

Sung-Min Ha

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

5,910
citations

8
h-index

20
g-index

20
ext. papers

8,528
ext. citations

4.6
avg, IF

6.18
L-index

#	Paper	IF	Citations
20	Genome insights into the pharmaceutical and plant growth promoting features of the novel species <i>Nocardia alni</i> sp. nov.. <i>BMC Genomics</i> , 2022 , 23, 70	4.5	4
19	Reliability of Genetic Alterations in Predicting Ceftriaxone Resistance in <i>Neisseria gonorrhoeae</i> Globally.. <i>Microbiology Spectrum</i> , 2022 , e0206521	8.9	0
18	PharmOmics: A species- and tissue-specific drug signature database and gene-network-based drug repositioning tool.. <i>IScience</i> , 2022 , 25, 104052	6.1	0
17	A Novel Species of the Genus Isolated From Human Blood Using Whole-Genome Sequencing. <i>Annals of Laboratory Medicine</i> , 2021 , 41, 323-327	3.1	0
16	Mergeomics 2.0: a web server for multi-omics data integration to elucidate disease networks and predict therapeutics. <i>Nucleic Acids Research</i> , 2021 , 49, W375-W387	20.1	4
15	Using a public database of <i>Neisseria gonorrhoeae</i> genomes to detect mutations associated with zoliflodacin resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 2847-2849	5.1	2
14	Isolation of a novel species in the genus <i>Cupriavidus</i> from a patient with sepsis using whole genome sequencing. <i>PLoS ONE</i> , 2020 , 15, e0232850	3.7	3
13	Improved Metagenomic Taxonomic Profiling Using a Curated Core Gene-Based Bacterial Database Reveals Unrecognized Species in the Genus. <i>Pathogens</i> , 2020 , 9,	4.5	3
12	Genome-based reclassification of <i>Aguilera</i> . 2001 as a later heterotypic synonym of (<i>Prazmowski</i> 1880) <i>Ash</i> . 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 3134-3138	2.2	3
11	Comparative Genomic Analysis of the 2016 Outbreak in South Korea. <i>Frontiers in Public Health</i> , 2019 , 7, 228	6	6
10	Genomic characterization of <i>Nocardia seriolae</i> strains isolated from diseased fish. <i>MicrobiologyOpen</i> , 2019 , 8, e00656	3.4	18
9	Application of the Whole Genome-Based Bacterial Identification System, TrueBac ID, Using Clinical Isolates That Were Not Identified With Three Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) Systems. <i>Annals of Laboratory Medicine</i> , 2019 , 39, 530-536	3.1	47
8	VCGIDB: A Database and Web Resource for the Genomic Islands from. <i>Pathogens</i> , 2019 , 8,	4.5	4
7	UBCG: Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. <i>Journal of Microbiology</i> , 2018 , 56, 280-285	3	505
6	Genome sequence of <i>Mycobacterium yongonense</i> RT 955-2015 isolate from a patient misdiagnosed with multidrug-resistant tuberculosis: First clinical detection in Tanzania. <i>International Journal of Infectious Diseases</i> , 2018 , 71, 82-88	10.5	3
5	A large-scale evaluation of algorithms to calculate average nucleotide identity. <i>Antonie Van Leeuwenhoek</i> , 2017 , 110, 1281-1286	2.1	1296
4	Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 1613-1617	2.2	3649

3	ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 2053-2057	2.2	200
2	Metagenomic insights into the bioaerosols in the indoor and outdoor environments of childcare facilities. <i>PLoS ONE</i> , 2015 , 10, e0126960	3.7	54
1	EzEditor: a versatile sequence alignment editor for both rRNA- and protein-coding genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014 , 64, 689-691	2.2	109