37	Dynamical Properties of a Boolean Model of Gene Regulatory Network with Memory. Journal of Computational Biology, 2011, 18, 1291-1303.	1.6	56
38	Information Transfer among Coupled Random Boolean Networks. Lecture Notes in Computer Science, 2010, , 1-11.	1.3	12
39	The Diffusion of Perturbations in a Model of Coupled Random Boolean Networks. Lecture Notes in Computer Science, 2008, , 315-322.	1.3	16
40	The role of backward reactions in a stochastic model of catalytic reaction networks. , 0, , .		2
41	Recent developments in research on catalytic reaction networks. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 3-13.	0.8	0