

Tae Kwon Lee

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,952
citations

430874

18
h-index

254184

43
g-index

48
all docs

48
docs citations

48
times ranked

3331
citing authors

#	ARTICLE	IF	CITATIONS
1	Tracking heavy water (D ₂ O) incorporation for identifying and sorting active microbial cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E194-203.	7.1	359
2	Ecological Patterns of <i>nifH</i> Genes in Four Terrestrial Climatic Zones Explored with Targeted Metagenomics Using FrameBot, a New Informatics Tool. MBio, 2013, 4, e00592-13.	4.1	279
3	Giant viruses with an expanded complement of translation system components. Science, 2017, 356, 82-85.	12.6	234
4	Molecular approaches for the detection and monitoring of microbial communities in bioaerosols: A review. Journal of Environmental Sciences, 2017, 51, 234-247.	6.1	113
5	Association of Biodiversity with the Rates of Micropollutant Biotransformations among Full-Scale Wastewater Treatment Plant Communities. Applied and Environmental Microbiology, 2015, 81, 666-675.	3.1	98
6	Treatment of Alcohol Distillery Wastewater Using a Bacteroidetes-Dominant Thermophilic Microbial Fuel Cell. Environmental Science & Technology, 2012, 46, 3022-3030.	10.0	97
7	Metagenomic Analysis of Chicken Gut Microbiota for Improving Metabolism and Health of Chickens â€” A Review. Asian-Australasian Journal of Animal Sciences, 2015, 28, 1217-1225.	2.4	90
8	Discovery of commonly existing anode biofilm microbes in two different wastewater treatment MFCs using FLX Titanium pyrosequencing. Applied Microbiology and Biotechnology, 2010, 87, 2335-2343.	3.6	70
9	Increased nitrous oxide accumulation by bioelectrochemical denitrification under autotrophic conditions: Kinetics and expression of denitrification pathway genes. Water Research, 2013, 47, 7087-7097.	11.3	64
10	The functional and taxonomic richness of wastewater treatment plant microbial communities are associated with each other and with ambient nitrogen and carbon availability. Environmental Microbiology, 2015, 17, 4851-4860.	3.8	59
11	Accelerating the Biodegradation of High-Density Polyethylene (HDPE) Using <i>Bjerkandera adusta</i> TBB-03 and Lignocellulose Substrates. Microorganisms, 2019, 7, 304.	3.6	38
12	Novel Biphenyl-Oxidizing Bacteria and Dioxygenase Genes from a Korean Tidal Mudflat. Applied and Environmental Microbiology, 2011, 77, 3888-3891.	3.1	36
13	A framework for establishing predictive relationships between specific bacterial 16S rRNA sequence abundances and biotransformation rates. Water Research, 2015, 70, 471-484.	11.3	31
14	The capacity of wastewater treatment plants drives bacterial community structure and its assembly. Scientific Reports, 2019, 9, 14809.	3.3	30
15	Nutritional status regulates algicidal activity of <i>Aeromonas</i> sp. L23 against cyanobacteria and green algae. PLoS ONE, 2019, 14, e0213370.	2.5	29
16	Characterization of microbial community structure and population dynamics of tetrachloroethene-dechlorinating tidal mudflat communities. Biodegradation, 2011, 22, 687-698.	3.0	27
17	A novel decoy strategy for polymyxin resistance in <i>Acinetobacter baumannii</i> . ELife, 2021, 10, .	6.0	26
18	Removal of pharmaceuticals and personal care products using native fungal enzymes extracted during the ligninolytic process. Environmental Research, 2021, 195, 110878.	7.5	24

