

Brett J Baker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5253598/publications.pdf>

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	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. ISME Journal, 2022, 16, 307-320.	4.4	71
2	Carbon metabolism and adaptation of hyperalkaliphilic microbes in serpentinizing spring of Manleluag, the Philippines. Environmental Microbiology Reports, 2022, 14, 308-319.	1.0	2
3	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. Nature Microbiology, 2022, 7, 953-961.	5.9	17
4	Compositional and Metabolic Responses of Autotrophic Microbial Community to Salinity in Lacustrine Environments. MSystems, 2022, 7, .	1.7	15
5	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
6	New Microbial Biodiversity in Marine Sediments. Annual Review of Marine Science, 2021, 13, 161-175.	5.1	49
7	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. Nature Communications, 2021, 12, 2404.	5.8	32
8	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. Frontiers in Microbiology, 2021, 12, 660052.	1.5	20
9	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i> . Environmental Microbiology, 2020, 22, 1764-1783.	1.8	28
10	Diversity, ecology and evolution of Archaea. Nature Microbiology, 2020, 5, 887-900.	5.9	262
11	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
12	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
13	Diversity, Ecology, and Prevalence of Antimicrobials in Nature. Frontiers in Microbiology, 2019, 10, 2518.	1.5	47
14	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. Applied and Environmental Microbiology, 2019, 85, .	1.4	36
15	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	5.8	165
16	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
17	Comparative genomic inference suggests mixotrophic lifestyle for Thorarchaeota. ISME Journal, 2018, 12, 1021-1031.	4.4	86
18	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. ISME Journal, 2018, 12, 756-775.	4.4	91

#	ARTICLE	IF	CITATIONS
19	Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. <i>Nature Communications</i> , 2018, 9, 4999.	5.8	205
20	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	14
21	Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. <i>ISME Journal</i> , 2018, 12, 2532-2543.	4.4	115
22	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
23	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
24	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
25	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017, 8, .	1.8	80
26	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
27	Genomic insights into potential interdependencies in microbial hydrocarbon and nutrient cycling in hydrothermal sediments. <i>Microbiome</i> , 2017, 5, 106.	4.9	168
28	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. <i>Frontiers in Microbiology</i> , 2016, 7, 1221.	1.5	25
29	Genomic evidence for distinct carbon substrate preferences and ecological niches of <i>Bathyarchaeota</i> in estuarine sediments. <i>Environmental Microbiology</i> , 2016, 18, 1200-1211.	1.8	195
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.	1.8	151
31	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
32	Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. <i>Nature Microbiology</i> , 2016, 1, 16057.	5.9	173
33	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
34	Genomic inference of the metabolism of cosmopolitan subsurface Archaea, Hadesarchaea. <i>Nature Microbiology</i> , 2016, 1, 16002.	5.9	118
35	Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. <i>ISME Journal</i> , 2016, 10, 1696-1705.	4.4	161
36	Genomic resolution of linkages in carbon, nitrogen, and sulfur cycling among widespread estuary sediment bacteria. <i>Microbiome</i> , 2015, 3, 14.	4.9	316

#	ARTICLE	IF	CITATIONS
37	Genomic and transcriptomic evidence for scavenging of diverse organic compounds by widespread deep-sea archaea. <i>Nature Communications</i> , 2015, 6, 8933.	5.8	151
38	Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. <i>Nature Communications</i> , 2014, 5, 3192.	5.8	75
39	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
40	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	6.0	439
41	Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. <i>ISME Journal</i> , 2013, 7, 1962-1973.	4.4	119
42	The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. <i>Frontiers in Microbiology</i> , 2013, 4, 124.	1.5	171
43	Omic Approaches in Microbial Ecology: Charting the Unknown. <i>Microbe Magazine</i> , 2013, 8, 353-360.	0.4	62
44	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
45	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	3.8	326
46	A novel three-unit tRNA splicing endonuclease found in ultrasmall Archaea possesses broad substrate specificity. <i>Nucleic Acids Research</i> , 2011, 39, 9695-9704.	6.5	32
47	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
48	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.	3.3	171
49	Insights into the Diversity of Eukaryotes in Acid Mine Drainage Biofilm Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2192-2199.	1.4	103
50	Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. <i>ISME Journal</i> , 2009, 3, 159-167.	4.4	110
51	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. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4599-4615.	1.4	168
52	Community-wide analysis of microbial genome sequence signatures. <i>Genome Biology</i> , 2009, 10, R85.	13.9	479
53	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. <i>Science</i> , 2006, 314, 1933-1935.	6.0	217
54	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

#	ARTICLE	IF	CITATIONS
55	Desulfotomaculum and Methanobacterium spp. Dominate a 4- to 5-Kilometer-Deep Fault. Applied and Environmental Microbiology, 2005, 71, 8773-8783.	1.4	172
56	Community proteomics of a natural microbial biofilm. Science, 2005, 308, 1915-20.	6.0	509
57	Community Proteomics of a Natural Microbial Biofilm. Science, 2005, 308, 1915-1920.	6.0	134
58	Metabolically Active Eukaryotic Communities in Extremely Acidic Mine Drainage. Applied and Environmental Microbiology, 2004, 70, 6264-6271.	1.4	159
59	Acid mine drainage biogeochemistry at Iron Mountain, California. Geochemical Transactions, 2004, 5, 1.	1.8	211
60	Microbial communities in acid mine drainage. FEMS Microbiology Ecology, 2003, 44, 139-152.	1.3	916
61	Related assemblages of sulphate-reducing bacteria associated with ultradeep gold mines of South Africa and deep basalt aquifers of Washington State. Environmental Microbiology, 2003, 5, 267-277.	1.8	96
62	Extremely Acidophilic Protists from Acid Mine Drainage Host Rickettsiales -Lineage Endosymbionts That Have Intervening Sequences in Their 16S rRNA Genes. Applied and Environmental Microbiology, 2003, 69, 5512-5518.	1.4	101
63	Origins and diversification of sulfate-respiring microorganisms. Antonie Van Leeuwenhoek, 2002, 81, 189-195.	0.7	59
64	Microbiological, molecular biological and stable isotopic evidence for nitrogen fixation in the open waters of Lake Michigan. Environmental Microbiology, 2001, 3, 205-219.	1.8	42
65	Seasonal and Spatial Variability in Lake Michigan Sediment Small-Subunit rRNA Concentrations. Applied and Environmental Microbiology, 2001, 67, 3908-3922.	1.4	35