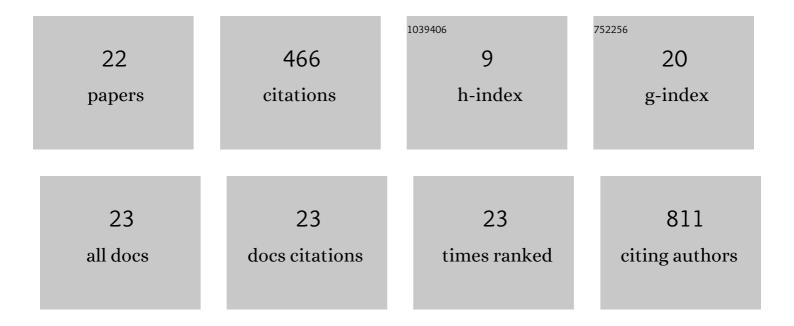
Se-Ran Jun

List of Publications by Year in descending order

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Version: 2024-02-01



SE-DAN LUN

#	Article	IF	CITATIONS
1	Whole-proteome phylogeny of prokaryotes by feature frequency profiles: An alignment-free method with optimal feature resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 133-138.	3.3	138
2	Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. Emerging Infectious Diseases, 2018, 24, 1758-1761.	2.0	75
3	Sulforaphane prevents ageâ€associated cardiac and muscular dysfunction through Nrf2 signaling. Aging Cell, 2020, 19, e13261.	3.0	64
4	Quality scores for 32,000 genomes. Standards in Genomic Sciences, 2014, 9, 20.	1.5	36
5	Sample storage conditions induce post-collection biases in microbiome profiles. BMC Microbiology, 2018, 18, 227.	1.3	23
6	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. BMC Bioinformatics, 2017, 18, 471.	1.2	20
7	Multi-Omic Analysis Reveals Different Effects of Sulforaphane on the Microbiome and Metabolome in Old Compared to Young Mice. Microorganisms, 2020, 8, 1500.	1.6	14
8	Effects of Housing Types on Cecal Microbiota of Two Different Strains of Laying Hens During the Late Production Phase. Frontiers in Veterinary Science, 2020, 7, 331.	0.9	12
9	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. Infection, Genetics and Evolution, 2019, 75, 103965.	1.0	11
10	KITSUNE: A Tool for Identifying Empirically Optimal K-mer Length for Alignment-Free Phylogenomic Analysis. Frontiers in Bioengineering and Biotechnology, 2020, 8, 556413.	2.0	11
11	Two Cases of Vancomycin-Resistant Enterococcus faecium Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. Open Forum Infectious Diseases, 2020, 7, ofaa180.	0.4	11
12	Isolation of AmpC- and extended spectrum β-lactamase-producing Enterobacterales from fresh vegetables in the United States. Food Control, 2022, 132, 108559.	2.8	11
13	Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 Outbreak in Arkansas, USA. Genome Announcements, 2017, 5, .	0.8	6
14	Genome-Based Comparison of Clostridioides difficile: Average Amino Acid Identity Analysis of Core Genomes. Microbial Ecology, 2018, 76, 801-813.	1.4	6
15	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant Enterococcus faecium with the <i>vanA</i> Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. Microbiology Resource Announcements, 2020, 9, .	0.3	6
16	Assessment of genome annotation using gene function similarity within the gene neighborhood. BMC Bioinformatics, 2017, 18, 345.	1.2	5
17	Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of <i>Hepatovirus</i> species. MicrobiologyOpen, 2020, 9, e973.	1.2	5
18	Cefiderocol heteroresistance in Klebsiella pneumoniae is linked to mutations in the siderophore receptor cirA and Î ² -lactamase activities. International Journal of Antimicrobial Agents, 2022, 60, 106635.	1.1	5

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#	Article	IF	CITATIONS
19	Draft Genome Sequences of 48 Vancomycin-Resistant Enterococcus faecium Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. Microbiology Resource Announcements, 2019, 8, .	0.3	3
20	Isolation and characterisation of carbapenemase-producing and polymyxin B-resistant Enterobacter bugandensis from a vegetable. Journal of Global Antimicrobial Resistance, 2021, 26, 264-265.	0.9	3
21	Plasma Metabolomics in a Nonhuman Primate Model of Abdominal Radiation Exposure. Metabolites, 2021, 11, 540.	1.3	0
22	869. Outbreak of Vancomycin Resistant Enterococcus faecium (VREfm) in a Hematology Unit Identified Through Whole Genome Sequencing. Open Forum Infectious Diseases, 2020, 7, S472-S474.	0.4	0