

Brian C Thomas

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

18,174
citations

20817

60
h-index

40979

93
g-index

105
all docs

105
docs citations

105
times ranked

16984
citing authors

#	ARTICLE	IF	CITATIONS
1	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	13.3	1,823
2	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	27.8	1,050
3	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
4	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	13.3	906
5	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. <i>Science</i> , 2012, 337, 1661-1665.	12.6	637
6	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	3.9	522
7	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. <i>Microbiome</i> , 2013, 1, 22.	11.1	493
8	Community-wide analysis of microbial genome sequence signatures. <i>Genome Biology</i> , 2009, 10, R85.	9.6	479
9	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	27.8	471
10	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. <i>Microbiome</i> , 2014, 2, 1.	11.1	437
11	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity. <i>Genome Research</i> , 2006, 16, 805-814.	5.5	421
12	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , 2013, 23, 111-120.	5.5	409
13	Following tetraploidy in an <i>Arabidopsis</i> ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes. <i>Genome Research</i> , 2006, 16, 934-946.	5.5	393
14	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , 2013, 2, e01102.	6.0	355
15	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. <i>ISME Journal</i> , 2018, 12, 1715-1728.	9.8	347
16	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	12.8	342
17	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	17.5	342
18	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	8.8	326

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19	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. <i>Nature</i> , 2018, 558, 440-444.	27.8	321
20	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. <i>MBio</i> , 2013, 4, e00708-13.	4.1	298
21	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	13.3	227
22	Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1128-1133.	7.1	224
23	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
24	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	3.8	212
25	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
26	Strong bias in the bacterial CRISPR elements that confer immunity to phage. <i>Nature Communications</i> , 2013, 4, 1430.	12.8	180
27	Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2383-2390.	7.1	171
28	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	9.8	170
29	Mediterranean grassland soil N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	13.3	170
30	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	3.8	164
31	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	5.5	163
32	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. <i>Nature Communications</i> , 2017, 8, 1814.	12.8	162
33	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. <i>PLoS ONE</i> , 2013, 8, e56018.	2.5	153
34	CRISPR Immunity Drives Rapid Phage Genome Evolution in <i>Streptococcus thermophilus</i> . <i>MBio</i> , 2015, 6, .	4.1	151
35	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , 2016, 7, e01669-15.	4.1	151
36	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	13.3	141

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37	Potential for microbial H ₂ and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	9.8	137
38	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.	3.1	136
39	Persisting Viral Sequences Shape Microbial CRISPR-based Immunity. <i>PLoS Computational Biology</i> , 2012, 8, e1002475.	3.2	136
40	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. <i>Environmental Microbiology</i> , 2015, 17, 4929-4941.	3.8	124
41	Proteogenomic analyses indicate bacterial methylophily and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	2.0	124
42	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
43	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	12.8	119
44	Unusual respiratory capacity and nitrogen metabolism in a <i>Parcubacterium</i> (OD1) of the Candidate Phyla Radiation. <i>Scientific Reports</i> , 2017, 7, 40101.	3.3	119
45	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	5.5	117
46	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. <i>ELife</i> , 2015, 4, .	6.0	111
47	Conserved Noncoding Sequences in the Grasses. <i>Genome Research</i> , 2003, 13, 2030-2041.	5.5	107
48	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. <i>Genome Research</i> , 2017, 27, 601-612.	5.5	99
49	Bio-stimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013, 7, 800-816.	9.8	98
50	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	9.8	98
51	Phage mutations in response to <i>CRISPR</i> diversification in a bacterial population. <i>Environmental Microbiology</i> , 2013, 15, 463-470.	3.8	97
52	Comparative genomics in acid mine drainage biofilm communities reveals metabolic and structural differentiation of co-occurring archaea. <i>BMC Genomics</i> , 2013, 14, 485.	2.8	96
53	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
54	Metabolites Associated with Adaptation of Microorganisms to an Acidophilic, Metal-Rich Environment Identified by Stable-Isotope-Enabled Metabolomics. <i>MBio</i> , 2013, 4, e00484-12.	4.1	87

