

Srijak Bhatnagar

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

3,327
citations

687220

13
h-index

839398

18
g-index

21
all docs

21
docs citations

21
times ranked

4802
citing authors

#	ARTICLE	IF	CITATIONS
1	Longitudinal SARS-CoV-2 RNA wastewater monitoring across a range of scales correlates with total and regional COVID-19 burden in a well-defined urban population. <i>Water Research</i> , 2022, 220, 118611.	5.3	34
2	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , 2021, 6, 885-898.	5.9	29
3	A multicenter study investigating SARS-CoV-2 in tertiary-care hospital wastewater. viral burden correlates with increasing hospitalized cases as well as hospital-associated transmissions and outbreaks. <i>Water Research</i> , 2021, 201, 117369.	5.3	64
4	CANT-HYD: A Curated Database of Phylogeny-Derived Hidden Markov Models for Annotation of Marker Genes Involved in Hydrocarbon Degradation. <i>Frontiers in Microbiology</i> , 2021, 12, 764058.	1.5	21
5	Microbial community dynamics and coexistence in a sulfide-driven phototrophic bloom. <i>Environmental Microbiomes</i> , 2020, 15, 3.	2.2	16
6	Fecal Microbial Communities in a Large Representative Cohort of California Dairy Cows. <i>Frontiers in Microbiology</i> , 2019, 10, 1093.	1.5	60
7	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018, 16, e2006352.	2.6	236
8	Transient exposure to oxygen or nitrate reveals ecophysiology of fermentative and sulfate-reducing benthic microbial populations. <i>Environmental Microbiology</i> , 2017, 19, 4866-4881.	1.8	26
9	Draft Genome Sequence of <i>Agrobacterium tumefaciens</i> Biovar 1 Strain 186, Isolated from Walnut. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
10	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain MR_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
11	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain CCM_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
12	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium <i>Thermodesulfobacterium yellowstonii</i> Strain DSM 11347 (Phylum <i>Nitrospirae</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	17
13	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, <i>Thermodesulfobacterium commune</i> DSM 2178 T (Phylum <i>Thermodesulfobacteria</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
14	Structure, variation, and assembly of the root-associated microbiomes of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E911-20.	3.3	2,016
15	Environmental Determinants of Transformation Efficiency in <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 2014, 196, 337-344.	1.0	14
16	The Impact of <i>Helicobacter pylori</i> Infection on the Gastric Microbiota of the Rhesus Macaque. <i>PLoS ONE</i> , 2013, 8, e76375.	1.1	46
17	Bacterial Communities of Diverse <i>Drosophila</i> Species: Ecological Context of a Host-Microbe Model System. <i>PLoS Genetics</i> , 2011, 7, e1002272.	1.5	650
18	Unsupervised statistical clustering of environmental shotgun sequences. <i>BMC Bioinformatics</i> , 2009, 10, 316.	1.2	84