

# 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  | Science depends on nomenclature, but nomenclature is not science. <i>Nature Reviews Microbiology</i> , 2022, 20, 123-124.   | 13.6 | 13        |
| 2  | Cryptic Methane-Cycling by Methanogens During Multi-Year Incubation of Estuarine Sediment. <i>Frontiers in Microbiology</i> , 2022, 13, 847563.   | 1.5  | 3         |
| 3  | Draft Genome Sequences of 10 <i>Pseudomonas</i> sp. Isolates from the Active Layer of Permafrost in Ny Ålesund, Svalbard, Norway. <i>Microbiology Resource Announcements</i> , 2022, , e0020122.                  | 0.3  | 0         |
| 4  | Time as a microbial resource. <i>Environmental Microbiology Reports</i> , 2021, 13, 18-21.  | 1.0  | 14        |
| 5  | <sc>ANME</sc> archaea may drive methane accumulation and removal in estuarine sediments. <i>Environmental Microbiology Reports</i> , 2021, 13, 185-194.   | 1.0  | 31        |
| 6  | On the Past, Present, and Future Role of Biology in NASA's Exploration of our Solar System. , 2021, 53, .   |      | 0         |
| 7  | Effect of tectonic processes on biosphere-geosphere feedbacks across a convergent margin. <i>Nature Geoscience</i> , 2021, 14, 301-306.   | 5.4  | 32        |
| 8  | Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. <i>Microbiome</i> , 2021, 9, 110.  | 4.9  | 17        |
| 9  | Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180.   | 4.4  | 54        |
| 10 | Microbial Taxonomy Run Amok. <i>Trends in Microbiology</i> , 2021, 29, 394-404.   | 3.5  | 38        |
| 11 | 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        |
| 12 | 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        |
| 13 | 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        |
| 14 | 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         |
| 15 | 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         |
| 16 | Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. <i>PLoS ONE</i> , 2020, 15, e0234839.   | 1.1  | 8         |
| 17 | Diversity, ecology and evolution of Archaea. <i>Nature Microbiology</i> , 2020, 5, 887-900.   | 5.9  | 262       |
| 18 | Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.  | 5.9  | 115       |

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|----|--|-----|-----------|
| 19 | Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.  |     | 0         |
| 20 | Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.  |     | 0         |
| 21 | Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.  |     | 0         |
| 22 | Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.  |     | 0         |
| 23 | High proportions of bacteria and archaea across most biomes remain uncultured. ISME Journal, 2019, 13, 3126-3130.  | 4.4 | 264       |
| 24 | The Genetics, Biochemistry, and Biophysics of Carbon Cycling by Deep Life. , 2019, , 556-584.  |     | 1         |
| 25 | Predominance of Anaerobic, Spore-Forming Bacteria in Metabolically Active Microbial Communities from Ancient Siberian Permafrost. Applied and Environmental Microbiology, 2019, 85, .                | 1.4 | 25        |
| 26 | Complex Microbial Communities Drive Iron and Sulfur Cycling in Arctic Fjord Sediments. Applied and Environmental Microbiology, 2019, 85, .   | 1.4 | 58        |
| 27 | Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. MBio, 2019, 10, .   | 1.8 | 45        |
| 28 | Helium, inorganic and organic carbon isotopes of fluids and gases across the Costa Rica convergent margin. Scientific Data, 2019, 6, 284.  | 2.4 | 17        |
| 29 | Microbial Organic Matter Degradation Potential in Baltic Sea Sediments Is Influenced by Depositional Conditions and <i>In Situ</i> Geochemistry. Applied and Environmental Microbiology, 2019, 85, . | 1.4 | 37        |
| 30 | 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        |
| 31 | Estimating Population Turnover Rates by Relative Quantification Methods Reveals Microbial Dynamics in Marine Sediment. Applied and Environmental Microbiology, 2018, 84, .                           | 1.4 | 31        |
| 32 | Phylogenetically Novel Uncultured Microbial Cells Dominate Earth Microbiomes. MSystems, 2018, 3, .   | 1.7 | 273       |
| 33 | Methanogens in the Antarctic Dry Valley permafrost. FEMS Microbiology Ecology, 2018, 94, .   | 1.3 | 22        |
| 34 | Thriving or surviving? Evaluating active microbial guilds in Baltic Sea sediment. Environmental Microbiology Reports, 2017, 9, 528-536.  | 1.0 | 39        |
| 35 | Inter-laboratory quantification of Bacteria and Archaea in deeply buried sediments of the Baltic Sea (IODP Expedition 347). FEMS Microbiology Ecology, 2017, 93, fix007.                             | 1.3 | 18        |
| 36 | Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. Frontiers in Microbiology, 2016, 7, 17.   | 1.5 | 72        |

