

Alexander Loy

List of Publications by Year in descending order

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104
papers

15,571
citations

18436

62
h-index

33814

99
g-index

120
all docs

120
docs citations

120
times ranked

16493
citing authors

#	ARTICLE	IF	CITATIONS
1	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. ISME Journal, 2021, 15, 833-847.	4.4	38
2	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. ISME Journal, 2021, 15, 2779-2791.	4.4	30
3	An Economical and Flexible Dual Barcoding, Two-Step PCR Approach for Highly Multiplexed Amplicon Sequencing. Frontiers in Microbiology, 2021, 12, 669776.	1.5	48
4	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. ISME Journal, 2021, 15, 3159-3180.	4.4	54
5	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. Nature Microbiology, 2021, 6, 885-898.	5.9	29
6	Environmental and Intestinal Phylum Firmicutes Bacteria Metabolize the Plant Sugar Sulfoquinovose via a 6-Deoxy-6-sulfofructose Transaldolase Pathway. IScience, 2020, 23, 101510.	1.9	32
7	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. PLoS ONE, 2020, 15, e0234839.	1.1	8
8	Microbiome definition re-visited: old concepts and new challenges. Microbiome, 2020, 8, 103.	4.9	903
9	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5972-6016.	0.8	830
10	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
11	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
12	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
13	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. , 2020, 15, e0234839.		0
14	Draft Genome Sequence of <i>Desulfosporosinus</i> sp. Strain Sb-LF, Isolated from an Acidic Peatland in Germany. Microbiology Resource Announcements, 2019, 8, .	0.3	8
15	Diversity decoupled from sulfur isotope fractionation in a sulfate-reducing microbial community. Geobiology, 2019, 17, 660-675.	1.1	7
16	Draft Genome Sequence of <i>Desulfosporosinus fructosivorans</i> Strain 63.6F T, Isolated from Marine Sediment in the Baltic Sea. Microbiology Resource Announcements, 2019, 8, .	0.3	1
17	A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome. Nature Communications, 2019, 10, 4366.	5.8	82
18	<i>Mucispirillum schaedleri</i> Antagonizes <i>Salmonella</i> Virulence to Protect Mice against Colitis. Cell Host and Microbe, 2019, 25, 681-694.e8.	5.1	205

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19	Historical Factors Associated With Past Environments Influence the Biogeography of Thermophilic Endospores in Arctic Marine Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 245.	1.5	21
20	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019, 10, .	1.8	35
21	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 2558.	1.5	16
22	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	23
23	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. <i>ISME Journal</i> , 2018, 12, 1715-1728.	4.4	347
24	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168
25	Draft Genome Sequence of <i>Telmatospirillum siberiense</i> 26-4b1, an Acidotolerant Peatland Alphaproteobacterium Potentially Involved in Sulfur Cycling. <i>Genome Announcements</i> , 2018, 6, .	0.8	13
26	Bacterial interactions during sequential degradation of cyanobacterial necromass in a sulfidic arctic marine sediment. <i>Environmental Microbiology</i> , 2018, 20, 2927-2940.	1.8	50
27	Stable-Isotope Probing of Human and Animal Microbiome Function. <i>Trends in Microbiology</i> , 2018, 26, 999-1007.	3.5	57
28	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of <i>Mucispirillum schaedleri</i> , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , 2017, 2, .	1.7	148
29	HuR Small-Molecule Inhibitor Elicits Differential Effects in Adenomatous Polyposis and Colorectal Carcinogenesis. <i>Cancer Research</i> , 2017, 77, 2424-2438.	0.4	75
30	The life sulfuric: microbial ecology of sulfur cycling in marine sediments. <i>Environmental Microbiology Reports</i> , 2017, 9, 323-344.	1.0	260
31	Depth Distribution and Assembly of Sulfate-Reducing Microbial Communities in Marine Sediments of Aarhus Bay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	53
32	Stable Isotope Techniques for the Assessment of Host and Microbiota Response During Gastrointestinal Dysfunction. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2017, 64, 8-14.	0.9	11
33	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	1.8	107
34	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , 2017, 2, 16215.	5.9	313
35	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. <i>Microbiome</i> , 2017, 5, 126.	4.9	26
36	Diversity analysis of sulfite- and sulfate-reducing microorganisms by multiplex <i>dsrA</i> and <i>dsrB</i> amplicon sequencing using new primers and mock community-optimized bioinformatics. <i>Environmental Microbiology</i> , 2016, 18, 2994-3009.	1.8	98

