

# Karen G Lloyd

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

5,343  
citations

159358

30  
h-index

133063

59  
g-index

73  
all docs

73  
docs citations

73  
times ranked

5264  
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterotrophic Archaea dominate sedimentary subsurface ecosystems off Peru. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3846-3851.	3.3	654
2	Predominant archaea in marine sediments degrade detrital proteins. Nature, 2013, 496, 215-218.	13.7	526
3	Life under extreme energy limitation: a synthesis of laboratory- and field-based investigations. FEMS Microbiology Reviews, 2015, 39, 688-728.	3.9	288
4	Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. ISME Journal, 2012, 6, 1949-1965.	4.4	281
5	Phylogenetically Novel Uncultured Microbial Cells Dominate Earth Microbiomes. MSystems, 2018, 3, .	1.7	273
6	High proportions of bacteria and archaea across most biomes remain uncultured. ISME Journal, 2019, 13, 3126-3130.	4.4	264
7	Diversity, ecology and evolution of Archaea. Nature Microbiology, 2020, 5, 887-900.	5.9	262
8	The bright side of microbial dark matter: lessons learned from the uncultivated majority. Current Opinion in Microbiology, 2016, 31, 217-226.	2.3	241
9	An Anaerobic Methane-Oxidizing Community of ANME-1b Archaea in Hypersaline Gulf of Mexico Sediments. Applied and Environmental Microbiology, 2006, 72, 7218-7230.	1.4	206
10	Genome sequencing of a single cell of the widely distributed marine subsurface <i>Dehalococcoidia</i> phylum <i>Chloroflexi</i> . ISME Journal, 2014, 8, 383-397.	4.4	172
11	Methanogen Diversity Evidenced by Molecular Characterization of Methyl Coenzyme M Reductase A ( <i>mcrA</i> ) Tj ETQq1 1 0.784314 rgBT /Over Microbiology, 2005, 71, 4592-4601.	1.4	152
12	Anaerobic oxidation of methane at different temperature regimes in Guaymas Basin hydrothermal sediments. ISME Journal, 2012, 6, 1018-1031.	4.4	149
13	Environmental evidence for net methane production and oxidation in putative ANaerobic MEthanotrophic (ANME) archaea. Environmental Microbiology, 2011, 13, 2548-2564.	1.8	146
14	Spatial Structure and Activity of Sedimentary Microbial Communities Underlying a <i>Beggiatoa</i> spp. Mat in a Gulf of Mexico Hydrocarbon Seep. PLoS ONE, 2010, 5, e8738.	1.1	117
15	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
16	Meta-Analysis of Quantification Methods Shows that Archaea and Bacteria Have Similar Abundances in the Subseafloor. Applied and Environmental Microbiology, 2013, 79, 7790-7799.	1.4	113
17	Metabolic variability in seafloor brines revealed by carbon and sulphur dynamics. Nature Geoscience, 2009, 2, 349-354.	5.4	111
18	Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermopfundales (MBC-D archaea). ISME Journal, 2019, 13, 885-901.	4.4	92

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19	The Guaymas Basin Hiking Guide to Hydrothermal Mounds, Chimneys, and Microbial Mats: Complex Seafloor Expressions of Subsurface Hydrothermal Circulation. <i>Frontiers in Microbiology</i> , 2016, 7, 75.	1.5	82
20	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
21	Spatial heterogeneity and underlying geochemistry of phylogenetically diverse orange and white <i>Beggiatoa</i> mats in Guaymas Basin hydrothermal sediments. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2012, 67, 21-31.	0.6	73
22	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. <i>Frontiers in Microbiology</i> , 2016, 7, 17.	1.5	72
23	Quantitative PCR methods for RNA and DNA in marine sediments: maximizing yield while overcoming inhibition. <i>FEMS Microbiology Ecology</i> , 2010, 72, 143-151.	1.3	62
24	Complex Microbial Communities Drive Iron and Sulfur Cycling in Arctic Fjord Sediments. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	58
25	Sulfide Ameliorates Metal Toxicity for Deep-Sea Hydrothermal Vent Archaea. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2551-2555.	1.4	56
26	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180.	4.4	54
27	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. <i>MBio</i> , 2019, 10, .	1.8	45
28	Thriving or surviving? Evaluating active microbial guilds in Baltic Sea sediment. <i>Environmental Microbiology Reports</i> , 2017, 9, 528-536.	1.0	39
29	Microbial Taxonomy Run Amok. <i>Trends in Microbiology</i> , 2021, 29, 394-404.	3.5	38
30	Microbial Organic Matter Degradation Potential in Baltic Sea Sediments Is Influenced by Depositional Conditions and <i>In Situ</i> Geochemistry. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	37
31	Effect of tectonic processes on biosphere-geosphere feedbacks across a convergent margin. <i>Nature Geoscience</i> , 2021, 14, 301-306.	5.4	32
32	Estimating Population Turnover Rates by Relative Quantification Methods Reveals Microbial Dynamics in Marine Sediment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
33	<i>ANME-1</i> archaea may drive methane accumulation and removal in estuarine sediments. <i>Environmental Microbiology Reports</i> , 2021, 13, 185-194.	1.0	31
34	Effects of Dissolved Sulfide, pH, and Temperature on Growth and Survival of Marine Hyperthermophilic Archaea. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6383-6387.	1.4	29
35	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. <i>Frontiers in Microbiology</i> , 2013, 4, 207.	1.5	28
36	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. <i>Frontiers in Microbiology</i> , 2016, 7, 1221.	1.5	25