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|----|---|------|-----------|
| 37 | 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        |
| 38 | Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. <i>Frontiers in Microbiology</i> , 2016, 7, 1221.  | 1.5  | 25        |
| 39 | Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. <i>Genome Announcements</i> , 2016, 4, .   | 0.8  | 2         |
| 40 | 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        |
| 41 | The bright side of microbial dark matter: lessons learned from the uncultivated majority. <i>Current Opinion in Microbiology</i> , 2016, 31, 217-226.   | 2.3  | 241       |
| 42 | 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        |
| 43 | Development and application of primers for the class <i>D</i> ( <i>Dehalococcoidia</i> ) (phylum <i>C</i> ( <i>Chloroflexi</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        |
| 44 | Life under extreme energy limitation: a synthesis of laboratory- and field-based investigations. <i>FEMS Microbiology Reviews</i> , 2015, 39, 688-728.  | 3.9  | 288       |
| 45 | New aminopeptidase from a microbial dark matter archaeon. <i>FASEB Journal</i> , 2015, 29, 4071-4079.   | 0.2  | 22        |
| 46 | Beyond known methanogens. <i>Science</i> , 2015, 350, 384-384.  | 6.0  | 17        |
| 47 | Genome sequencing of a single cell of the widely distributed marine subsurface <i>Dehalococcoidia</i> phylum <i>Chloroflexi</i> . <i>ISME Journal</i> , 2014, 8, 383-397.   | 4.4  | 172       |
| 48 | Predominant archaea in marine sediments degrade detrital proteins. <i>Nature</i> , 2013, 496, 215-218.  | 13.7 | 526       |
| 49 | Meta-Analysis of Quantification Methods Shows that Archaea and Bacteria Have Similar Abundances in the Subseafloor. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7790-7799.  | 1.4  | 113       |
| 50 | Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. <i>Frontiers in Microbiology</i> , 2013, 4, 207.  | 1.5  | 28        |
| 51 | Anaerobic oxidation of methane at different temperature regimes in Guaymas Basin hydrothermal sediments. <i>ISME Journal</i> , 2012, 6, 1018-1031.  | 4.4  | 149       |
| 52 | Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. <i>ISME Journal</i> , 2012, 6, 1949-1965.   | 4.4  | 281       |
| 53 | Spatial heterogeneity and underlying geochemistry of phylogenetically diverse orange and white Beggiatoa mats in Guaymas Basin hydrothermal sediments. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2012, 67, 21-31.  | 0.6  | 73        |
| 54 | Environmental evidence for net methane production and oxidation in putative Anaerobic Methanotrophic (ANME) archaea. <i>Environmental Microbiology</i> , 2011, 13, 2548-2564.   | 1.8  | 146       |

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|----|--|-----|-----------|
| 55 | 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        |
| 56 | Spatial Structure and Activity of Sedimentary Microbial Communities Underlying a <i>Beggiatoa</i> spp. Mat in a Gulf of Mexico Hydrocarbon Seep. <i>PLoS ONE</i> , 2010, 5, e8738.   | 1.1 | 117       |
| 57 | Metabolic variability in seafloor brines revealed by carbon and sulphur dynamics. <i>Nature Geoscience</i> , 2009, 2, 349-354.   | 5.4 | 111       |
| 58 | 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        |
| 59 | Heterotrophic Archaea dominate sedimentary subsurface ecosystems off Peru. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3846-3851.  | 3.3 | 654       |
| 60 | An Anaerobic Methane-Oxidizing Community of ANME-1b Archaea in Hypersaline Gulf of Mexico Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7218-7230.  | 1.4 | 206       |
| 61 | Methanogen Diversity Evidenced by Molecular Characterization of Methyl Coenzyme M Reductase A ( ) Tj ETQq1 1 0.784314 rgBT /Over<br><i>Microbiology</i> , 2005, 71, 4592-4601.   | 1.4 | 152       |
| 62 | 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        |
| 63 | Sulfide Ameliorates Metal Toxicity for Deep-Sea Hydrothermal Vent Archaea. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2551-2555.  | 1.4 | 56        |
| 64 | 6. Quantifying microbes in the marine subseafloor: some notes of caution. , 0, , .   |     | 2         |