Daniel Machado

List of Publications by Year
in descending order

27	2,190	430442	500791
papers	citations	18	28
		h-index	g-index

35	35	35	2523
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	2.0	9
2	Ecological modelling approaches for predicting emergent properties in microbial communities. Nature Ecology and Evolution, 2022, 6, 855-865.	3.4	54
3	Polarization of microbial communities between competitive and cooperative metabolism. Nature Ecology and Evolution, 2021, 5, 195-203.	3.4	131
4	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021, 6, 196-208.	5.9	138
5	Metabolic memory underlying minimal residual disease in breast cancer. Molecular Systems Biology, 2021, 17, e10141.	3.2	14
6	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
7	Linking genetic, metabolic, and phenotypic diversity among *Saccharomyces cerevisiae* strains using multi-omics associations. GigaScience, 2019, 8, .	3.3	25
8	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. Metabolic Engineering, 2018, 45, 149-157.	3.6	27
9	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. Nucleic Acids Research, 2018, 46, 7542-7553.	6.5	410
10	Stoichiometric Representation of Gene–Protein–Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. PLoS Computational Biology, 2016, 12, e1005140.	1.5	48
11	A Comparative Analysis of Dynamic Models of the Central Carbon Metabolism of Escherichia coli. IFAC-PapersOnLine, 2016, 49, 270-276.	0.5	6
12	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	2.9	124
13	Current state and challenges for dynamic metabolic modeling. Current Opinion in Microbiology, 2016, 33, 97-104.	2.3	40
14	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.	2.0	31
15	Editorial: Current Challenges in Modeling Cellular Metabolism. Frontiers in Bioengineering and Biotechnology, 2015, 3, 193.	2.0	7
16	Co-evolution of strain design methods based on flux balance and elementary mode analysis. Metabolic Engineering Communications, 2015, 2, 85-92.	1.9	66
17	A kinetic model for curcumin production in Escherichia coli. BioSystems, 2014, 125, 16-21.	0.9	12
18	Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism. PLoS Computational Biology, 2014, 10, e1003580.	1.5	357

#	ARTICLE	IF	CITATIONS
19	Random sampling of elementary flux modes in large-scale metabolic networks. Bioinformatics, 2012, 28, i515-i521.	1.8	66
20	Exploring the gap between dynamic and constraint-based models of metabolism. Metabolic Engineering, 2012, 14, 112-119.	3.6	33
21	Critical perspective on the consequences of the limited availability of kinetic data in metabolic dynamic modelling. IET Systems Biology, 2011, 5, 157-163.	0.8	18
22	Modeling formalisms in Systems Biology. AMB Express, 2011, 1, 45.	1.4	139
23	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
24	Hybrid dynamic modeling of Escherichia coli central metabolic network combining Michaelis–Menten and approximate kinetic equations. BioSystems, 2010, 100, 150-157.	0.9	49
25	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. Lecture Notes in Computer Science, 2009, , 1063-1070.	1.0	2
26	Large Scale Dynamic Model Reconstruction for the Central Carbon Metabolism of Escherichia coli. Lecture Notes in Computer Science, 2009, , 1079-1083.	1.0	2
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.	0.7	1