

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	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
2	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydotroph. <i>Environmental Microbiology Reports</i> , 2020, 12, 525-533.	2.4	3
3	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	13.3	141
4	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
5	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
6	Mediterranean grassland soil C-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
7	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. <i>ISME Journal</i> , 2018, 12, 1715-1728.	9.8	347
8	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	5.5	163
9	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. <i>MBio</i> , 2018, 9, .	4.1	34
10	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
11	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
12	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
13	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
14	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	13.3	906
15	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
16	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. <i>Nature</i> , 2018, 558, 440-444.	27.8	321
17	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
18	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

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19	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. <i>MBio</i> , 2017, 8, .	4.1	17
20	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
21	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
22	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
23	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
24	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	13.3	62
25	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	27.8	471
26	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
27	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	3.9	82
28	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
29	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
30	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
31	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
32	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	17.5	342
33	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
34	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	13.3	1,823
35	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
36	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

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37	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
38	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
39	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. <i>ISME Journal</i> , 2016, 10, 858-870.	9.8	80
40	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
41	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	2.0	124
42	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. <i>Environmental Microbiology</i> , 2015, 17, 4929-4941.	3.8	124
43	CRISPR Immunity Drives Rapid Phage Genome Evolution in <i>Streptococcus thermophilus</i> . <i>MBio</i> , 2015, 6, .	4.1	151
44	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
45	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
46	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	12.8	342
47	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
48	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	27.8	1,050
49	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
50	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	3.8	32
51	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. <i>ISME Journal</i> , 2015, 9, 1014-1023.	9.8	59
52	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. <i>ISME Journal</i> , 2015, 9, 180-194.	9.8	57
53	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. <i>ELife</i> , 2015, 4, .	6.0	111
54	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	12.8	119

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55	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
56	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
57	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	9.8	170
58	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
59	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
60	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
61	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
62	Biostimulation 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
63	Strong bias in the bacterial CRISPR elements that confer immunity to phage. <i>Nature Communications</i> , 2013, 4, 1430.	12.8	180
64	Phage mutations in response to <scf>CRISPR</scf> diversification in a bacterial population. <i>Environmental Microbiology</i> , 2013, 15, 463-470.	3.8	97
65	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
66	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
67	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. <i>MBio</i> , 2013, 4, e00708-13.	4.1	298
68	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
69	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
70	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	82
71	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. <i>PLoS ONE</i> , 2013, 8, e56018.	2.5	153
72	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

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73	Persisting Viral Sequences Shape Microbial CRISPR-based Immunity. PLoS Computational Biology, 2012, 8, e1002475.	3.2	136
74	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. Applied and Environmental Microbiology, 2012, 78, 6309-6320.	3.1	83
75	Heterotrophic Archaea Contribute to Carbon Cycling in Low-pH, Suboxic Biofilm Communities. Applied and Environmental Microbiology, 2012, 78, 8321-8330.	3.1	52
76	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. Science, 2012, 337, 1661-1665.	12.6	637
77	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. Genome Biology, 2011, 12, R44.	8.8	326
78	Proteome changes in the initial bacterial colonist during ecological succession in an acid mine drainage biofilm community. Environmental Microbiology, 2011, 13, 2279-2292.	3.8	49
79	Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1128-1133.	7.1	224
80	A Semi-Quantitative, Synteny-Based Method to Improve Functional Predictions for Hypothetical and Poorly Annotated Bacterial and Archaeal Genes. PLoS Computational Biology, 2011, 7, e1002230.	3.2	32
81	Metabolome-Proteome Differentiation Coupled to Microbial Divergence. MBio, 2010, 1, .	4.1	28
82	Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2383-2390.	7.1	171
83	Ecological distribution and population physiology defined by proteomics in a natural microbial community. Molecular Systems Biology, 2010, 6, 374.	7.2	63
84	Community-wide analysis of microbial genome sequence signatures. Genome Biology, 2009, 10, R85.	9.6	479
85	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. Applied and Environmental Microbiology, 2009, 75, 6591-6599.	3.1	136
86	G-Boxes, Bigfoot Genes, and Environmental Response: Characterization of Intragenomic Conserved Noncoding Sequences in Arabidopsis. Plant Cell, 2007, 19, 1441-1457.	6.6	42
87	Arabidopsis intragenomic conserved noncoding sequence. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3348-3353.	7.1	55
88	Following tetraploidy in an Arabidopsis ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes. Genome Research, 2006, 16, 934-946.	5.5	393
89	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity. Genome Research, 2006, 16, 805-814.	5.5	421
90	Conserved Noncoding Sequences in the Grasses. Genome Research, 2003, 13, 2030-2041.	5.5	107

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91	Chloroplast ribonuclease P does not utilize the ribozyme-type pre-tRNA cleavage mechanism. <i>Rna</i> , 2000, 6, 545-553.	3.5	60
92	Evidence for an RNA-based catalytic mechanism in eukaryotic nuclear ribonuclease P. <i>Rna</i> , 2000, 6, 554-562.	3.5	42