

# Daniel Machado

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

2,190  
citations

430442

18  
h-index

500791

28  
g-index

35  
all docs

35  
docs citations

35  
times ranked

2523  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. <i>Nucleic Acids Research</i> , 2018, 46, 7542-7553.	6.5	410
2	Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism. <i>PLoS Computational Biology</i> , 2014, 10, e1003580.	1.5	357
3	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
4	Modeling formalisms in Systems Biology. <i>AMB Express</i> , 2011, 1, 45.	1.4	139
5	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	5.9	138
6	Polarization of microbial communities between competitive and cooperative metabolism. <i>Nature Ecology and Evolution</i> , 2021, 5, 195-203.	3.4	131
7	Multi-omics Quantification of Species Variation of <i>Escherichia coli</i> Links Molecular Features with Strain Phenotypes. <i>Cell Systems</i> , 2016, 3, 238-251.e12.	2.9	124
8	Random sampling of elementary flux modes in large-scale metabolic networks. <i>Bioinformatics</i> , 2012, 28, i515-i521.	1.8	66
9	Co-evolution of strain design methods based on flux balance and elementary mode analysis. <i>Metabolic Engineering Communications</i> , 2015, 2, 85-92.	1.9	66
10	Ecological modelling approaches for predicting emergent properties in microbial communities. <i>Nature Ecology and Evolution</i> , 2022, 6, 855-865.	3.4	54
11	Hybrid dynamic modeling of <i>Escherichia coli</i> central metabolic network combining Michaelis-Menten and approximate kinetic equations. <i>BioSystems</i> , 2010, 100, 150-157.	0.9	49
12	Stoichiometric Representation of Gene-Protein-Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. <i>PLoS Computational Biology</i> , 2016, 12, e1005140.	1.5	48
13	Current state and challenges for dynamic metabolic modeling. <i>Current Opinion in Microbiology</i> , 2016, 33, 97-104.	2.3	40
14	Exploring the gap between dynamic and constraint-based models of metabolism. <i>Metabolic Engineering</i> , 2012, 14, 112-119.	3.6	33
15	Modeling the Contribution of Allosteric Regulation for Flux Control in the Central Carbon Metabolism of <i>E. coli</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 154.	2.0	31
16	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	3.6	27
17	Linking genetic, metabolic, and phenotypic diversity among <i>Saccharomyces cerevisiae</i> strains using multi-omics associations. <i>GigaScience</i> , 2019, 8, .	3.3	25
18	Critical perspective on the consequences of the limited availability of kinetic data in metabolic dynamic modelling. <i>IET Systems Biology</i> , 2011, 5, 157-163.	0.8	18

#	ARTICLE	IF	CITATIONS
19	Metabolic memory underlying minimal residual disease in breast cancer. <i>Molecular Systems Biology</i> , 2021, 17, e10141.	3.2	14
20	A kinetic model for curcumin production in <i>Escherichia coli</i> . <i>BioSystems</i> , 2014, 125, 16-21.	0.9	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. <i>Microbial Biotechnology</i> , 2022, 15, 6-12.	2.0	9
22	Editorial: Current Challenges in Modeling Cellular Metabolism. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 193.	2.0	7
23	A Comparative Analysis of Dynamic Models of the Central Carbon Metabolism of <i>Escherichia coli</i> . <i>IFAC-PapersOnLine</i> , 2016, 49, 270-276.	0.5	6
24	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. <i>Lecture Notes in Computer Science</i> , 2009, , 1063-1070.	1.0	2
25	Large Scale Dynamic Model Reconstruction for the Central Carbon Metabolism of <i>Escherichia coli</i> . <i>Lecture Notes in Computer Science</i> , 2009, , 1079-1083.	1.0	2
26	Evaluating the integration of proteomic data for the prediction of intracellular fluxes after knockout experiments. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 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. <i>Studies in Computational Intelligence</i> , 2008, , 35-44.	0.7	1