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37	Predominance of Anaerobic, Spore-Forming Bacteria in Metabolically Active Microbial Communities from Ancient Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
38	Development and application of primers for the class <i>D</i> (phylum <i>C</i> ) enables deep insights into diversity and stratification of subgroups in the marine subsurface. <i>Environmental Microbiology</i> , 2015, 17, 3540-3556.	1.8	22
39	New aminopeptidase from a microbial dark matter archaeon. <i>FASEB Journal</i> , 2015, 29, 4071-4079.	0.2	22
40	Methanogens in the Antarctic Dry Valley permafrost. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	22
41	Inter-laboratory quantification of Bacteria and Archaea in deeply buried sediments of the Baltic Sea (IODP Expedition 347). <i>FEMS Microbiology Ecology</i> , 2017, 93, fix007.	1.3	18
42	Survival and growth of two heterotrophic hydrothermal vent archaea, <i>Pyrococcus</i> strain GB-D and <i>Thermococcus fumicolans</i> , under low pH and high sulfide concentrations in combination with high temperature and pressure regimes. <i>Extremophiles</i> , 2007, 11, 329-342.	0.9	17
43	Beyond known methanogens. <i>Science</i> , 2015, 350, 384-384.	6.0	17
44	Helium, inorganic and organic carbon isotopes of fluids and gases across the Costa Rica convergent margin. <i>Scientific Data</i> , 2019, 6, 284.	2.4	17
45	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. <i>Microbiome</i> , 2021, 9, 110.	4.9	17
46	Microbial community structure and methane-cycling activity of subsurface sediments at Mississippi Canyon 118 before the Deepwater Horizon disaster. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 129, 148-156.	0.6	15
47	Time as a microbial resource. <i>Environmental Microbiology Reports</i> , 2021, 13, 18-21.	1.0	14
48	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0097221.	1.4	13
49	Science depends on nomenclature, but nomenclature is not science. <i>Nature Reviews Microbiology</i> , 2022, 20, 123-124.	13.6	13
50	High <sup>3</sup> He/ <sup>4</sup> He in central Panama reveals a distal connection to the Galápagos plume. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
51	Potential Activities and Long Lifetimes of Organic Carbon-Degrading Extracellular Enzymes in Deep Subsurface Sediments of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2021, 12, 702015.	1.5	10
52	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. <i>PLoS ONE</i> , 2020, 15, e0234839.	1.1	8
53	Permafrost Active Layer Microbes From Ny Ålesund, Svalbard (79°N) Show Autotrophic and Heterotrophic Metabolisms With Diverse Carbon-Degrading Enzymes. <i>Frontiers in Microbiology</i> , 2021, 12, 757812.	1.5	7
54	Evidence for a Growth Zone for Deep-Subsurface Microbial Clades in Near-Surface Anoxic Sediments. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	5

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55	Cryptic Methane-Cycling by Methanogens During Multi-Year Incubation of Estuarine Sediment. <i>Frontiers in Microbiology</i> , 2022, 13, 847563.	1.5	3
56	6. Quantifying microbes in the marine subseafloor: some notes of caution. , 0, , .		2
57	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
58	The Genetics, Biochemistry, and Biophysics of Carbon Cycling by Deep Life. , 2019, , 556-584.		1
59	On the Past, Present, and Future Role of Biology in NASA's Exploration of our Solar System. , 2021, 53, .		0
60	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
61	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
62	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
63	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
64	Draft Genome Sequences of 10 <i>Pseudomonas</i> sp. Isolates from the Active Layer of Permafrost in Ny Å..lesund, Svalbard, Norway. <i>Microbiology Resource Announcements</i> , 2022, , e0020122.	0.3	0