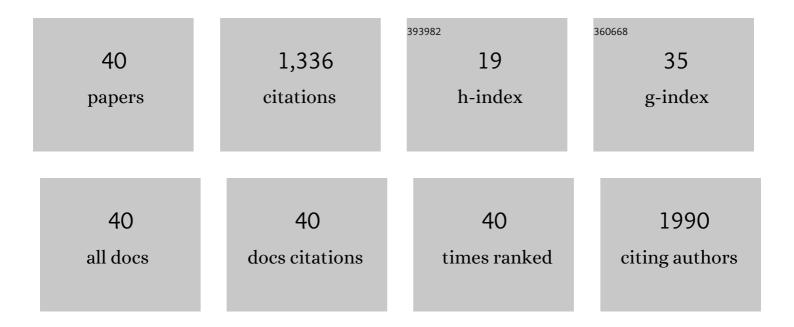
Jaejoon Jung

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Nonlabens ponticola sp. nov., isolated from seawater and reclassification of Nonlabens sediminis as a later heterotypic synonym of Nonlabens tegetincola. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	12
2	Mesorhizobium microcysteis sp. nov., isolated from a culture of Microcystis aeruginosa. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
3	Flavihumibacter soli sp. nov., Isolated from Soil. Current Microbiology, 2020, 77, 3179-3184.	1.0	7
4	Identification and characterization of a marine-derived chitinolytic fungus, Acremonium sp. YS2-2. Journal of Microbiology, 2019, 57, 372-380.	1.3	24
5	Tamlana carrageenivorans sp. nov., a carrageenan-degrading bacterium isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1355-1360.	0.8	12
6	Complete Genome Sequence of <i>Marinobacterium aestuarii</i> ST58-10 ^T , a Benzene-Degrading Bacterium Isolated from Estuarine Sediment. Microbiology Resource Announcements, 2018, 7, .	0.3	9
7	Marinobacterium aestuarii sp. nov., a benzene-degrading marine bacterium isolated from estuary sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 651-656.	0.8	22
8	Metabolic and stress responses of <i>Acinetobacter oleivorans </i> <scp>DR</scp> 1 during long hain alkane degradation. Microbial Biotechnology, 2017, 10, 1809-1823.	2.0	34
9	Role of Glyoxylate Shunt in Oxidative Stress Response. Journal of Biological Chemistry, 2016, 291, 11928-11938.	1.6	184
10	Metagenomic and functional analyses of the consequences of reduction of bacterial diversity on soil functions and bioremediation in diesel-contaminated microcosms. Scientific Reports, 2016, 6, 23012.	1.6	103
11	High Concentration of Red Clay as an Alternative for Antibiotics in Aquaculture. Journal of Microbiology and Biotechnology, 2016, 26, 130-138.	0.9	4
12	Calcium Carbonate Precipitation by Bacillus and Sporosarcina Strains Isolated from Concrete and Analysis of the Bacterial Community of Concrete. Journal of Microbiology and Biotechnology, 2016, 26, 540-548.	0.9	56
13	Acinetobacter species as model microorganisms in environmental microbiology: current state and perspectives. Applied Microbiology and Biotechnology, 2015, 99, 2533-2548.	1.7	158
14	Molecular Mechanisms of Enhanced Bacterial Growth on Hexadecane with Red Clay. Microbial Ecology, 2015, 70, 912-921.	1.4	14
15	Plasmid-Encoded Tetracycline Efflux Pump Protein Alters Bacterial Stress Responses and Ecological Fitness of Acinetobacter oleivorans. PLoS ONE, 2014, 9, e107716.	1.1	22
16	Pyrosequencing-based analysis of bacterial community and metabolites profiles in Korean traditional seafood fermentation: a flatfish-fermented seafood. Bioscience, Biotechnology and Biochemistry, 2014, 78, 908-910.	0.6	10
17	Comparative genomic and transcriptomic analyses of NaCl-tolerant Staphylococcus sp. OJ82 isolated from fermented seafood. Applied Microbiology and Biotechnology, 2014, 98, 807-822.	1.7	21
18	Effect of Red Clay on Diesel Bioremediation and Soil Bacterial Community. Microbial Ecology, 2014, 68, 314-323.	1.4	17

