Daniel Machado

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3383707/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. Nucleic Acids Research, 2018, 46, 7542-7553.	14.5	410
2	Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism. PLoS Computational Biology, 2014, 10, e1003580.	3.2	357
3	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
4	Modeling formalisms in Systems Biology. AMB Express, 2011, 1, 45.	3.0	139
5	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021, 6, 196-208.	13.3	138
6	Polarization of microbial communities between competitive and cooperative metabolism. Nature Ecology and Evolution, 2021, 5, 195-203.	7.8	131
7	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	6.2	124
8	Random sampling of elementary flux modes in large-scale metabolic networks. Bioinformatics, 2012, 28, i515-i521.	4.1	66
9	Co-evolution of strain design methods based on flux balance and elementary mode analysis. Metabolic Engineering Communications, 2015, 2, 85-92.	3.6	66
10	Ecological modelling approaches for predicting emergent properties in microbial communities. Nature Ecology and Evolution, 2022, 6, 855-865.	7.8	54
11	Hybrid dynamic modeling of Escherichia coli central metabolic network combining Michaelis–Menten and approximate kinetic equations. BioSystems, 2010, 100, 150-157.	2.0	49
12	Stoichiometric Representation of Gene–Protein–Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. PLoS Computational Biology, 2016, 12, e1005140.	3.2	48
13	Current state and challenges for dynamic metabolic modeling. Current Opinion in Microbiology, 2016, 33, 97-104.	5.1	40
14	Exploring the gap between dynamic and constraint-based models of metabolism. Metabolic Engineering, 2012, 14, 112-119.	7.0	33
15	Modeling the Contribution of Allosteric Regulation for Flux Control in the Central Carbon Metabolism of E. coli. Frontiers in Bioengineering and Biotechnology, 2015, 3, 154.	4.1	31
16	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. Metabolic Engineering, 2018, 45, 149-157.	7.0	27
17	Linking genetic, metabolic, and phenotypic diversity among <i>Saccharomyces cerevisiae</i> strains using multi-omics associations. GigaScience, 2019, 8, .	6.4	25
18	Critical perspective on the consequences of the limited availability of kinetic data in metabolic dynamic modelling. IET Systems Biology, 2011, 5, 157-163.	1.5	18

DANIEL MACHADO

#	Article	IF	CITATIONS
19	Metabolic memory underlying minimal residual disease in breast cancer. Molecular Systems Biology, 2021, 17, e10141.	7.2	14
20	A kinetic model for curcumin production in Escherichia coli. BioSystems, 2014, 125, 16-21.	2.0	12
21	Unlocking the genomic potential of aerobes and phototrophs for the production of nutritious and palatable microbial food without arable land or fossil fuels. Microbial Biotechnology, 2022, 15, 6-12.	4.2	9
22	Editorial: Current Challenges in Modeling Cellular Metabolism. Frontiers in Bioengineering and Biotechnology, 2015, 3, 193.	4.1	7
23	A Comparative Analysis of Dynamic Models of the Central Carbon Metabolism of Escherichia coli. IFAC-PapersOnLine, 2016, 49, 270-276.	0.9	6
24	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. Lecture Notes in Computer Science, 2009, , 1063-1070.	1.3	2
25	Large Scale Dynamic Model Reconstruction for the Central Carbon Metabolism of Escherichia coli. Lecture Notes in Computer Science, 2009, , 1079-1083.	1.3	2
26	Evaluating the integration of proteomic data for the prediction of intracellular fluxes after knockout experiments. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2010, 43, 114-119.	0.4	1
27	getALife - An Artificial Life Environment for the Evaluation of Agent-Based Systems and Evolutionary Algorithms for Reinforcement Learning, Studies in Computational Intelligence, 2008, , 35-44.	0.9	1