

# Srijak Bhatnagar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7295606/publications.pdf>

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