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19	Gut Microbiota of Tenebrio molitor and Their Response to Environmental Change. Journal of Microbiology and Biotechnology, 2014, 24, 888-897.	0.9	49
20	Biochemical Characterization of L-Asparaginase in NaCl-Tolerant Staphylococcus sp. OJ82 Isolated from Fermented Seafood. Journal of Microbiology and Biotechnology, 2014, 24, 1096-1104.	0.9	29
21	Primers for amplification of nitrous oxide reductase genes associated with Firmicutes and Bacteroidetes in organic-compound-rich soils. Microbiology (United Kingdom), 2013, 159, 307-315.	0.7	24
22	The effect of toxic malachite green on the bacterial community in Antarctic soil and the physiology of malachite green-degrading Pseudomonas sp. MGO. Applied Microbiology and Biotechnology, 2013, 97, 4511-4521.	1.7	8
23	Comparative Genomic and Transcriptomic Analyses Reveal Habitat Differentiation and Different Transcriptional Responses during Pectin Metabolism in Alishewanella Species. Applied and Environmental Microbiology, 2013, 79, 6351-6361.	1.4	11
24	Short-Term Effect of Elevated Temperature on the Abundance and Diversity of Bacterial and Archaeal amoA Genes in Antarctic Soils. Journal of Microbiology and Biotechnology, 2013, 23, 1187-1196.	0.9	21
25	Pyrosequencing-Based Analysis of the Bacterial Community in Korean Traditional Seafood, Ojingeo Jeotgal. Journal of Microbiology and Biotechnology, 2013, 23, 1428-1433.	0.9	17
26	Genome Sequence of Extracellular-Protease-Producing Alishewanella jeotgali Isolated from Traditional Korean Fermented Seafood. Journal of Bacteriology, 2012, 194, 2097-2097.	1.0	15
27	Genome Sequence of Pectin-Degrading Alishewanella aestuarii Strain B11 ^T , Isolated from Tidal Flat Sediment. Journal of Bacteriology, 2012, 194, 5476-5476.	1.0	12
28	Genome Sequence of Pectin-Degrading Alishewanella agri, Isolated from Landfill Soil. Journal of Bacteriology, 2012, 194, 5135-5136.	1.0	11
29	Complexity of cell–cell interactions between Pseudomonas sp. AS1 and Acinetobacter oleivorans DR1: metabolic commensalism, biofilm formation and quorum quenching. Research in Microbiology, 2012, 163, 173-181.	1.0	18
30	Pedobacter jeongneungensis sp. nov., isolated from forest soil. Journal of Microbiology, 2012, 50, 660-664.	1.3	11
31	Effects of nutritional input and diesel contamination on soil enzyme activities and microbial communities in antarctic soils. Journal of Microbiology, 2012, 50, 916-924.	1.3	21
32	Seasonal changes in nitrogen-cycle gene abundances and in bacterial communities in acidic forest soils. Journal of Microbiology, 2012, 50, 365-373.	1.3	39
33	Detection of genetically modified microorganisms in soil using the most-probable-number method with multiplex PCR and DNA dot blot. Research in Microbiology, 2011, 162, 807-816.	1.0	2
34	Change in gene abundance in the nitrogen biogeochemical cycle with temperature and nitrogen addition in Antarctic soils. Research in Microbiology, 2011, 162, 1018-1026.	1.0	124
35	Acinetobacter oleivorans sp. nov. Is capable of adhering to and growing on diesel-oil. Journal of Microbiology, 2011, 49, 29-34.	1.3	64
36	Physiological and metabolic responses for hexadecane degradation in Acinetobacter oleivorans DR1. Journal of Microbiology, 2011, 49, 208-215.	1.3	27

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37	Comparative Genomic Analysis of Acinetobacter oleivorans DR1 To Determine Strain-Specific Genomic Regions and Gentisate Biodegradation. Applied and Environmental Microbiology, 2011, 77, 7418-7424.	1.4	27
38	Phenotypic and physiological alterations by heterologous acylhomoserine lactone synthase expression in Pseudomonas putida. Microbiology (United Kingdom), 2010, 156, 3762-3772.	0.7	13
39	Complete Genome Sequence of the Diesel-Degrading <i>Acinetobacter</i> sp. Strain DR1. Journal of Bacteriology, 2010, 192, 4794-4795.	1.0	62
40	Inhibitory Effect of Aged Petroleum Hydrocarbons on the Survival of Inoculated Microorganism in a Crude-Oil-Contaminated Site. Journal of Microbiology and Biotechnology, 2009, 19, 1672-1678.	0.9	14