

# Kim Handley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7435045/publications.pdf>

Version: 2024-02-01

54  
papers

3,917  
citations

159525

30  
h-index

168321

53  
g-index

60  
all docs

60  
docs citations

60  
times ranked

6432  
citing authors

#	ARTICLE	IF	CITATIONS
1	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751
2	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. <i>MBio</i> , 2013, 4, e00708-13.	1.8	298
3	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	248
4	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	6.5	177
5	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	4.4	170
6	Genome reduction in an abundant and ubiquitous soil bacterium <i>Candidatus Udaeobacter copiosus</i> <sup>™</sup> . <i>Nature Microbiology</i> , 2017, 2, 16198.	5.9	168
7	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. <i>PLoS ONE</i> , 2013, 8, e56018.	1.1	153
8	Metabolic Reconstruction and Modeling Microbial Electrosynthesis. <i>Scientific Reports</i> , 2017, 7, 8391.	1.6	117
9	Lifestyle Evolution in Cyanobacterial Symbionts of Sponges. <i>MBio</i> , 2015, 6, e00391-15.	1.8	103
10	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013, 7, 800-816.	4.4	98
11	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.	1.5	85
12	Phylogenetic Distribution of Plastic-Degrading Microorganisms. <i>MSystems</i> , 2021, 6, .	1.7	83
13	Vanadate and Acetate Biostimulation of Contaminated Sediments Decreases Diversity, Selects for Specific Taxa, and Decreases Aqueous V <sup>5+</sup> Concentration. <i>Environmental Science &amp; Technology</i> , 2013, 47, 6500-6509.	4.6	80
14	<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, 886-892.	0.8	71
15	Functional diversity of bacteria in a ferruginous hydrothermal sediment. <i>ISME Journal</i> , 2010, 4, 1193-1205.	4.4	71
16	Silicifying Biofilm Exopolymers on a Hot-Spring Microstromatolite: Templating Nanometer-Thick Laminae. <i>Astrobiology</i> , 2008, 8, 747-770.	1.5	69
17	The complete genome sequence for putative <i>H<sub>2</sub>S</i> -oxidizer <i>Candidatus Sulfuricum</i> sp., assembled <i>de novo</i> from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014, 16, 3443-3462.	1.8	69
18	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, 2740-2744.	4.4	69

#	ARTICLE	IF	CITATIONS
19	Tracing Biosignature Preservation of Geothermally Silicified Microbial Textures into the Geological Record. <i>Astrobiology</i> , 2015, 15, 858-882.	1.5	68
20	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.	1.1	66
21	Responses of Microbial Communities to Hydrocarbon Exposures. <i>Oceanography</i> , 2016, 29, 136-149.	0.5	59
22	Bicarbonate impact on U(VI) bioreduction in a shallow alluvial aquifer. <i>Geochimica Et Cosmochimica Acta</i> , 2015, 150, 106-124.	1.6	58
23	Methods for the extraction, storage, amplification and sequencing of DNA from environmental samples. , 2018, , .		58
24	Speciation and Reactivity of Uranium Products Formed during <i>in Situ</i> Bioremediation in a Shallow Alluvial Aquifer. <i>Environmental Science &amp; Technology</i> , 2014, 48, 12842-12850.	4.6	56
25	PlasticDB: a database of microorganisms and proteins linked to plastic biodegradation. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	49
26	Redox cycling of arsenic by the hydrothermal marine bacterium <i>Marinobacter santoriniensis</i> . <i>Environmental Microbiology</i> , 2009, 11, 1601-1611.	1.8	45
27	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.	1.3	43
28	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017, 11, 2569-2583.	4.4	39
29	Divalent metal adsorption by the thermophile <i>Anoxybacillus flavithermus</i> in single and multi-metal systems. <i>Chemical Geology</i> , 2007, 244, 493-506.	1.4	35
30	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.	1.6	34
31	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. <i>ISME Journal</i> , 2020, 14, 2164-2178.	4.4	33
32	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	1.8	32
33	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.	1.4	30
34	Life at Home and on the Roam: Genomic Adaptions Reflect the Dual Lifestyle of an Intracellular, Facultative Symbiont. <i>MSystems</i> , 2019, 4, .	1.7	30
35	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021, 9, 190.	4.9	29
36	Characterization of sponge-associated <i>Verrucomicrobia</i> : microcompartment-based sugar utilization and enhanced toxin-antitoxin modules as features of host-associated <i>Opitutaes</i> . <i>Environmental Microbiology</i> , 2020, 22, 4669-4688.	1.8	26

#	ARTICLE	IF	CITATIONS
37	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.	1.8	25
38	Genomic adaptations enabling <i>Acidithiobacillus</i> distribution across wide-ranging hot spring temperatures and pHs. <i>Microbiome</i> , 2021, 9, 135.	4.9	22
39	Fluctuations in Species-Level Protein Expression Occur during Element and Nutrient Cycling in the Subsurface. <i>PLoS ONE</i> , 2013, 8, e57819.	1.1	21
40	Stromatolitic digitate sinters form under wide-ranging physicochemical conditions with diverse hot spring microbial communities. <i>Geobiology</i> , 2020, 18, 619-640.	1.1	18
41	Genomic Insights Into the Lifestyles of Thaumarchaeota Inside Sponges. <i>Frontiers in Microbiology</i> , 2020, 11, 622824.	1.5	16
42	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, .	3.3	15
43	Functional predictions from inference and observation in sequence-based inflammatory bowel disease research. <i>Genome Biology</i> , 2012, 13, 169.	13.9	14
44	Metabolic Diversity and Aero-Tolerance in Anammox Bacteria from Geochemically Distinct Aquifers. <i>MSystems</i> , 2022, 7, e0125521.	1.7	13
45	Lineage-specific energy and carbon metabolism of sponge symbionts and contributions to the host carbon pool. <i>ISME Journal</i> , 2022, 16, 1163-1175.	4.4	13
46	Estuarine microbial diversity and nitrogen cycling increase along sand-mud gradients independent of salinity and distance. <i>Environmental Microbiology</i> , 2022, 24, 50-65.	1.8	12
47	Functional predictions from inference and observation in sequence-based inflammatory bowel disease research. <i>Genome Biology</i> , 2012, 13, 169.	3.8	11
48	Determining Microbial Roles in Ecosystem Function: Redefining Microbial Food Webs and Transcending Kingdom Barriers. <i>MSystems</i> , 2019, 4, .	1.7	11
49	Genome Streamlining, Plasticity, and Metabolic Versatility Distinguish Co-occurring Toxic and Nontoxic Cyanobacterial Strains of <i>Microcoleus</i> . <i>MBio</i> , 2021, 12, e0223521.	1.8	11
50	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.	0.3	10
51	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, .	1.3	9
52	Biogeochemical controls on microbial diversity in seafloor sulphidic sediments. <i>Geobiology</i> , 2010, 8, 309-326.	1.1	7
53	Genome Sequence of Hydrothermal Arsenic-Respiring Bacterium <i>Marinobacter santoriniensis</i> NKSG1. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
54	Opportunities for modern genetic technologies to maintain and enhance Aotearoa New Zealand's bioheritage. <i>New Zealand Journal of Ecology</i> , 2020, 44, .	1.1	4