

# Meiyappan Lakshmanan

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

2,265  
citations

361413  
20  
h-index

254184  
43  
g-index

51  
all docs

51  
docs citations

51  
times ranked

3321  
citing authors

#	ARTICLE	IF	CITATIONS
1	Harnessing the potential of machine learning for advancing "Quality by Design" in biomanufacturing. <i>MAbs</i> , 2022, 14, 2013593.	5.2	21
2	Systems Biology of Gut Microbiota-Human Receptor Interactions: Toward Anti-inflammatory Probiotics. <i>Frontiers in Microbiology</i> , 2022, 13, 846555.	3.5	3
3	Combined multivariate statistical and flux balance analyses uncover media bottlenecks to the growth and productivity of Chinese hamster ovary cell cultures. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1740-1754.	3.3	7
4	Multi-omics profiling of a CHO cell culture system unravels the effect of culture pH on cell growth, antibody titer, and product quality. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4305-4316.	3.3	11
5	Enhancing Microbiome Research through Genome-Scale Metabolic Modeling. <i>MSystems</i> , 2021, 6, e0059921.	3.8	15
6	In silico model-based characterization of metabolic response to harsh sparging stress in fed-batch CHO cell cultures. <i>Journal of Biotechnology</i> , 2020, 308, 10-20.	3.8	10
7	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
8	Genome-scale metabolic reconstruction and in silico analysis of the rice leaf blight pathogen, <i>Xanthomonas oryzae</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 527-540.	4.2	11
9	Enzyme capacity-based genome scale modelling of CHO cells. <i>Metabolic Engineering</i> , 2020, 60, 138-147.	7.0	51
10	Oral microbiome-systemic link studies: perspectives on current limitations and future artificial intelligence-based approaches. <i>Critical Reviews in Microbiology</i> , 2020, 46, 288-299.	6.1	12
11	Multi-omics profiling of CHO parental hosts reveals cell line-specific variations in bioprocessing traits. <i>Biotechnology and Bioengineering</i> , 2019, 116, 2117-2129.	3.3	38
12	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136
13	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018, 18, 62.	3.6	73
14	Kinetic Modeling of Mammalian Cell Culture Bioprocessing: The Quest to Advance Biomanufacturing. <i>Biotechnology Journal</i> , 2018, 13, e1700229.	3.5	63
15	Towards next generation CHO cell line development and engineering by systems approaches. <i>Current Opinion in Chemical Engineering</i> , 2018, 22, 1-10.	7.8	43
16	In silico model-guided identification of transcriptional regulator targets for efficient strain design. <i>Microbial Cell Factories</i> , 2018, 17, 167.	4.0	10
17	Comparative phenotypic analysis of CHO clones and culture media for lactate shift. <i>Journal of Biotechnology</i> , 2018, 283, 97-104.	3.8	17
18	Genome-scale model-driven strain design for dicarboxylic acid production in <i>Yarrowia lipolytica</i> . <i>BMC Systems Biology</i> , 2018, 12, 12.	3.0	58

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19	Metabolic Modeling of Microbial Community Interactions for Health, Environmental and Biotechnological Applications. <i>Current Genomics</i> , 2018, 19, 712-722.	1.6	28
20	Mammalian Systems Biotechnology Reveals Global Cellular Adaptations in a Recombinant CHO Cell Line. <i>Cell Systems</i> , 2017, 4, 530-542.e6.	6.2	84
21	Integrative metabolomic analysis reveals diet supplementation with green tea alleviates UVB-damaged mouse skin correlated with ascorbate metabolism and urea cycle. <i>Metabolomics</i> , 2017, 13, 1.	3.0	3
22	Genome-scale modeling and transcriptome analysis of <i>Leuconostoc mesenteroides</i> unravel the redox governed metabolic states in obligate heterofermentative lactic acid bacteria. <i>Scientific Reports</i> , 2017, 7, 15721.	3.3	33
23	Modeling Rice Metabolism: From Elucidating Environmental Effects on Cellular Phenotype to Guiding Crop Improvement. <i>Frontiers in Plant Science</i> , 2016, 7, 1795.	3.6	18
24	Transcriptomics-based strain optimization tool for designing secondary metabolite overproducing strains of <i>Streptomyces coelicolor</i> . <i>Biotechnology and Bioengineering</i> , 2016, 113, 651-660.	3.3	38
25	Genome-scale metabolic modeling and in silico analysis of lipid accumulating yeast <i>Candida tropicalis</i> for dicarboxylic acid production. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1993-2004.	3.3	55
26	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , 2016, 3, 434-443.e8.	6.2	205
27	Light-specific transcriptional regulation of the accumulation of carotenoids and phenolic compounds in rice leaves. <i>Plant Signaling and Behavior</i> , 2016, 11, e1184808.	2.4	22
28	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	3.0	243
29	A genetic algorithm-based approach for pre-processing metabolomics and lipidomics LC-MS data. <i>Metabolomics</i> , 2016, 12, 1.	3.0	4
30	Identification of candidate network hubs involved in metabolic adjustments of rice under drought stress by integrating transcriptome data and genome-scale metabolic network. <i>Plant Science</i> , 2016, 242, 224-239.	3.6	39
31	Flux-sum analysis identifies metabolite targets for strain improvement. <i>BMC Systems Biology</i> , 2015, 9, 73.	3.0	15
32	In silico model-driven cofactor engineering strategies for improving the overall NADP(H) turnover in microbial cell factories. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 1401-1414.	3.0	12
33	Unraveling the light-specific metabolic and regulatory signatures of rice through combined in silico modeling and multi-omics analysis. <i>Plant Physiology</i> , 2015, 169, pp.01379.2015.	4.8	68
34	Metabolic and transcriptional regulatory mechanisms underlying the anoxic adaptation of rice coleoptile. <i>AoB PLANTS</i> , 2014, 6, .	2.3	9
35	Software applications for flux balance analysis. <i>Briefings in Bioinformatics</i> , 2014, 15, 108-122.	6.5	94
36	Genome-scale metabolic network reconstruction and in silico flux analysis of the thermophilic bacterium <i>Thermus thermophilus</i> HB27. <i>Microbial Cell Factories</i> , 2014, 13, 61.	4.0	17

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37	Genome-scale in silico modeling and analysis for designing synthetic terpenoid-producing microbial cell factories. <i>Chemical Engineering Science</i> , 2013, 103, 100-108.	3.8	22
38	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , 2013, 6, 1.	4.0	186
39	Identifying essential genes/reactions of the rice photorespiration by in silico model-based analysis. <i>Rice</i> , 2013, 6, 20.	4.0	11
40	Metabolic reconstruction and flux analysis of industrial <i>Pichia</i> yeasts. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1865-1873.	3.6	13
41	Elucidating Rice Cell Metabolism under Flooding and Drought Stresses Using Flux-Based Modeling and Analysis. <i>Plant Physiology</i> , 2013, 162, 2140-2150.	4.8	69
42	COFACTOR MODIFICATION ANALYSIS: A COMPUTATIONAL FRAMEWORK TO IDENTIFY COFACTOR SPECIFICITY ENGINEERING TARGETS FOR STRAIN IMPROVEMENT. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1343006.	0.8	16