

Adam R Rivers

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

14,803
citations

516710

16
h-index

454955

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, .	1.5	0
2	GuideMaker: Software to design CRISPR-Cas guide RNA pools in non-model genomes. GigaScience, 2022, 11, .	6.4	7
3	Intrinsic variation in the vertically transmitted core virome of the mosquito <i>Aedes aegypti</i> . Molecular Ecology, 2022, 31, 2545-2561.	3.9	18
4	Rice Plant–Soil Microbiome Interactions Driven by Root and Shoot Biomass. Diversity, 2021, 13, 125.	1.7	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.	8.8	14
6	AT Homopolymer Strings in Salmonella enterica Subspecies I Contribute to Speciation and Serovar Diversity. Microorganisms, 2021, 9, 2075.	3.6	1
7	Advancing Equity and Inclusion in Microbiome Research and Training. MSystems, 2021, 6, e0115121.	3.8	9
8	Under-the-Radar Dengue Virus Infections in Natural Populations of Aedes aegypti Mosquitoes. MSphere, 2020, 5, .	2.9	19
9	AI Down on the Farm. IT Professional, 2020, 22, 22-26.	1.5	6
10	Harnessing AI to Transform Agriculture and Inform Agricultural Research. IT Professional, 2020, 22, 16-21.	1.5	11
11	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
12	Nine new RNA viruses associated with the fire ant Solenopsis invicta from its native range. Virus Genes, 2019, 55, 368-380.	1.6	22
13	ITSxpress: Software to rapidly trim internally transcribed spacer sequences with quality scores for marker gene analysis. F1000Research, 2018, 7, 1418.	1.6	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.	17.5	1,512
15	Patterns and drivers of fungal community depth stratification in Sphagnum peat. FEMS Microbiology Ecology, 2017, 93, .	2.7	28
16	Experimental Identification of Small Non-Coding RNAs in the Model Marine Bacterium Ruegeria pomeroyi DSS-3. Frontiers in Microbiology, 2016, 7, 380.	3.5	14
17	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	14.5	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.	2.5	20

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19	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. ISME Journal, 2015, 9, 1141-1151.	9.8	20
20	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. Environmental Microbiology, 2015, 17, 3466-3480.	3.8	55
21	An Updated genome annotation for the model marine bacterium Ruegeria pomeroyi DSS-3. Standards in Genomic Sciences, 2014, 9, 11.	1.5	20
22	An online calculator for marine phytoplankton iron culturing experiments. Journal of Phycology, 2013, 49, 1017-1021.	2.3	1
23	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. ISME Journal, 2013, 7, 2315-2329.	9.8	172
24	Sizing up metatranscriptomics. ISME Journal, 2013, 7, 237-243.	9.8	298
25	A molecular and physiological survey of a diverse collection of hydrothermal vent Thermococcus and Pyrococcus isolates. Extremophiles, 2009, 13, 905-915.	2.3	32
26	Iron stress genes in marine <i>Synechococcus</i> and the development of a flow cytometric iron stress assay. Environmental Microbiology, 2009, 11, 382-396.	3.8	40
27	Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181.	4.7	40