

# Lin Wang

## List of Publications by Year in descending order

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

Version: 2024-02-01

15  
papers

1,270  
citations

933447

10  
h-index

1058476

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.	7.0	26
2	Building kinetic models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2021, 67, 35-41.	6.6	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.	2.9	4
4	Computationally Prospecting Potential Pathways from Lignin Monomers and Dimers toward Aromatic Compounds. <i>ACS Synthetic Biology</i> , 2021, 10, 1064-1076.	3.8	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.	3.2	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.	7.8	7
7	Pareto Optimality Explanation of the Glycolytic Alternatives in Nature. <i>Scientific Reports</i> , 2019, 9, 2633.	3.3	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.	12.0	833
9	Principles of Systems Biology, No. 26. <i>Cell Systems</i> , 2018, 6, 143-145.	6.2	0
10	Exploring the combinatorial space of complete pathways to chemicals. <i>Biochemical Society Transactions</i> , 2018, 46, 513-522.	3.4	14
11	MinGenome: An <i>In Silico</i> Top-Down Approach for the Synthesis of Minimized Genomes. <i>ACS Synthetic Biology</i> , 2018, 7, 462-473.	3.8	45
12	Pathway design using de novo steps through uncharted biochemical spaces. <i>Nature Communications</i> , 2018, 9, 184.	12.8	77
13	Accelerating flux balance calculations in genome-scale metabolic models by localizing the application of loopless constraints. <i>Bioinformatics</i> , 2018, 34, 4248-4255.	4.1	22
14	Standardizing biomass reactions and ensuring complete mass balance in genome-scale metabolic models. <i>Bioinformatics</i> , 2017, 33, 3603-3609.	4.1	86
15	A review of computational tools for design and reconstruction of metabolic pathways. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 243-252.	3.7	98