

# Zhou Li

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

1,572  
citations

394421

19  
h-index

677142

22  
g-index

24  
all docs

24  
docs citations

24  
times ranked

2673  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic Comparison of Label-Free, Metabolic Labeling, and Isobaric Chemical Labeling for Quantitative Proteomics on LTQ Orbitrap Velos. <i>Journal of Proteome Research</i> , 2012, 11, 1582-1590.	3.7	301
2	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	13.3	170
3	Microbial metaproteomics for characterizing the range of metabolic functions and activities of human gut microbiota. <i>Proteomics</i> , 2015, 15, 3424-3438.	2.2	126
4	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	2.0	124
5	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. <i>Nature Ecology and Evolution</i> , 2018, 2, 499-509.	7.8	116
6	Nutrients drive transcriptional changes that maintain metabolic homeostasis but alter genome architecture in <i>Microcystis</i> . <i>ISME Journal</i> , 2014, 8, 2080-2092.	9.8	84
7	Phylogenetically conserved resource partitioning in the coastal microbial loop. <i>ISME Journal</i> , 2017, 11, 2781-2792.	9.8	82
8	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	3.5	66
9	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. <i>ISME Journal</i> , 2015, 9, 180-194.	9.8	57
10	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. <i>Nature Communications</i> , 2014, 5, 4405.	12.8	51
11	<sup>15</sup> N- and <sup>2</sup> H proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. <i>Environmental Microbiology</i> , 2014, 16, 3224-3237.	3.8	48
12	Microbial Community Structure-Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	3.5	48
13	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. <i>MSystems</i> , 2016, 1, .	3.8	43
14	Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungal-endobacterial system. <i>Environmental Microbiology</i> , 2017, 19, 1041-1053.	3.8	38
15	Phytoplankton exudates and lysates support distinct microbial consortia with specialized metabolic and ecophysiological traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	37
16	Sipros Ensemble improves database searching and filtering for complex metaproteomics. <i>Bioinformatics</i> , 2018, 34, 795-802.	4.1	35
17	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 563.	3.5	34
18	Sipros/ProRata: a versatile informatics system for quantitative community proteomics. <i>Bioinformatics</i> , 2013, 29, 2064-2065.	4.1	30

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19	Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2014, 13, 1359-1372.	3.7	24
20	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using <sup>13</sup> CO <sub>2</sub> and <sup>13</sup> C-Methanol. <i>Frontiers in Microbiology</i> , 2019, 10, 2706.	3.5	23
21	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. <i>Microbiome</i> , 2021, 9, 110.	11.1	17
22	Metagenome Sequencing of a Coastal Marine Microbial Community from Monterey Bay, California. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
23	Genome Sequences of 42 Bacteria Isolated from <i>Sorghum bicolor</i> Roots. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1