

Luke R Thompson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4268276/publications.pdf>

Version: 2024-02-01

40
papers

21,632
citations

218381

26
h-index

288905

40
g-index

59
all docs

59
docs citations

59
times ranked

25108
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
3	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
4	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
5	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
6	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
7	Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E757-64.	3.3	394
8	Prevalence and Evolution of Core Photosystem II Genes in Marine Cyanobacterial Viruses and Their Hosts. <i>PLoS Biology</i> , 2006, 4, e234.	2.6	394
9	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	6.0	381
10	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. <i>Environmental Microbiology</i> , 2010, 12, 3035-3056.	1.8	318
11	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	295
12	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	4.4	236
13	Exploring the Vast Diversity of Marine Viruses. <i>Oceanography</i> , 2007, 20, 135-139.	0.5	224
14	Choreography of the Transcriptome, Photophysiology, and Cell Cycle of a Minimal Photoautotroph, <i>Prochlorococcus</i> . <i>PLoS ONE</i> , 2009, 4, e5135.	1.1	184
15	Physiology and evolution of nitrate acquisition in <i>Prochlorococcus</i> . <i>ISME Journal</i> , 2015, 9, 1195-1207.	4.4	130
16	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. <i>Nature Communications</i> , 2018, 9, 2017.	5.8	103
17	DNA Sequencing as a Tool to Monitor Marine Ecological Status. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	92
18	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019, 15, e1008028.	2.1	50

#	ARTICLE	IF	CITATIONS
19	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. <i>Molecular Biology and Evolution</i> , 2015, 32, 2738-2748.	3.5	47
20	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016, 3, 160050.	2.4	47
21	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	2.9	46
22	Patterns of ecological specialization among microbial populations in the <sc>R</sc>ed Sea and diverse oligotrophic marine environments. <i>Ecology and Evolution</i> , 2013, 3, 1780-1797.	0.8	45
23	Gene Expression Patterns during Light and Dark Infection of <i>Prochlorococcus</i> by Cyanophage. <i>PLoS ONE</i> , 2016, 11, e0165375.	1.1	44
24	Environmental radiation alters the gut microbiome of the bank vole <i>Myodes glareolus</i>. <i>ISME Journal</i> , 2018, 12, 2801-2806.	4.4	44
25	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. <i>ISME Journal</i> , 2017, 11, 138-151.	4.4	40
26	Distribution and diversity of <i>Prochlorococcus</i> ecotypes in the Red Sea. <i>FEMS Microbiology Letters</i> , 2014, 356, 118-126.	0.7	29
27	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	1.7	28
28	Transcriptional characterization of <i>Vibrio fischeri</i> during colonization of juvenile <i>Euprymna scolopes</i>. <i>Environmental Microbiology</i> , 2017, 19, 1845-1856.	1.8	24
29	Expanding the temporal and spatial scales of environmental DNA research with autonomous sampling. <i>Environmental DNA</i> , 2022, 4, 972-984.	3.1	18
30	Distribution of <i>Prochlorococcus</i> Ecotypes in the Red Sea Basin Based on Analyses of rpoC1 Sequences. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	17
31	Subsurface automated samplers for eDNA (SASe) for biological monitoring and research. <i>HardwareX</i> , 2021, 10, e00239.	1.1	16
32	Draft Genome Sequence of Uncultured SAR324 Bacterium lautmerah10, Binned from a Red Sea Metagenome. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
33	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
34	Mitohelper: A mitochondrial reference sequence analysis tool for fish eDNA studies. <i>Environmental DNA</i> , 2021, 3, 706-715.	3.1	9
35	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	8
36	Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. <i>Environmental DNA</i> , 2022, 4, 291-303.	3.1	6

#	ARTICLE	IF	CITATIONS
37	The genome of a novel isolate of <i>Prochlorococcus</i> from the Red Sea contains transcribed genes for compatible solute biosynthesis. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	5
38	MixS-SA: a MixS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. <i>ISME Communications</i> , 2022, 2, .	1.7	3
39	Dominance of <i>Sulfurospirillum</i> in Metagenomes Associated with the Methane Ice Worm (<i>Sirsoe</i>) Tj ETQq1 1,0,784314,rgBT /Otel	1.4	2
40	Red Sea Metagenomics. , 2014, , 1-9.		0