#	ARTICLE	IF	CITATIONS
19	Effect of Algal Inoculation on COD and Nitrogen Removal, and Indigenous Bacterial Dynamics in Municipal Wastewater. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 900-908.	2.1	24
20	Development and Characterization of PCE-to-Ethene Dechlorinating Microcosms with Contaminated River Sediment. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 120-129.	2.1	18
21	Microbial phenomics linking the phenotype to function: The potential of Raman spectroscopy. <i>Journal of Microbiology</i> , 2021, 59, 249-258.	2.8	17
22	Cancer and non-cancer risk associated with PM10-bound metals in subways. <i>Transportation Research, Part D: Transport and Environment</i> , 2020, 89, 102618.	6.8	15
23	In-Depth Characterization of Wastewater Bacterial Community in Response to Algal Growth Using Pyrosequencing. <i>Journal of Microbiology and Biotechnology</i> , 2013, 23, 1472-1477.	2.1	14
24	Metagenomic SMRT Sequencing-Based Exploration of Novel Lignocellulose-Degrading Capability in Wood Detritus from <i>Torreya nucifera</i> in Bija Forest on Jeju Island. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 1670-1680.	2.1	14
25	Characterization of a <i>nifH</i> -Harboring Bacterial Community in the Soil-Limited Gotjawal Forest. <i>Frontiers in Microbiology</i> , 2019, 10, 1858.	3.5	13
26	Bacillus-Dominant Airborne Bacterial Communities Identified During Asian Dust Events. <i>Microbial Ecology</i> , 2019, 78, 677-687.	2.8	13
27	Transcriptional Response and Plant Growth Promoting Activity of <i>Pseudomonas fluorescens</i> DR397 under Drought Stress Conditions. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	13
28	Improved detection of microbial risk of releasing genetically modified bacteria in soil by using massive sequencing and antibiotic resistance selection. <i>Journal of Hazardous Materials</i> , 2012, 227-228, 172-178.	12.4	11
29	Commuters health risk associated with particulate matter exposures in subway system “ Globally. <i>Building and Environment</i> , 2022, 216, 109036.	6.9	11
30	Regional effects on chimera formation in 454 pyrosequenced amplicons from a mock community. <i>Journal of Microbiology</i> , 2014, 52, 566-573.	2.8	10
31	Degradation of crude oil in a contaminated tidal flat area and the resilience of bacterial community. <i>Marine Pollution Bulletin</i> , 2017, 114, 296-301.	5.0	10
32	Pollution level and reusability of the waste soil generated from demolition of a rural railway. <i>Environmental Pollution</i> , 2018, 240, 867-874.	7.5	9
33	Unveiling of Concealed Processes for the Degradation of Pharmaceutical Compounds by <i>Neopetalotriopsis</i> sp.. <i>Microorganisms</i> , 2019, 7, 264.	3.6	7
34	Role of Algal Community Stability in Harmful Algal Blooms in River-Connected Lakes. <i>Microbial Ecology</i> , 2021, 82, 309-318.	2.8	7
35	Raman-Deuterium Isotope Probing and Metagenomics Reveal the Drought Tolerance of the Soil Microbiome and Its Promotion of Plant Growth. <i>MSystems</i> , 2022, 7, e0124921.	3.8	7
36	Shifts in benthic bacterial communities associated with farming stages and a microbiological proxy for assessing sulfidic sediment conditions at fish farms. <i>Marine Pollution Bulletin</i> , 2022, 178, 113603.	5.0	7

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37	Raman spectroscopy reveals alteration of spore compositions under different nutritional conditions in <i>Lysinibacillus boronitolerans</i> YS11. <i>Journal of Microbiology</i> , 2021, 59, 491-499.	2.8	6
38	Enhanced deflocculation of dehydrated sludge by rhamnolipid treatment coupled with thermal hydrolysis. <i>Waste Management</i> , 2020, 110, 66-73.	7.4	5
39	The effect of engineered PLGA nanoparticles on nitrifying bacteria in the soil environment. <i>Journal of Industrial and Engineering Chemistry</i> , 2020, 84, 297-304.	5.8	5
40	Short-term Effects of Great Cormorant Droppings on Water Quality and Microbial Community of an Artificial Agricultural Reservoir. <i>Journal of Environmental Quality</i> , 2017, 46, 470-476.	2.0	4
41	Short-Term Legacy Effects of Mercury Contamination on Plant Growth and nifH-Harboring Microbial Community in Rice Paddy Soil. <i>Microbial Ecology</i> , 2021, 82, 932-941.	2.8	4
42	A comparison study of the potential risks induced in arable land and forest soils by carcass-derived pollutants. <i>Environmental Geochemistry and Health</i> , 2018, 40, 451-460.	3.4	2
43	Water quality drives the regional patterns of an algal metacommunity in interconnected lakes. <i>Scientific Reports</i> , 2021, 11, 13601.	3.3	1
44	Flow cytometric monitoring of the bacterial phenotypic diversity in aquatic ecosystems. <i>Journal of Microbiology</i> , 2021, 59, 879-885.	2.8	1
45	Bacterial Resuscitation from Starvation-Induced Dormancy Results in Phenotypic Diversity Coupled with Translational Activity Depending on Carbon Substrate Availability. <i>Microbial Ecology</i> , 0, , .	2.8	0