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55	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
56	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6309-6320.	3.1	83
57	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	82
58	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	3.9	82
59	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. <i>ISME Journal</i> , 2016, 10, 858-870.	9.8	80
60	Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. <i>Environmental Microbiology</i> , 2016, 18, 1686-1703.	3.8	78
61	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1435.	3.5	73
62	Comparison of environmental and isolate <i>Sulfobacillus</i> genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. <i>BMC Genomics</i> , 2014, 15, 1107.	2.8	65
63	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. <i>Microbiome</i> , 2018, 6, 112.	11.1	65
64	Ecological distribution and population physiology defined by proteomics in a natural microbial community. <i>Molecular Systems Biology</i> , 2010, 6, 374.	7.2	63
65	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	13.3	62
66	Chloroplast ribonuclease P does not utilize the ribozyme-type pre-tRNA cleavage mechanism. <i>Rna</i> , 2000, 6, 545-553.	3.5	60
67	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. <i>ISME Journal</i> , 2015, 9, 1014-1023.	9.8	59
68	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. <i>ISME Journal</i> , 2018, 12, 31-47.	9.8	59
69	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. <i>ISME Journal</i> , 2015, 9, 180-194.	9.8	57
70	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. <i>PeerJ</i> , 2016, 4, e1607.	2.0	57
71	<i>Arabidopsis</i> intragenomic conserved noncoding sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3348-3353.	7.1	55
72	Heterotrophic Archaea Contribute to Carbon Cycling in Low-pH, Suboxic Biofilm Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8321-8330.	3.1	52

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73	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. <i>Environmental Science & Technology</i> , 2017, 51, 2944-2953.	10.0	51
74	Genome resolved analysis of a premature infant gut microbial community reveals a <i>Varibaculum cambriense</i> genome and a shift towards fermentation-based metabolism during the third week of life. <i>Microbiome</i> , 2013, 1, 30.	11.1	50
75	Proteome changes in the initial bacterial colonist during ecological succession in an acid mine drainage biofilm community. <i>Environmental Microbiology</i> , 2011, 13, 2279-2292.	3.8	49
76	New Group in the <i>Leptospirillum</i> Clade: Cultivation-Independent Community Genomics, Proteomics, and Transcriptomics of the New Species <i>Leptospirillum</i> Group IV UBA BS. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5384-5393.	3.1	49
77	Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. <i>ISME Journal</i> , 2016, 10, 2817-2830.	9.8	47
78	Evidence for an RNA-based catalytic mechanism in eukaryotic nuclear ribonuclease P. <i>Rna</i> , 2000, 6, 554-562.	3.5	42
79	G-Boxes, Bigfoot Genes, and Environmental Response: Characterization of Intragenomic Conserved Noncoding Sequences in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 1441-1457.	6.6	42
80	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6755-6764.	3.1	37
81	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
82	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. <i>MBio</i> , 2018, 9, .	4.1	34
83	A Semi-Quantitative, Synteny-Based Method to Improve Functional Predictions for Hypothetical and Poorly Annotated Bacterial and Archaeal Genes. <i>PLoS Computational Biology</i> , 2011, 7, e1002230.	3.2	32
84	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	3.8	32
85	Metabolome-Proteome Differentiation Coupled to Microbial Divergence. <i>MBio</i> , 2010, 1, .	4.1	28
86	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. <i>Environmental Microbiology</i> , 2018, 20, 800-814.	3.8	27
87	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock. <i>Ecology and Evolution</i> , 2019, 9, 6869-6900.	1.9	24
88	Genome-resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. <i>MicrobiologyOpen</i> , 2017, 6, e00446.	3.0	22
89	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	19
90	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. <i>MBio</i> , 2017, 8, .	4.1	17

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91	Complete 4.55-Megabase-Pair Genome of <i>Candidatus</i> <i>Fluviicola riflensis</i> , Curated from Short-Read Metagenomic Sequences. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
92	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydrotroph. <i>Environmental Microbiology Reports</i> , 2020, 12, 525-533.	2.4	3