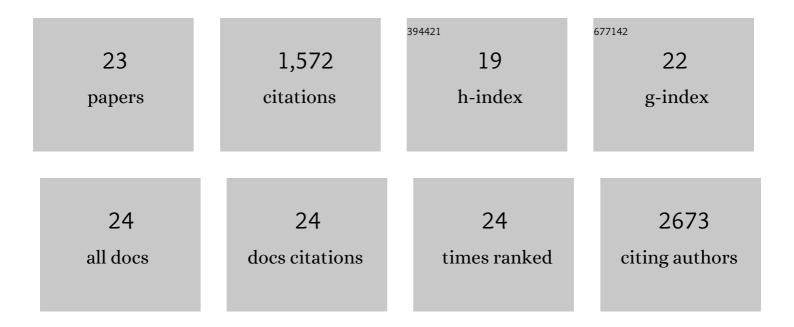
## Zhou Li

## List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. Microbiome, 2021, 9, 110.	11.1	17
2	Phytoplankton exudates and lysates support distinct microbial consortia with specialized metabolic and ecophysiological traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
3	Genome Sequences of 42 Bacteria Isolated from Sorghum bicolor Roots. Microbiology Resource Announcements, 2020, 9, .	0.6	1
4	Mediterranean grassland soil C–N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. Nature Microbiology, 2019, 4, 1356-1367.	13.3	170
5	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using 13CO2 and 13C-Methanol. Frontiers in Microbiology, 2019, 10, 2706.	3.5	23
6	Sipros Ensemble improves database searching and filtering for complex metaproteomics. Bioinformatics, 2018, 34, 795-802.	4.1	35
7	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. Nature Ecology and Evolution, 2018, 2, 499-509.	7.8	116
8	Microbial Community Structure–Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. Frontiers in Microbiology, 2018, 9, 1282.	3.5	48
9	Phylogenetically conserved resource partitioning in the coastal microbial loop. ISME Journal, 2017, 11, 2781-2792.	9.8	82
10	Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungalâ€endobacterial system. Environmental Microbiology, 2017, 19, 1041-1053.	3.8	38
11	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Frontiers in Microbiology, 2016, 7, 238.	3.5	66
12	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. Frontiers in Microbiology, 2016, 7, 563.	3.5	34
13	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. MSystems, 2016, 1, .	3.8	43
14	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. PeerJ, 2016, 4, e2687.	2.0	124
15	Metagenome Sequencing of a Coastal Marine Microbial Community from Monterey Bay, California. Genome Announcements, 2015, 3, .	0.8	6
16	Microbial metaproteomics for characterizing the range of metabolic functions and activities of human gut microbiota. Proteomics, 2015, 15, 3424-3438.	2.2	126
17	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. ISME Journal, 2015, 9, 180-194.	9.8	57
18	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. Nature Communications, 2014, 5, 4405.	12.8	51

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19	<sup>15</sup> <scp>N</scp> ―and <sup>2</sup> <scp>H</scp> proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. Environmental Microbiology, 2014, 16, 3224-3237.	3.8	48
20	Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in <i>Arabidopsis</i> . Journal of Proteome Research, 2014, 13, 1359-1372.	3.7	24
21	Nutrients drive transcriptional changes that maintain metabolic homeostasis but alter genome architecture in <i>Microcystis</i> . ISME Journal, 2014, 8, 2080-2092.	9.8	84
22	Sipros/ProRata: a versatile informatics system for quantitative community proteomics. Bioinformatics, 2013, 29, 2064-2065.	4.1	30
23	Systematic Comparison of Label-Free, Metabolic Labeling, and Isobaric Chemical Labeling for Quantitative Proteomics on LTQ Orbitrap Velos. Journal of Proteome Research, 2012, 11, 1582-1590.	3.7	301