

Patrick F Suthers

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,625
citations

516710

16
h-index

794594

19
g-index

22
all docs

22
docs citations

22
times ranked

1951
citing authors

#	ARTICLE	IF	CITATIONS
1	Examining organic acid production potential and growth-coupled strategies in <i>Issatchenkia orientalis</i> using constraint-based modeling. <i>Biotechnology Progress</i> , 2022, 38, .	2.6	4
2	Recent advances in constraint and machine learning-based metabolic modeling by leveraging stoichiometric balances, thermodynamic feasibility and kinetic law formalisms. <i>Metabolic Engineering</i> , 2021, 63, 13-33.	7.0	26
3	Building kinetic models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2021, 67, 35-41.	6.6	30
4	Genome-scale metabolic reconstruction of the non-model yeast <i>Issatchenkia orientalis</i> SD108 and its application to organic acids production. <i>Metabolic Engineering Communications</i> , 2020, 11, e00148.	3.6	20
5	Challenges of cultivated meat production and applications of genome-scale metabolic modeling. <i>AIChE Journal</i> , 2020, 66, e16235.	3.6	7
6	A comprehensive genome-scale model for <i>Rhodospiridium toruloides</i> IFO0880 accounting for functional genomics and phenotypic data. <i>Metabolic Engineering Communications</i> , 2019, 9, e00101.	3.6	55
7	Mathematical optimization applications in metabolic networks. <i>Metabolic Engineering</i> , 2012, 14, 672-686.	7.0	123
8	Orchestrating hi-fi annotations. <i>Nature Chemical Biology</i> , 2012, 8, 810-811.	8.0	0
9	MetRxn: a knowledgebase of metabolites and reactions spanning metabolic models and databases. <i>BMC Bioinformatics</i> , 2012, 13, 6.	2.6	120
10	<i>Zea mays</i> iRS1563: A Comprehensive Genome-Scale Metabolic Reconstruction of Maize Metabolism. <i>PLoS ONE</i> , 2011, 6, e21784.	2.5	189
11	Construction of an <i>E. Coli</i> genome-scale atom mapping model for MFA calculations. <i>Biotechnology and Bioengineering</i> , 2011, 108, 1372-1382.	3.3	42
12	Improved computational performance of MFA using elementary metabolite units and flux coupling. <i>Metabolic Engineering</i> , 2010, 12, 123-128.	7.0	27
13	OptForce: An Optimization Procedure for Identifying All Genetic Manipulations Leading to Targeted Overproductions. <i>PLoS Computational Biology</i> , 2010, 6, e1000744.	3.2	346
14	A Genome-Scale Metabolic Reconstruction of <i>Mycoplasma genitalium</i> , iPS189. <i>PLoS Computational Biology</i> , 2009, 5, e1000285.	3.2	119
15	Genome Scale Reconstruction of a <i>Salmonella</i> Metabolic Model. <i>Journal of Biological Chemistry</i> , 2009, 284, 29480-29488.	3.4	85
16	Genome-scale gene/reaction essentiality and synthetic lethality analysis. <i>Molecular Systems Biology</i> , 2009, 5, 301.	7.2	143
17	Using Systems Engineering to Reconstruct, Analyze and Redesign Metabolism. <i>Computer Aided Chemical Engineering</i> , 2009, , 113-115.	0.5	0
18	Identification of optimal measurement sets for complete flux elucidation in metabolic flux analysis experiments. <i>Biotechnology and Bioengineering</i> , 2008, 100, 1039-1049.	3.3	35

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19	Rapid responses of ribosomal RNA synthesis to nutrient shifts. <i>Biotechnology and Bioengineering</i> , 2007, 97, 1230-1245.	3.3	4
20	Metabolic flux elucidation for large-scale models using ¹³ C labeled isotopes. <i>Metabolic Engineering</i> , 2007, 9, 387-405.	7.0	104
21	Effects of <i>Escherichia coli</i> Physiology on Growth of Phage T7 In Vivo and In Silico. <i>Journal of Bacteriology</i> , 2002, 184, 1888-1894.	2.2	146