

Adam R Rivers

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

14,803
citations

516215

16
h-index

454577

30
g-index

35
all docs

35
docs citations

35
times ranked

18451
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Journal of Insect Science, 2022, 22, .	0.6	0
2	GuideMaker: Software to design CRISPR-Cas guide RNA pools in non-model genomes. GigaScience, 2022, 11, .	3.3	7
3	Intrinsic variation in the vertically transmitted core virome of the mosquito <i>Aedes aegypti</i> . Molecular Ecology, 2022, 31, 2545-2561.	2.0	18
4	Rice Plant-Soil Microbiome Interactions Driven by Root and Shoot Biomass. Diversity, 2021, 13, 125.	0.7	4
5	Changes in rhizosphere soil microbial communities across plant developmental stages of high and low methane emitting rice genotypes. Soil Biology and Biochemistry, 2021, 156, 108233.	4.2	14
6	AT Homopolymer Strings in Salmonella enterica Subspecies I Contribute to Speciation and Serovar Diversity. Microorganisms, 2021, 9, 2075.	1.6	1
7	Advancing Equity and Inclusion in Microbiome Research and Training. MSystems, 2021, 6, e0115121.	1.7	9
8	Under-the-Radar Dengue Virus Infections in Natural Populations of Aedes aegypti Mosquitoes. MSphere, 2020, 5, .	1.3	19
9	AI Down on the Farm. IT Professional, 2020, 22, 22-26.	1.4	6
10	Harnessing AI to Transform Agriculture and Inform Agricultural Research. IT Professional, 2020, 22, 16-21.	1.4	11
11	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
12	Nine new RNA viruses associated with the fire ant Solenopsis invicta from its native range. Virus Genes, 2019, 55, 368-380.	0.7	22
13	ITSxpress: Software to rapidly trim internally transcribed spacer sequences with quality scores for marker gene analysis. F1000Research, 2018, 7, 1418.	0.8	155
14	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
15	Patterns and drivers of fungal community depth stratification in Sphagnum peat. FEMS Microbiology Ecology, 2017, 93, .	1.3	28
16	Experimental Identification of Small Non-Coding RNAs in the Model Marine Bacterium Ruegeria pomeroyi DSS-3. Frontiers in Microbiology, 2016, 7, 380.	1.5	14
17	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	6.5	177
18	Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral Acropora palmata. PLoS ONE, 2015, 10, e0143790.	1.1	20

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19	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. <i>ISME Journal</i> , 2015, 9, 1141-1151.	4.4	20
20	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. <i>Environmental Microbiology</i> , 2015, 17, 3466-3480.	1.8	55
21	An Updated genome annotation for the model marine bacterium <i>Ruegeria pomeroyi</i> DSS-3. <i>Standards in Genomic Sciences</i> , 2014, 9, 11.	1.5	20
22	An online calculator for marine phytoplankton iron culturing experiments. <i>Journal of Phycology</i> , 2013, 49, 1017-1021.	1.0	1
23	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2013, 7, 2315-2329.	4.4	172
24	Sizing up metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 237-243.	4.4	298
25	A molecular and physiological survey of a diverse collection of hydrothermal vent <i>Thermococcus</i> and <i>Pyrococcus</i> isolates. <i>Extremophiles</i> , 2009, 13, 905-915.	0.9	32
26	Iron stress genes in marine <i>Synechococcus</i> and the development of a flow cytometric iron stress assay. <i>Environmental Microbiology</i> , 2009, 11, 382-396.	1.8	40
27	Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. <i>Conservation Biology</i> , 2005, 19, 171-181.	2.4	40