

Brett J Baker

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

13,592
citations

41258

49
h-index

85405

71
g-index

78
all docs

78
docs citations

78
times ranked

12863
citing authors

#	ARTICLE	IF	CITATIONS
1	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
2	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
3	Microbial communities in acid mine drainage. <i>FEMS Microbiology Ecology</i> , 2003, 44, 139-152.	1.3	916
4	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
5	Community proteomics of a natural microbial biofilm. <i>Science</i> , 2005, 308, 1915-20.	6.0	509
6	Community-wide analysis of microbial genome sequence signatures. <i>Genome Biology</i> , 2009, 10, R85.	13.9	479
7	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
8	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	6.0	439
9	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	3.8	326
10	Genomic resolution of linkages in carbon, nitrogen, and sulfur cycling among widespread estuary sediment bacteria. <i>Microbiome</i> , 2015, 3, 14.	4.9	316
11	Enigmatic, ultrasmall, uncultivated Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8806-8811.	3.3	306
12	Diversity, ecology and evolution of Archaea. <i>Nature Microbiology</i> , 2020, 5, 887-900.	5.9	262
13	Genome-Directed Isolation of the Key Nitrogen Fixer <i>Leptospirillum ferrodiazotrophum</i> sp. nov. from an Acidophilic Microbial Community. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6319-6324.	1.4	225
14	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. <i>Science</i> , 2006, 314, 1933-1935.	6.0	217
15	Acid mine drainage biogeochemistry at Iron Mountain, California. <i>Geochemical Transactions</i> , 2004, 5, 1.	1.8	211
16	Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. <i>Nature Communications</i> , 2018, 9, 4999.	5.8	205
17	Genomic evidence for distinct carbon substrate preferences and ecological niches of <i>Scp</i> -B- <i>Scp</i> -athyarchaeota in estuarine sediments. <i>Environmental Microbiology</i> , 2016, 18, 1200-1211.	1.8	195
18	Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. <i>Nature Microbiology</i> , 2016, 1, 16057.	5.9	173

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19	Desulfotomaculum and Methanobacterium spp. Dominate a 4- to 5-Kilometer-Deep Fault. Applied and Environmental Microbiology, 2005, 71, 8773-8783.	1.4	172
20	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.	3.3	171
21	The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. Frontiers in Microbiology, 2013, 4, 124.	1.5	171
22	Community Genomic and Proteomic Analyses of Chemoautotrophic Iron-Oxidizing <i>Leptospirillum rubrum</i> (Group II) and <i>Leptospirillum ferrodiazotrophum</i> (Group III) Bacteria in Acid Mine Drainage Biofilms. Applied and Environmental Microbiology, 2009, 75, 4599-4615.	1.4	168
23	Genomic insights into potential interdependencies in microbial hydrocarbon and nutrient cycling in hydrothermal sediments. Microbiome, 2017, 5, 106.	4.9	168
24	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	5.8	165
25	Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. ISME Journal, 2016, 10, 1696-1705.	4.4	161
26	Metabolically Active Eukaryotic Communities in Extremely Acidic Mine Drainage. Applied and Environmental Microbiology, 2004, 70, 6264-6271.	1.4	159
27	Genomic and transcriptomic evidence for scavenging of diverse organic compounds by widespread deep-sea archaea. Nature Communications, 2015, 6, 8933.	5.8	151
28	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. MBio, 2016, 7, e01669-15.	1.8	151
29	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. Nature Microbiology, 2019, 4, 1138-1148.	5.9	143
30	Community Proteomics of a Natural Microbial Biofilm. Science, 2005, 308, 1915-1920.	6.0	134
31	Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. ISME Journal, 2013, 7, 1962-1973.	4.4	119
32	Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea. Nature Microbiology, 2016, 1, 16002.	5.9	118
33	Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. ISME Journal, 2018, 12, 2532-2543.	4.4	115
34	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
35	Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. ISME Journal, 2009, 3, 159-167.	4.4	110
36	Insights into the Diversity of Eukaryotes in Acid Mine Drainage Biofilm Communities. Applied and Environmental Microbiology, 2009, 75, 2192-2199.	1.4	103

