Adam R Rivers

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

27	5,817	15	35
papers	citations	h-index	g-index
35 ext. papers	10,667 ext. citations	8.7 avg, IF	4.36 L-index

#	Paper	IF	Citations
27	AT Homopolymer Strings in Subspecies I Contribute to Speciation and Serovar Diversity. <i>Microorganisms</i> , 2021 , 9,	4.9	1
26	Advancing Equity and Inclusion in Microbiome Research and Training. MSystems, 2021, 6, e0115121	7.6	1
25	Rice PlantBoil Microbiome Interactions Driven by Root and Shoot Biomass. <i>Diversity</i> , 2021 , 13, 125	2.5	O
24	Changes in rhizosphere soil microbial communities across plant developmental stages of high and low methane emitting rice genotypes. <i>Soil Biology and Biochemistry</i> , 2021 , 156, 108233	7.5	4
23	Under-the-Radar Dengue Virus Infections in Natural Populations of Aedes aegypti Mosquitoes. <i>MSphere</i> , 2020 , 5,	5	9
22	Al Down on the Farm. IT Professional, 2020, 22, 22-26	1.9	4
21	Harnessing AI to Transform Agriculture and Inform Agricultural Research. IT Professional, 2020, 22, 16-2	1 1.9	5
20	Nine new RNA viruses associated with the fire ant Solenopsis invicta from its native range. <i>Virus Genes</i> , 2019 , 55, 368-380	2.3	7
19	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
18	ITSxpress: Software to rapidly trim internally transcribed spacer sequences with quality scores for marker gene analysis. <i>F1000Research</i> , 2018 , 7, 1418	3.6	65
17	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018,		78
16	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
15	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
14	Patterns and drivers of fungal community depth stratification in Sphagnum peat. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	20
13	Experimental Identification of Small Non-Coding RNAs in the Model Marine Bacterium Ruegeria pomeroyi DSS-3. <i>Frontiers in Microbiology</i> , 2016 , 7, 380	5.7	9
12	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. <i>ISME Journal</i> , 2015 , 9, 1141-51	11.9	11
11	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. <i>Environmental Microbiology</i> , 2015 , 17, 3466-80	5.2	23

LIST OF PUBLICATIONS

An Olpdated genome annotation for the model marine bacterium Ruegeria pomeroyi DSS-3. Standards in Genomic Sciences, 2014, 9, 11 An online calculator for marine phytoplankton iron culturing experiments. Journal of Phycology, 2013, 49, 1017-21 Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. ISME Journal, 2013, 7, 2315-29 Sizing up metatranscriptomics. ISME Journal, 2013, 7, 237-43 11.9 209 A molecular and physiological survey of a diverse collection of hydrothermal vent Thermococcus and Pyrococcus isolates. Extremophiles, 2009, 13, 905-15 Ilron stress genes in marine Synechococcus and the development of a flow cytometric iron stress assay. Environmental Microbiology, 2009, 11, 382-96 Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 138	10	Spatial Homogeneity of Bacterial Communities Associated with the Surface Mucus Layer of the Reef-Building Coral Acropora palmata. <i>PLoS ONE</i> , 2015 , 10, e0143790	3.7	11
Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. ISME Journal, 2013, 7, 2315-29 11.9 118 Sizing up metatranscriptomics. ISME Journal, 2013, 7, 237-43 11.9 209 A molecular and physiological survey of a diverse collection of hydrothermal vent Thermococcus and Pyrococcus isolates. Extremophiles, 2009, 13, 905-15 Iron stress genes in marine Synechococcus and the development of a flow cytometric iron stress assay. Environmental Microbiology, 2009, 11, 382-96 Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 3 36	9			11
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A molecular and physiological survey of a diverse collection of hydrothermal vent Thermococcus and Pyrococcus isolates. Extremophiles, 2009, 13, 905-15 Iron stress genes in marine Synechococcus and the development of a flow cytometric iron stress assay. Environmental Microbiology, 2009, 11, 382-96 Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181 2 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 3 25 26 37	7		11.9	118
lron stress genes in marine Synechococcus and the development of a flow cytometric iron stress assay. Environmental Microbiology, 2009, 11, 382-96 Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 3 25 25 27 28 4 25 4 27 29 2009, 11, 382-96 5-2 33 6 37 2019 2	6	Sizing up metatranscriptomics. <i>ISME Journal</i> , 2013 , 7, 237-43	11.9	209
assay. Environmental Microbiology, 2009, 11, 382-96 Individual- and Assemblage-Level Effects of Anthropogenic Sedimentation on Snails in Lake Tanganyika. Conservation Biology, 2005, 19, 171-181 2 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 36	5		3	25
Tanganyika. Conservation Biology, 2005, 19, 171-181 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 36	4		5.2	33
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