

Alexander Crits-Christoph

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,232
citations

331259

21
h-index

525886

27
g-index

30
all docs

30
docs citations

30
times ranked

4257
citing authors

#	ARTICLE	IF	CITATIONS
1	Priority effects in microbiome assembly. <i>Nature Reviews Microbiology</i> , 2022, 20, 109-121.	13.6	180
2	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs). <i>ISME Journal</i> , 2022, 16, 1348-1362.	4.4	17
3	Species- and site-specific genome editing in complex bacterial communities. <i>Nature Microbiology</i> , 2022, 7, 34-47.	5.9	127
4	Good microbes, bad genes? The dissemination of antimicrobial resistance in the human microbiome. <i>Gut Microbes</i> , 2022, 14, 2055944.	4.3	50
5	Interactions of Non-Nutritive Artificial Sweeteners with the Microbiome in Metabolic Syndrome. <i>Immunometabolism</i> , 2022, 4, .	0.7	6
6	Sewage, Salt, Silica, and SARS-CoV-2 (4S): An Economical Kit-Free Method for Direct Capture of SARS-CoV-2 RNA from Wastewater. <i>Environmental Science & Technology</i> , 2021, 55, 4880-4888.	4.6	72
7	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. <i>Microbiome</i> , 2021, 9, 121.	4.9	11
8	Tools for interpretation of wastewater SARS-CoV-2 temporal and spatial trends demonstrated with data collected in the San Francisco Bay Area. <i>Water Research X</i> , 2021, 12, 100111.	2.8	67
9	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. <i>Cell Reports Medicine</i> , 2021, 2, 100393.	3.3	39
10	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
11	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. <i>Nature Biotechnology</i> , 2021, 39, 727-736.	9.4	238
12	Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. <i>MBio</i> , 2021, 12, .	1.8	284
13	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2021, 31, 239-250.	2.4	24
14	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
15	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	1.7	135
16	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. <i>MBio</i> , 2020, 11, .	1.8	116
17	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. <i>ISME Journal</i> , 2020, 14, 1834-1846.	4.4	43
18	High proportions of bacteria and archaea across most biomes remain uncultured. <i>ISME Journal</i> , 2019, 13, 3126-3130.	4.4	264

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19	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
20	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using ¹³ C ₂ O ₂ and ¹³ C-Methanol. <i>Frontiers in Microbiology</i> , 2019, 10, 2706.	1.5	23
21	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. <i>Science Advances</i> , 2019, 5, eaax5727.	4.7	120
22	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. <i>Nature</i> , 2018, 558, 440-444.	13.7	321
23	Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 301.	1.5	60
24	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016, 18, 2064-2077.	1.8	107
25	Microbial diversity and the presence of algae in halite endolithic communities are correlated to atmospheric moisture in the hyper-arid zone of the Atacama Desert. <i>Environmental Microbiology</i> , 2015, 17, 299-315.	1.8	108
26	Colonization patterns of soil microbial communities in the Atacama Desert. <i>Microbiome</i> , 2013, 1, 28.	4.9	215