Jinlyung Choi

List of Publications by Year
in descending order

15	521	933447 10	996975 15
papers	citations	h-index	g-index

18	18	18	1059
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A meta-analysis of global fungal distribution reveals climate-driven patterns. Nature Communications, 2019, 10, 5142.	12.8	232
2	Strategies to improve reference databases for soil microbiomes. ISME Journal, 2017, 11, 829-834.	9.8	106
3	Characterizing the soil microbiome and quantifying antibiotic resistance gene dynamics in agricultural soil following swine CAFO manure application. PLoS ONE, 2019, 14, e0220770.	2.5	42
4	Toward Antibiotic Stewardship: Route of Antibiotic Administration Impacts the Microbiota and Resistance Gene Diversity in Swine Feces. Frontiers in Veterinary Science, 2020, 7, 255.	2.2	26
5	The Impact of Stand Age and Fertilization on the Soil Microbiome of Miscanthus Ã— giganteus. Phytobiomes Journal, 2021, 5, 51-59.	2.7	22
6	Identification of Soil Microbes Capable of Utilizing Cellobiosan. PLoS ONE, 2016, 11, e0149336.	2.5	16
7	RefSoil+: a Reference Database for Genes and Traits of Soil Plasmids. MSystems, 2019, 4, .	3.8	16
8	Improved detection of mcyA genes and their phylogenetic origins in harmful algal blooms. Water Research, 2020, 176, 115730.	11.3	13
9	Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance. FEMS Microbiology Ecology, 2018, 94, .	2.7	12
10	Strategies for Building Computing Skills To Support Microbiome Analysis: a Five-Year Perspective from the EDAMAME Workshop. MSystems, 2019, 4, .	3.8	10
11	The LacI family protein GlyR3 co-regulates the celC operon and manB in Clostridium thermocellum. Biotechnology for Biofuels, 2017, 10, 163.	6.2	8
12	Diversity of Antibiotic Resistance genes and Transfer Elements-Quantitative Monitoring (DARTE-QM): a method for detection of antimicrobial resistance in environmental samples. Communications Biology, 2022, 5, 216.	4.4	7
13	Spatial Structuring of Cellulase Gene Abundance and Activity in Soil. Frontiers in Environmental Science, 2018, 6, .	3.3	4
14	MetaFunPrimer: an Environment-Specific, High-Throughput Primer Design Tool for Improved Quantification of Target Genes. MSystems, 2021, 6, e0020121.	3.8	2
15	Response of Total (DNA) and Metabolically Active (RNA) Microbial Communities in Miscanthus Ã— Giganteus Cultivated Soil to Different Nitrogen Fertilization Rates. Microbiology Spectrum, 2022, 10, e0211621.	3.0	2