

Luke R Thompson

List of Publications by Citations

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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.

52 papers	10,132 citations	26 h-index	59 g-index
59 ext. papers	16,509 ext. citations	10.5 avg, IF	5.46 L-index

#	Paper	IF	Citations
52	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
51	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
50	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.6	763
49	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422	22.2	668
48	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018 , 15, 962-968	21.6	608
47	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
46	Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts. <i>PLoS Biology</i> , 2006 , 4, e234	9.7	326
45	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	11.5	262
44	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016 , 351, 158-62	33.3	256
43	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. <i>Environmental Microbiology</i> , 2010 , 12, 3035-56	5.2	237
42	Exploring the Vast Diversity of Marine Viruses. <i>Oceanography</i> , 2007 , 20, 135-139	2.3	173
41	Choreography of the transcriptome, photophysiology, and cell cycle of a minimal photoautotroph, prochlorococcus. <i>PLoS ONE</i> , 2009 , 4, e5135	3.7	147
40	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
39	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019 , 4,	7.6	137
38	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019 , 13, 576-587	11.9	132
37	Physiology and evolution of nitrate acquisition in Prochlorococcus. <i>ISME Journal</i> , 2015 , 9, 1195-207	11.9	84
36	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78

35	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. <i>Nature Communications</i> , 2018 , 9, 2017	17.4	61
34	DNA Sequencing as a Tool to Monitor Marine Ecological Status. <i>Frontiers in Marine Science</i> , 2017 , 4,	4.5	55
33	Patterns of ecological specialization among microbial populations in the Red Sea and diverse oligotrophic marine environments. <i>Ecology and Evolution</i> , 2013 , 3, 1780-97	2.8	38
32	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
31	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016 , 3, 160058.2		34
30	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2738-48	8.3	33
29	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. <i>ISME Journal</i> , 2017 , 11, 138-151	11.9	27
28	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	10.6	26
27	Environmental radiation alters the gut microbiome of the bank vole <i>Myodes glareolus</i> . <i>ISME Journal</i> , 2018 , 12, 2801-2806	11.9	23
26	Gene Expression Patterns during Light and Dark Infection of <i>Prochlorococcus</i> by Cyanophage. <i>PLoS ONE</i> , 2016 , 11, e0165375	3.7	23
25	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019 , 15, e1008028	7.6	22
24	Distribution and diversity of <i>Prochlorococcus</i> ecotypes in the Red Sea. <i>FEMS Microbiology Letters</i> , 2014 , 356, 118-26	2.9	22
23	Transcriptional characterization of <i>Vibrio fischeri</i> during colonization of juvenile <i>Euprymna scolopes</i> . <i>Environmental Microbiology</i> , 2017 , 19, 1845-1856	5.2	21
22	Distribution of <i>Prochlorococcus</i> Ecotypes in the Red Sea Basin Based on Analyses of <i>rpoC1</i> Sequences. <i>Frontiers in Marine Science</i> , 2016 , 3,	4.5	14
21	Draft Genome Sequence of Uncultured SAR324 Bacterium lautmerah10, Binned from a Red Sea Metagenome. <i>Genome Announcements</i> , 2016 , 4,		13
20	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
19	Red Sea SAR11 and Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	7
18	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021 , 6,	7.6	7

17	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	5
16	EMP 18S Illumina Amplicon Protocol v1		4
15	EMP ITS Illumina Amplicon Protocol v1		4
14	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,	4.3	4
13	Earth Microbiome Project (EMP) high throughput (HTP) DNA extraction protocol v1		3
12	Metagenomic Covariation Along Densely Sampled Environmental Gradients in the Red Sea		3
11	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
10	EMP DNA Extraction Protocol v1		2
9	EMP Sample Submission Guide v1		2
8	Mitohelper: A mitochondrial reference sequence analysis tool for fish eDNA studies. <i>Environmental DNA</i> , 2021 , 3, 706-715	7.6	2
7	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
6	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides		1
5	Red Sea SAR11 and <i>Prochlorococcus</i> Single-cell Genomes Reflect Globally Distributed Pangenomes		1
4	Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. <i>Environmental DNA</i> ,	7.6	1
3	Subsurface automated samplers for eDNA (SASe) for biological monitoring and research. <i>HardwareX</i> , 2021 , 10, e00239	2.7	0
2	Mikrobielle Biologie des Roten Meeres. <i>BioSpektrum</i> , 2012 , 18, 582-584	0.1	
1	Red Sea Metagenomics 2014 , 1-9		