

Kim Handley

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56
papers

2,572
citations

28
h-index

50
g-index

60
ext. papers

3,442
ext. citations

8.4
avg, IF

4.84
L-index

#	Paper	IF	Citations
56	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	33.3	543
55	Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. <i>MBio</i> , 2013 , 4, e00708-13	7.8	204
54	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	146
53	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014 , 8, 1452-63	11.9	131
52	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
51	Genome reduction in an abundant and ubiquitous soil bacterium 'Candidatus Udaeobacter copiosus'. <i>Nature Microbiology</i> , 2016 , 2, 16198	26.6	99
50	Short-read assembly of full-length 16S amplicons reveals bacterial diversity in subsurface sediments. <i>PLoS ONE</i> , 2013 , 8, e56018	3.7	81
49	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013 , 7, 800-16	11.9	78
48	Lifestyle evolution in cyanobacterial symbionts of sponges. <i>MBio</i> , 2015 , 6, e00391-15	7.8	76
47	Metabolic Reconstruction and Modeling Microbial Electrosynthesis. <i>Scientific Reports</i> , 2017 , 7, 8391	4.9	67
46	Vanadate and acetate biostimulation of contaminated sediments decreases diversity, selects for specific taxa, and decreases aqueous V5+ concentration. <i>Environmental Science & Technology</i> , 2013 , 47, 6500-9	10.3	58
45	Silicifying biofilm exopolymers on a hot-spring microstromatolite: templating nanometer-thick laminae. <i>Astrobiology</i> , 2008 , 8, 747-70	3.7	58
44	Abiotic/Biotic controls on the origin and development of spicular sinter: in situ growth experiments, Champagne Pool, Waiotapu, New Zealand. <i>Geobiology</i> , 2005 , 3, 93-114	4.3	57
43	Tracing Biosignature Preservation of Geothermally Silicified Microbial Textures into the Geological Record. <i>Astrobiology</i> , 2015 , 15, 858-82	3.7	54
42	Biogeochemical implications of the ubiquitous colonization of marine habitats and redox gradients by <i>Marinobacter</i> species. <i>Frontiers in Microbiology</i> , 2013 , 4, 136	5.7	53
41	<i>Marinobacter santoriniensis</i> sp. nov., an arsenate-respiring and arsenite-oxidizing bacterium isolated from hydrothermal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009 , 59, 886-92	2.2	52
40	The complete genome sequence for putative H ₂ and S-oxidizer <i>Candidatus Sulfuricum</i> sp., assembled de novo from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014 , 16, 3443-62	5.2	51

39	Responses of Microbial Communities to Hydrocarbon Exposures. <i>Oceanography</i> , 2016 , 29, 136-149	2.3	47
38	Metabolic potential of fatty acid oxidation and anaerobic respiration by abundant members of Thaumarchaeota and Thermoplasmata in deep anoxic peat. <i>ISME Journal</i> , 2015 , 9, 2740-4	11.9	46
37	Bicarbonate impact on U(VI) bioreduction in a shallow alluvial aquifer. <i>Geochimica Et Cosmochimica Acta</i> , 2015 , 150, 106-124	5.5	44
36	Functional diversity of bacteria in a ferruginous hydrothermal sediment. <i>ISME Journal</i> , 2010 , 4, 1193-205	11.9	44
35	Speciation and reactivity of uranium products formed during in situ bioremediation in a shallow alluvial aquifer. <i>Environmental Science & Technology</i> , 2014 , 48, 12842-50	10.3	42
34	High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. <i>FEMS Microbiology Ecology</i> , 2012 , 81, 188-204	4.3	42
33	Redox cycling of arsenic by the hydrothermal marine bacterium <i>Marinobacter santoriniensis</i> . <i>Environmental Microbiology</i> , 2009 , 11, 1601-11	5.2	38
32	Divalent metal adsorption by the thermophile <i>Anoxybacillus flavithermus</i> in single and multi-metal systems. <i>Chemical Geology</i> , 2007 , 244, 493-506	4.2	32
31	Effect of iron redox transformations on arsenic solid-phase associations in an arsenic-rich, ferruginous hydrothermal sediment. <i>Geochimica Et Cosmochimica Acta</i> , 2013 , 102, 124-142	5.5	30
30	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015 , 17, 622-36	5.2	28
29	Methods for the extraction, storage, amplification and sequencing of DNA from environmental samples 2018 ,		28
28	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017 , 11, 2569-2583	11.9	27
27	Phylogenetic Distribution of Plastic-Degrading Microorganisms. <i>MSystems</i> , 2021 , 6,	7.6	23
26	Following Rapoport's Rule: the geographic range and genome size of bacterial taxa decline at warmer latitudes. <i>Environmental Microbiology</i> , 2017 , 19, 3152-3162	5.2	20
25	A New N-Acyl Homoserine Lactone Synthase in an Uncultured Symbiont of the Red Sea Sponge <i>Theonella swinhoei</i> . <i>Applied and Environmental Microbiology</i> , 2016 , 82, 1274-1285	4.8	19
24	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. <i>ISME Journal</i> , 2020 , 14, 2164-2178	11.9	15
23	Fluctuations in species-level protein expression occur during element and nutrient cycling in the subsurface. <i>PLoS ONE</i> , 2013 , 8, e57819	3.7	15
22	Functional predictions from inference and observation in sequence-based inflammatory bowel disease research 2012 , 13, 169		14