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37	Environmental Enteric Dysfunction and Growth Failure/Stunting in Global Child Health. <i>Pediatrics</i> , 2016, 138, .	1.0	184
38	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
39	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
40	Bacterial nutrient foraging in a mouse model of enteral nutrient deprivation: insight into the gut origin of sepsis. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, G734-G743.	1.6	25
41	Gypsum amendment to rice paddy soil stimulated bacteria involved in sulfur cycling but largely preserved the phylogenetic composition of the total bacterial community. <i>Environmental Microbiology Reports</i> , 2016, 8, 413-423.	1.0	29
42	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. <i>ISME Journal</i> , 2016, 10, 2365-2375.	4.4	159
43	probeBase™ an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Research</i> , 2016, 44, D586-D589.	6.5	163
44	Phylogenetic and genomic analysis of <i>Methanomassiliicoccales</i> in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv149.	1.3	110
45	Activity and community structures of sulfate-reducing microorganisms in polar, temperate and tropical marine sediments. <i>ISME Journal</i> , 2016, 10, 796-809.	4.4	85
46	A flexible and economical barcoding approach for highly multiplexed amplicon sequencing of diverse target genes. <i>Frontiers in Microbiology</i> , 2015, 6, 731.	1.5	164
47	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , 2015, 6, 1408.	1.5	106
48	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , 2015, 9, 1152-1165.	4.4	331
49	Intestinal Epithelial Cell Tyrosine Kinase 2 Transduces IL-22 Signals To Protect from Acute Colitis. <i>Journal of Immunology</i> , 2015, 195, 5011-5024.	0.4	40
50	Functionally relevant diversity of closely related <i>Nitrospira</i> in activated sludge. <i>ISME Journal</i> , 2015, 9, 643-655.	4.4	172
51	Type I interferons have opposing effects during the emergence and recovery phases of colitis. <i>European Journal of Immunology</i> , 2014, 44, 2749-2760.	1.6	39
52	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <i>ISME Journal</i> , 2014, 8, 1153-1165.	4.4	139
53	<i>NxrB</i> encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing <i>Nitrospira</i> . <i>Environmental Microbiology</i> , 2014, 16, 3055-3071.	1.8	280
54	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014, 8, 1101-1114.	4.4	174

