

Lin Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6919828/publications.pdf>

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14
papers

1,270
citations

933264

10
h-index

1058333

14
g-index

16
all docs

16
docs citations

16
times ranked

2035
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.6	26
2	Building kinetic models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2021, 67, 35-41.	3.3	30
3	A Genome-Scale Metabolic Model of <i>Anabaena</i> 33047 to Guide Genetic Modifications to Overproduce Nylon Monomers. <i>Metabolites</i> , 2021, 11, 168.	1.3	4
4	Computationally Prospecting Potential Pathways from Lignin Monomers and Dimers toward Aromatic Compounds. <i>ACS Synthetic Biology</i> , 2021, 10, 1064-1076.	1.9	4
5	dGPredictor: Automated fragmentation method for metabolic reaction free energy prediction and de novo pathway design. <i>PLoS Computational Biology</i> , 2021, 17, e1009448.	1.5	8
6	Metabolic flux analysis reaching genome wide coverage: lessons learned and future perspectives. <i>Current Opinion in Chemical Engineering</i> , 2020, 30, 17-25.	3.8	7
7	Pareto Optimality Explanation of the Glycolytic Alternatives in Nature. <i>Scientific Reports</i> , 2019, 9, 2633.	1.6	16
8	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	5.5	833
9	Exploring the combinatorial space of complete pathways to chemicals. <i>Biochemical Society Transactions</i> , 2018, 46, 513-522.	1.6	14
10	MinGenome: An <i>In Silico</i> Top-Down Approach for the Synthesis of Minimized Genomes. <i>ACS Synthetic Biology</i> , 2018, 7, 462-473.	1.9	45
11	Pathway design using de novo steps through uncharted biochemical spaces. <i>Nature Communications</i> , 2018, 9, 184.	5.8	77
12	Accelerating flux balance calculations in genome-scale metabolic models by localizing the application of loopless constraints. <i>Bioinformatics</i> , 2018, 34, 4248-4255.	1.8	22
13	Standardizing biomass reactions and ensuring complete mass balance in genome-scale metabolic models. <i>Bioinformatics</i> , 2017, 33, 3603-3609.	1.8	86
14	A review of computational tools for design and reconstruction of metabolic pathways. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 243-252.	1.8	98