

David W Waite

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

6,257
citations

279798

23
h-index

254184

43
g-index

52
all docs

52
docs citations

52
times ranked

7789
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	9.8	89
2	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. <i>ISME Journal</i> , 2021, 15, 3339-3356.	9.8	48
3	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	13.3	198
4	Termite gas emissions select for hydrogenotrophic microbial communities in termite mounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	15
5	Application of Oxford Nanopore Technology to Plant Virus Detection. <i>Viruses</i> , 2021, 13, 1424.	3.3	42
6	Kinetic and Structural Characterization of the First B3 Metallo- β -Lactamase with an Active-Site Glutamic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0093621.	3.2	7
7	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021, 9, 190.	11.1	29
8	Characterising clinical <i>Staphylococcus aureus</i> isolates from the sinuses of patients with chronic rhinosinusitis. <i>Scientific Reports</i> , 2021, 11, 21940.	3.3	6
9	Bacterial Signatures of Paediatric Respiratory Disease: An Individual Participant Data Meta-Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 711134.	3.5	5
10	Molecular identification of <i>Bactrocera passiflorae</i> (Diptera: Tephritidae): Challenge and solution for DNA barcoding. <i>Journal of Applied Entomology</i> , 2020, 144, 877-884.	1.8	2
11	A Novel Description of the Human Sinus Archaeome During Health and Chronic Rhinosinusitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 398.	3.9	8
12	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. <i>ISME Journal</i> , 2020, 14, 2715-2731.	9.8	21
13	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. <i>ISME Journal</i> , 2020, 14, 2164-2178.	9.8	33
14	Broad spectrum antibiotic-degrading metallo- β -lactamases are phylogenetically diverse. <i>Protein and Cell</i> , 2020, 11, 613-617.	11.0	21
15	Probing the Chemical Transformation of Seawater-Soluble Crude Oil Components during Microbial Oxidation. <i>ACS Earth and Space Chemistry</i> , 2020, 4, 690-701.	2.7	5
16	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5972-6016.	1.7	830
17	DNA barcoding and real-time PCR detection of <i>Bactrocera xanthodes</i> (Tephritidae: Diptera) complex. <i>Bulletin of Entomological Research</i> , 2019, 109, 102-110.	1.0	5
18	Bacterial communities associated with tail fan necrosis in spiny lobster, <i>Jasus edwardsii</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	14

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19	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. <i>Nature Microbiology</i> , 2019, 4, 1014-1023.	13.3	76
20	The microbiome in threatened species conservation. <i>Biological Conservation</i> , 2019, 229, 85-98.	4.1	185
21	Characterization of mid-intestinal microbiota of farmed Chinook salmon using 16S rRNA gene metabarcoding. <i>Archives of Biological Sciences</i> , 2019, 71, 577-587.	0.5	22
22	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science & Technology</i> , 2018, 52, 5386-5397.	10.0	52
23	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. <i>Environmental Microbiology</i> , 2018, 20, 561-576.	3.8	32
24	Active migration is associated with specific and consistent changes to gut microbiota in <i>Calidris</i> shorebirds. <i>Journal of Animal Ecology</i> , 2018, 87, 428-437.	2.8	73
25	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	3.3	11
26	Molecular detection of small hive beetle <i>Aethina tumida</i> Murray (Coleoptera: Nitidulidae): DNA barcoding and development of a real-time PCR assay. <i>Scientific Reports</i> , 2018, 8, 9623.	3.3	11
27	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	17.5	2,615
28	Assessment of microbial DNA enrichment techniques from sino-nasal swab samples for metagenomics. <i>Rhinology</i> , 2018, 1, 160-193.	0.3	11
29	Development and validation of a real-time PCR assay for the glassy-winged sharpshooter <i>Homalodisca vitripennis</i> (Hemiptera: Cicadellidae). <i>Bulletin of Entomological Research</i> , 2017, 107, 332-339.	1.0	0
30	Bacterial community collapse: a meta-analysis of the sinonasal microbiota in chronic rhinosinusitis. <i>Environmental Microbiology</i> , 2017, 19, 381-392.	3.8	174
31	Gut microbiota of a long-distance migrant demonstrates resistance against environmental microbe incursions. <i>Molecular Ecology</i> , 2017, 26, 5842-5854.	3.9	51
32	What Thrives Inside; The World Within the Gut. <i>Frontiers for Young Minds</i> , 2017, 5, .	0.8	0
33	Moving beyond descriptions of diversity: clinical and research implications of bacterial imbalance in chronic rhinosinusitis. <i>Rhinology</i> , 2017, 55, 291-297.	1.3	0
34	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	3.5	409
35	Real-Time PCR Assay for the Identification of the Brown Marmorated Stink Bug (<i>Halyomorpha halys</i>). <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 5.	3.5	18
36	Integrity of the Human Faecal Microbiota following Long-Term Sample Storage. <i>PLoS ONE</i> , 2016, 11, e0163666.	2.5	41

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37	Rapid and accurate identification of <i>Xanthomonas citri</i> subspecies <i>citri</i> by fluorescence in situ hybridization. <i>Letters in Applied Microbiology</i> , 2016, 63, 315-321.	2.2	1
38	Exploring the avian gut microbiota: current trends and future directions. <i>Frontiers in Microbiology</i> , 2015, 6, 673.	3.5	216
39	Evaluating variation in human gut microbiota profiles due to DNA extraction method and inter-subject differences. <i>Frontiers in Microbiology</i> , 2015, 6, 130.	3.5	152
40	Microbial community structure in the gut of the New Zealand insect Auckland tree weta (<i>Hemideina tjiriki</i>). <i>Journal of Insect Science and Technology</i> , 2015, 15, 10.	2.2	15
41	Development and Validation of a Real-Time PCR Assay for Rapid Detection of Two-Spotted Spider Mite, <i>Tetranychus urticae</i> (Acari: Tetranychidae). <i>PLoS ONE</i> , 2015, 10, e0131887.	2.5	17
42	Characterizing the avian gut microbiota: membership, driving influences, and potential function. <i>Frontiers in Microbiology</i> , 2014, 5, 223.	3.5	328
43	Influence of Hand Rearing and Bird Age on the Fecal Microbiota of the Critically Endangered Kakapo. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4650-4658.	3.1	42
44	Quantifying the impact of storage procedures for faecal bacteriotherapy in the critically endangered New Zealand Parrot, the Kakapo (<i>Strigops habroptilus</i>). <i>Zoo Biology</i> , 2013, 32, 620-625.	1.2	19
45	Gut Microbiome of the Critically Endangered New Zealand Parrot, the Kakapo (<i>Strigops habroptilus</i>). <i>PLoS ONE</i> , 2012, 7, e35803.	2.5	75