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55	Colonization resistance and microbial ecophysiology: using gnotobiotic mouse models and single-cell technology to explore the intestinal jungle. <i>FEMS Microbiology Reviews</i> , 2013, 37, 793-829.	3.9	85
56	Temporal Bacterial Community Dynamics Vary Among Ulcerative Colitis Patients After Fecal Microbiota Transplantation. <i>American Journal of Gastroenterology</i> , 2013, 108, 1620-1630.	0.2	298
57	Host-compound foraging by intestinal microbiota revealed by single-cell stable isotope probing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4720-4725.	3.3	210
58	Dispersal of thermophilic <i>Desulfotomaculum</i> endospores into Baltic Sea sediments over thousands of years. <i>ISME Journal</i> , 2013, 7, 72-84.	4.4	82
59	Intestinal Bacteria Modify Lymphoma Incidence and Latency by Affecting Systemic Inflammatory State, Oxidative Stress, and Leukocyte Genotoxicity. <i>Cancer Research</i> , 2013, 73, 4222-4232.	0.4	68
60	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765, <i>Desulfosporosinus youngiae</i> DSM17734, <i>Desulfosporosinus meridiei</i> DSM13257, and <i>Desulfosporosinus acidiphilus</i> DSM22704. <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	1.0	73
61	Barcoded Primers Used in Multiplex Amplicon Pyrosequencing Bias Amplification. <i>Applied and Environmental Microbiology</i> , 2012, 78, 612-612.	1.4	146
62	Sulfate-reducing microorganisms in wetlands –“fameless actors in carbon cycling and climate change. <i>Frontiers in Microbiology</i> , 2012, 3, 72.	1.5	264
63	Three manganese oxide-rich marine sediments harbor similar communities of acetate-oxidizing manganese-reducing bacteria. <i>ISME Journal</i> , 2012, 6, 2078-2090.	4.4	95
64	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <i>ISME Journal</i> , 2012, 6, 2091-2106.	4.4	291
65	<i>amoA</i> -based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of <i>amoA</i> genes from soils of four different geographic regions. <i>Environmental Microbiology</i> , 2012, 14, 525-539.	1.8	485
66	Modeling Formamide Denaturation of Probe-Target Hybrids for Improved Microarray Probe Design in Microbial Diagnostics. <i>PLoS ONE</i> , 2012, 7, e43862.	1.1	16
67	Barcoded Primers Used in Multiplex Amplicon Pyrosequencing Bias Amplification. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7846-7849.	1.4	514
68	Systematic Spatial Bias in DNA Microarray Hybridization Is Caused by Probe Spot Position-Dependent Variability in Lateral Diffusion. <i>PLoS ONE</i> , 2011, 6, e23727.	1.1	18
69	Microorganisms with Novel Dissimilatory (Bi)Sulfite Reductase Genes Are Widespread and Part of the Core Microbiota in Low-Sulfate Peatlands. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1231-1242.	1.4	49
70	<i>Paracatenula</i> , an ancient symbiosis between thiotrophic <i>Alphaproteobacteria</i> and catenulid flatworms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12078-12083.	3.3	75
71	Phylogenetic Microarrays for Cultivation-Independent Identification and Metabolic Characterization of Microorganisms in Complex Samples. <i>Methods in Molecular Biology</i> , 2011, 688, 187-206.	0.4	5
72	A “rare biosphere” microorganism contributes to sulfate reduction in a peatland. <i>ISME Journal</i> , 2010, 4, 1591-1602.	4.4	303

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73	Thermophilic anaerobes in Arctic marine sediments induced to mineralize complex organic matter at high temperature. <i>Environmental Microbiology</i> , 2010, 12, 1089-1104.	1.8	61
74	Probing Identity and Physiology of Uncultured Microorganisms with Isotope Labeling Techniques. , 2010, , 127-145.		4
75	Isotope array analysis of <i>Rhodocyclales</i> uncovers functional redundancy and versatility in an activated sludge. <i>ISME Journal</i> , 2009, 3, 1349-1364.	4.4	86
76	High genetic similarity between two geographically distinct strains of the sulfur-oxidizing symbiont <i>Candidatus Thiobios zoothamnicoli</i> ™. <i>FEMS Microbiology Ecology</i> , 2009, 67, 229-241.	1.3	35
77	Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. <i>Environmental Microbiology</i> , 2009, 11, 289-299.	1.8	162
78	16S rRNA gene-based phylogenetic microarray for simultaneous identification of members of the genus <i>Burkholderia</i> . <i>Environmental Microbiology</i> , 2009, 11, 779-800.	1.8	22
79	A Constant Flux of Diverse Thermophilic Bacteria into the Cold Arctic Seabed. <i>Science</i> , 2009, 325, 1541-1544.	6.0	189
80	Biogeography of sulfate-reducing prokaryotes in river floodplains. <i>FEMS Microbiology Ecology</i> , 2008, 64, 395-406.	1.3	36
81	probeCheck – a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898.	1.8	170
82	Multiple bacterial symbionts in two species of co-occurring gutless oligochaete worms from Mediterranean sea grass sediments. <i>Environmental Microbiology</i> , 2008, 10, 3404-3416.	1.8	55
83	Evolution and Ecology of Microbes Dissimilating Sulfur Compounds: Insights from Siroheme Sulfite Reductases. , 2008, , 46-59.		24
84	probeBase—an online resource for rRNA-targeted oligonucleotide probes: new features 2007. <i>Nucleic Acids Research</i> , 2007, 35, D800-D804.	6.5	421
85	Molecular strategies for studies of natural populations of sulphate-reducing microorganisms. , 2007, , 39-116.		12
86	Improved 16S rRNA-targeted probe set for analysis of sulfate-reducing bacteria by fluorescence in situ hybridization. <i>Journal of Microbiological Methods</i> , 2007, 69, 523-528.	0.7	98
87	Diversity and abundance of sulfate-reducing microorganisms in the sulfate and methane zones of a marine sediment, Black Sea. <i>Environmental Microbiology</i> , 2007, 9, 131-142.	1.8	233
88	Diversity of sulfate-reducing bacteria from an extreme hypersaline sediment, Great Salt Lake (Utah). <i>FEMS Microbiology Ecology</i> , 2007, 60, 287-298.	1.3	117
89	Unravelling Microbial Communities with DNA-Microarrays: Challenges and Future Directions. <i>Microbial Ecology</i> , 2007, 53, 498-506.	1.4	95
90	Highly parallel microbial diagnostics using oligonucleotide microarrays. <i>Clinica Chimica Acta</i> , 2006, 363, 106-119.	0.5	123