21	Functional predictions from inference and observation in sequence-based inflammatory bowel disease research. <i>Genome Biology</i> , 2012 , 13, 169	18.3	11
20	Characterization of sponge-associated Verrucomicrobia: microcompartment-based sugar utilization and enhanced toxin-antitoxin modules as features of host-associated Opitutales. <i>Environmental Microbiology</i> , 2020 , 22, 4669-4688	5.2	11
19	Character, Analysis, and Preservation of Biogenicity in Terrestrial Siliceous Stromatolites from Geothermal Settings. <i>Cellular Origin and Life in Extreme Habitats</i> , 2011 , 359-381		10
18	Life at Home and on the Roam: Genomic Adaptions Reflect the Dual Lifestyle of an Intracellular, Facultative Symbiont. <i>MSystems</i> , 2019 , 4,	7.6	7
17	Stromatolitic digitate sinters form under wide-ranging physicochemical conditions with diverse hot spring microbial communities. <i>Geobiology</i> , 2020 , 18, 619-640	4.3	6
16	Genomic adaptations enabling <i>Acidithiobacillus</i> distribution across wide-ranging hot spring temperatures and pHs. <i>Microbiome</i> , 2021 , 9, 135	16.6	6
15	Determining Microbial Roles in Ecosystem Function: Redefining Microbial Food Webs and Transcending Kingdom Barriers. <i>MSystems</i> , 2019 , 4,	7.6	5
14	Genome Sequence of Hydrothermal Arsenic-Respiring Bacterium <i>Marinobacter santoriniensis</i> NKSG1T. <i>Genome Announcements</i> , 2013 , 1,		5
13	Biogeochemical controls on microbial diversity in seafloor sulphidic sediments. <i>Geobiology</i> , 2010 , 8, 309-319	4.6	5
12	From pine to pasture: land use history has long-term impacts on soil bacterial community composition and functional potential. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	4
11	PlasticDB: a database of microorganisms and proteins linked to plastic biodegradation.. <i>Database: the Journal of Biological Databases and Curation</i> , 2022 , 2022,	5	4
10	Metabolic Reconstruction and Modeling Microbial Electrosynthesis		4
9	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021 , 9, 190	16.6	4
8	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,	11.5	3
7	Opportunities for modern genetic technologies to maintain and enhance Aotearoa New Zealand's bioheritage. <i>New Zealand Journal of Ecology</i> , 2020 , 44,	1.9	2
6	Genome reduction in an abundant and ubiquitous soil bacterial lineage		2
5	Estuarine microbial diversity and nitrogen cycling increase along sand-mud gradients independent of salinity and distance. <i>Environmental Microbiology</i> , 2021 ,	5.2	2
4	Metabolic Diversity and Aero-Tolerance in Anammox Bacteria from Geochemically Distinct Aquifers.. <i>MSystems</i> , 2022 , 7, e0125521	7.6	2

3	Genome Streamlining, Plasticity, and Metabolic Versatility Distinguish Co-occurring Toxic and Nontoxic Cyanobacterial Strains of. <i>MBio</i> , 2021 , 12, e0223521	7.8	1
2	Effect of dietary zinc supplementation on the gastrointestinal microbiota and host gene expression in the Shank3B ^{fl/fl} mouse model of autism spectrum disorder		1
1	Genomic Insights Into the Lifestyles of Thaumarchaeota Inside Sponges. <i>Frontiers in Microbiology</i> , 2020 , 11, 622824	5.7	0