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37	Extremely Acidophilic Protists from Acid Mine Drainage Host Rickettsiales -Lineage Endosymbionts That Have Intervening Sequences in Their 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5512-5518.	1.4	101
38	Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume. <i>ISME Journal</i> , 2012, 6, 2269-2279.	4.4	100
39	Related assemblages of sulphate-reducing bacteria associated with ultradeep gold mines of South Africa and deep basalt aquifers of Washington State. <i>Environmental Microbiology</i> , 2003, 5, 267-277.	1.8	96
40	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <i>ISME Journal</i> , 2018, 12, 756-775.	4.4	91
41	Comparative genomic inference suggests mixotrophic lifestyle for Thorarchaeota. <i>ISME Journal</i> , 2018, 12, 1021-1031.	4.4	86
42	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico â€œDead Zoneâ€. <i>MBio</i> , 2017, 8, .	1.8	80
43	Genomic reconstruction of multiple lineages of uncultured benthic archaea suggests distinct biogeochemical roles and ecological niches. <i>ISME Journal</i> , 2017, 11, 1118-1129.	4.4	79
44	Single-Cell Genome and Group-Specific <i>dsrAB</i> Sequencing Implicate Marine Members of the Class <i>Dehalococcoidia</i> (Phylum <i>Chloroflexi</i>) in Sulfur Cycling. <i>MBio</i> , 2016, 7, .	1.8	78
45	Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. <i>Nature Communications</i> , 2014, 5, 3192.	5.8	75
46	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. <i>ISME Journal</i> , 2022, 16, 307-320.	4.4	71
47	Omic Approaches in Microbial Ecology: Charting the Unknown. <i>Microbe Magazine</i> , 2013, 8, 353-360.	0.4	62
48	Origins and diversification of sulfate-respiring microorganisms. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 189-195.	0.7	59
49	Novel hydrocarbon monooxygenase genes in the metatranscriptome of a natural deep-sea hydrocarbon plume. <i>Environmental Microbiology</i> , 2014, 16, 60-71.	1.8	59
50	New Microbial Biodiversity in Marine Sediments. <i>Annual Review of Marine Science</i> , 2021, 13, 161-175.	5.1	49
51	Diversity, Ecology, and Prevalence of Antimicrobials in Nature. <i>Frontiers in Microbiology</i> , 2019, 10, 2518.	1.5	47
52	Microbiological, molecular biological and stable isotopic evidence for nitrogen fixation in the open waters of Lake Michigan. <i>Environmental Microbiology</i> , 2001, 3, 205-219.	1.8	42
53	Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids. <i>Genome Biology and Evolution</i> , 2018, 10, 2380-2393.	1.1	37
54	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	36

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55	Seasonal and Spatial Variability in Lake Michigan Sediment Small-Subunit rRNA Concentrations. Applied and Environmental Microbiology, 2001, 67, 3908-3922.	1.4	35
56	A novel three-unit tRNA splicing endonuclease found in ultrasmall Archaea possesses broad substrate specificity. Nucleic Acids Research, 2011, 39, 9695-9704.	6.5	32
57	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. Nature Communications, 2021, 12, 2404.	5.8	32
58	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i> . Environmental Microbiology, 2020, 22, 1764-1783.	1.8	28
59	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. Frontiers in Microbiology, 2016, 7, 1221.	1.5	25
60	Kinetics and Identities of Extracellular Peptidases in Subsurface Sediments of the White Oak River Estuary, North Carolina. Applied and Environmental Microbiology, 2019, 85, .	1.4	25
61	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. Frontiers in Microbiology, 2021, 12, 660052.	1.5	20
62	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. Nature Microbiology, 2022, 7, 953-961.	5.9	17
63	Compositional and Metabolic Responses of Autotrophic Microbial Community to Salinity in Lacustrine Environments. MSystems, 2022, 7, .	1.7	15
64	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". Microbiology Resource Announcements, 2018, 7, .	0.3	14
65	Carbon metabolism and adaptation of hyperalkaliphilic microbes in serpentinizing spring of Manleluag, the Philippines. Environmental Microbiology Reports, 2022, 14, 308-319.	1.0	2