Luke R Thompson

List of Publications by Year in Descending Order

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	MIxS-SA: a MIxS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. *ISME Communications*, **2022**, 2,		1
51	Subsurface automated samplers for eDNA (SASe) for biological monitoring and research. *HardwareX*, **2021**, 10, e00239	2.7	0
50	Mitohelper: A mitochondrial reference sequence analysis tool for fish eDNA studies. *Environmental DNA*, **2021**, 3, 706-715	7.6	2
49	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. *MSystems*, **2021**, 6,	7.6	7
48	Red Sea SAR11 and Single-Cell Genomes Reflect Globally Distributed Pangenomes. *Applied and Environmental Microbiology*, **2019**, 85,	4.8	7
47	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. *ISME Journal*, **2019**, 13, 576-587	11.9	132
46	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
45	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. *Cell Systems*, **2019**, 9, 600-608.e4	10.6	26
44	Parasite microbiome project: Grand challenges. *PLoS Pathogens*, **2019**, 15, e1008028	7.6	22
43	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. *MSystems*, **2019**, 4,	7.6	137
42	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. *FEMS Microbiology Ecology*, **2018**, 94,	4.3	5
41	Environmental radiation alters the gut microbiome of the bank vole Myodes glareolus. *ISME Journal*, **2018**, 12, 2801-2806	11.9	23
40	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science **2018**,		78
39	Species-level functional profiling of metagenomes and metatranscriptomes. *Nature Methods*, **2018**, 15, 962-968	21.6	608
38	The genome of a novel isolate of Prochlorococcus from the Red Sea contains transcribed genes for compatible solute biosynthesis. *FEMS Microbiology Ecology*, **2018**, 94,	4.3	4
37	American Gut: an Open Platform for Citizen Science Microbiome Research. *MSystems*, **2018**, 3,	7.6	336
36	Best practices for analysing microbiomes. *Nature Reviews Microbiology*, **2018**, 16, 410-422	22.2	668

35	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. *Nature Communications*, **2018**, 9, 2017	17.4	61
34	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. *MSystems*, **2017**, 2,	7.6	763
33	Transcriptional characterization of Vibrio fischeri during colonization of juvenile Euprymna scolopes. *Environmental Microbiology*, **2017**, 19, 1845-1856	5.2	21
32	A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **2017**, 551, 457-463	50.4	1076
31	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. *ISME Journal*, **2017**, 11, 138-151	11.9	27
30	DNA Sequencing as a Tool to Monitor Marine Ecological Status. *Frontiers in Marine Science*, **2017**, 4,	4.5	55
29	Draft Genome Sequence of Uncultured SAR324 Bacterium lautmerah10, Binned from a Red Sea Metagenome. *Genome Announcements*, **2016**, 4,		13
28	Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science*, **2016**, 351, 158-62	33.3	256
27	Distribution of Prochlorococcus Ecotypes in the Red Sea Basin Based on Analyses of rpoC1 Sequences. *Frontiers in Marine Science*, **2016**, 3,	4.5	14
26	Gene Expression Patterns during Light and Dark Infection of Prochlorococcus by Cyanophage. *PLoS ONE*, **2016**, 11, e0165375	3.7	23
25	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. *Scientific Data*, **2016**, 3, 160050	8.2	34
24	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. *Molecular Biology and Evolution*, **2015**, 32, 2738-48	8.3	33
23	Physiology and evolution of nitrate acquisition in Prochlorococcus. *ISME Journal*, **2015**, 9, 1195-207	11.9	84
22	Distribution and diversity of Prochlorococcus ecotypes in the Red Sea. *FEMS Microbiology Letters*, **2014**, 356, 118-26	2.9	22
21	Red Sea Metagenomics **2014**, 1-9		
20	Patterns of ecological specialization among microbial populations in the Red Sea and diverse oligotrophic marine environments. *Ecology and Evolution*, **2013**, 3, 1780-97	2.8	38
19	Mikrobielle Ökologie des Roten Meeres. *BioSpektrum*, **2012**, 18, 582-584	0.1	
18	Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E757-64	11.5	262

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17	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. *Environmental Microbiology*, **2010**, 12, 3035-56	5.2	237
16	Choreography of the transcriptome, photophysiology, and cell cycle of a minimal photoautotroph, prochlorococcus. *PLoS ONE*, **2009**, 4, e5135	3.7	147
15	Exploring the Vast Diversity of Marine Viruses. *Oceanography*, **2007**, 20, 135-139	2.3	173
14	Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts. *PLoS Biology*, **2006**, 4, e234	9.7	326
13	EMP DNA Extraction Protocol v1		2
12	EMP 18S Illumina Amplicon Protocol v1		4
11	Earth Microbiome Project (EMP) high throughput (HTP) DNA extraction protocol v1		3
10	EMP Sample Submission Guide v1		2
9	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
8	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
7	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides		1
6	EMP ITS Illumina Amplicon Protocol v1		4
5	Red Sea SAR11 andProchlorococcusSingle-cell Genomes Reflect Globally Distributed Pangenomes		1
4	Metagenomic Covariation Along Densely Sampled Environmental Gradients in the Red Sea		3
3	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
2	Multi-omics profiling of Earth biomes reveals that microbial and metabolite composition are shaped by the environment		3
1	Optimizing an enclosed bead beating extraction method for microbial and fish environmental DNA. *Environmental DNA*,	7.6	1