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91	Linking microbial community structure with function: fluorescence in situ hybridization-microautoradiography and isotope arrays. <i>Current Opinion in Biotechnology</i> , 2006, 17, 83-91.	3.3	166
92	Non-Sulfate-Reducing, Syntrophic Bacteria Affiliated with Desulfotomaculum Cluster I Are Widely Distributed in Methanogenic Environments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2080-2091.	1.4	165
93	Oligonucleotide microarray for identification of <i>Enterococcus</i> species. <i>FEMS Microbiology Letters</i> , 2005, 246, 133-142.	0.7	47
94	New Insights into Metabolic Properties of Marine Bacteria Encoding Proteorhodopsins. <i>PLoS Biology</i> , 2005, 3, e273.	2.6	218
95	Lateral Gene Transfer of Dissimilatory (Bi)Sulfite Reductase Revisited. <i>Journal of Bacteriology</i> , 2005, 187, 2203-2208.	1.0	153
96	Diversity of Bacteria Growing in Natural Mineral Water after Bottling. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3624-3632.	1.4	78
97	16S rRNA Gene-Based Oligonucleotide Microarray for Environmental Monitoring of the Betaproteobacterial Order <i>Rhodocyclales</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 1373-1386.	1.4	231
98	Functional Marker Genes for Identification of Sulfate-Reducing Prokaryotes. <i>Methods in Enzymology</i> , 2005, 397, 469-489.	0.4	86
99	Microarray and Functional Gene Analyses of Sulfate-Reducing Prokaryotes in Low-Sulfate, Acidic Fens Reveal Cooccurrence of Recognized Genera and Novel Lineages. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6998-7009.	1.4	188
100	probeBase: an online resource for rRNA-targeted oligonucleotide probes. <i>Nucleic Acids Research</i> , 2003, 31, 514-516.	6.5	345
101	Oligonucleotide Microarray for 16S rRNA Gene-Based Detection of All Recognized Lineages of Sulfate-Reducing Prokaryotes in the Environment. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5064-5081.	1.4	622
102	The Microbial Community Composition of a Nitrifying-Denitrifying Activated Sludge from an Industrial Sewage Treatment Plant Analyzed by the Full-Cycle rRNA Approach. <i>Systematic and Applied Microbiology</i> , 2002, 25, 84-99.	1.2	338
103	Bacterial community composition and function in sewage treatment systems. <i>Current Opinion in Biotechnology</i> , 2002, 13, 218-227.	3.3	488
104	Microbial community composition and function in wastewater treatment plants. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 665-680.	0.7	341