

# Alexander Loy

## List of Publications by Year in Descending Order

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**Version:** 2024-04-23

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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.

110  
papers

10,362  
citations

55  
h-index

101  
g-index

120  
ext. papers

13,711  
ext. citations

8.6  
avg, IF

6.12  
L-index

#	Paper	IF	Citations
110	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , <b>2021</b> , 15, 2779-2791	11.9	5
109	An Economical and Flexible Dual Barcoding, Two-Step PCR Approach for Highly Multiplexed Amplicon Sequencing. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 669776	5.7	7
108	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , <b>2021</b> , 15, 3159-3180	11.9	12
107	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , <b>2021</b> , 6, 885-898	26.6	1
106	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. <i>ISME Journal</i> , <b>2021</b> , 15, 833-847	11.9	5
105	Microbiome definition re-visited: old concepts and new challenges. <i>Microbiome</i> , <b>2020</b> , 8, 103	16.6	271
104	Proposal to reclassify the proteobacterial classes and , and the phylum into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 5972-6016	2.2	205
103	Environmental and Intestinal Phylum Firmicutes Bacteria Metabolize the Plant Sugar Sulfoquinovose via a 6-Deoxy-6-sulfofructose Transaldolase Pathway. <i>IScience</i> , <b>2020</b> , 23, 101510	6.1	17
102	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment. <i>PLoS ONE</i> , <b>2020</b> , 15, e0234839	3.7	6
101	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment <b>2020</b> , 15, e0234839		
100	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment <b>2020</b> , 15, e0234839		
99	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment <b>2020</b> , 15, e0234839		
98	Woeseiales transcriptional response to shallow burial in Arctic fjord surface sediment <b>2020</b> , 15, e0234839		
97	Draft Genome Sequence of <i>Desulfosporosinus fructosivorans</i> Strain 63.6F, Isolated from Marine Sediment in the Baltic Sea. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
96	A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome. <i>Nature Communications</i> , <b>2019</b> , 10, 4366	17.4	34
95	<i>Mucispirillum schaedleri</i> Antagonizes <i>Salmonella</i> Virulence to Protect Mice against Colitis. <i>Cell Host and Microbe</i> , <b>2019</b> , 25, 681-694.e8	23.4	96
94	Historical Factors Associated With Past Environments Influence the Biogeography of Thermophilic Endospores in Arctic Marine Sediments. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 245	5.7	5

93	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , <b>2019</b> , 10,	7.8	22
92	Draft Genome Sequence of sp. Strain Sb-LF, Isolated from an Acidic Peatland in Germany. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
91	Diversity decoupled from sulfur isotope fractionation in a sulfate-reducing microbial community. <i>Geobiology</i> , <b>2019</b> , 17, 660-675	4.3	3
90	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2558	5.7	10
89	Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy. <i>Science Translational Medicine</i> , <b>2019</b> , 11,	17.5	11
88	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. <i>ISME Journal</i> , <b>2018</b> , 12, 1715-1728	11.9	165
87	Peatland Acidobacteria with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , <b>2018</b> , 12, 1729-1742	11.9	58
86	Draft Genome Sequence of 26-4b1, an Acidotolerant Peatland Alphaproteobacterium Potentially Involved in Sulfur Cycling. <i>Genome Announcements</i> , <b>2018</b> , 6,		6
85	Bacterial interactions during sequential degradation of cyanobacterial necromass in a sulfidic arctic marine sediment. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2927-2940	5.2	27
84	Stable-Isotope Probing of Human and Animal Microbiome Function. <i>Trends in Microbiology</i> , <b>2018</b> , 26, 999-1007	12.4	36
83	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , <b>2017</b> , 2,	7.6	88
82	HuR Small-Molecule Inhibitor Elicits Differential Effects in Adenomatosis Polyposis and Colorectal Carcinogenesis. <i>Cancer Research</i> , <b>2017</b> , 77, 2424-2438	10.1	48
81	The life sulfuric: microbial ecology of sulfur cycling in marine sediments. <i>Environmental Microbiology Reports</i> , <b>2017</b> , 9, 323-344	3.7	142
80	Depth Distribution and Assembly of Sulfate-Reducing Microbial Communities in Marine Sediments of Aarhus Bay. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	36
79	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. <i>Microbiome</i> , <b>2017</b> , 5, 126	16.6	19
78	Stable Isotope Techniques for the Assessment of Host and Microbiota Response During Gastrointestinal Dysfunction. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , <b>2017</b> , 64, 8-14	2.8	7
77	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 4939-4952	5.2	57
76	Activity and community structures of sulfate-reducing microorganisms in polar, temperate and tropical marine sediments. <i>ISME Journal</i> , <b>2016</b> , 10, 796-809	11.9	41

75	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , <b>2016</b> , 537, 689-693	50.4	400
74	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> , <b>2016</b> , 311, G734-G743	5.1	20
73	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> , <b>2016</b> , 8, 413-23	3.7	19
72	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. <i>ISME Journal</i> , <b>2016</b> , 10, 2365-75	11.9	87
71	probeBase--an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D586-9	20.1	119
70	Phylogenetic and genomic analysis of Methanomassiliicoccales in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , <b>2016</b> , 92,	4.3	78
69	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16215	26.6	168
68	Diversity analysis of sulfite- and sulfate-reducing microorganisms by multiplex dsrA and dsrB amplicon sequencing using new primers and mock community-optimized bioinformatics. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 2994-3009	5.2	50
67	Environmental Enteric Dysfunction and Growth Failure/Stunting in Global Child Health. <i>Pediatrics</i> , <b>2016</b> , 138,	7.4	108
66	Single-Cell Genome and Group-Specific dsrAB Sequencing Implicate Marine Members of the Class Dehalococcoidia (Phylum Chloroflexi) in Sulfur Cycling. <i>MBio</i> , <b>2016</b> , 7,	7.8	33
65	Intestinal Epithelial Cell Tyrosine Kinase 2 Transduces IL-22 Signals To Protect from Acute Colitis. <i>Journal of Immunology</i> , <b>2015</b> , 195, 5011-24	5.3	33
64	Functionally relevant diversity of closely related Nitrospira in activated sludge. <i>ISME Journal</i> , <b>2015</b> , 9, 643-55	11.9	112
63	A flexible and economical barcoding approach for highly multiplexed amplicon sequencing of diverse target genes. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 731	5.7	106
62	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1408	5.7	67
61	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , <b>2015</b> , 9, 1152-65	11.9	176
60	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , <b>2014</b> , 8, 1101-14	11.9	121
59	Type I interferons have opposing effects during the emergence and recovery phases of colitis. <i>European Journal of Immunology</i> , <b>2014</b> , 44, 2749-60	6.1	23
58	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. <i>ISME Journal</i> , <b>2014</b> , 8, 1153-65	11.9	85

57	NxrB encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing Nitrospira. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 3055-71	5.2	193
56	Colonization resistance and microbial ecophysiology: using gnotobiotic mouse models and single-cell technology to explore the intestinal jungle. <i>FEMS Microbiology Reviews</i> , <b>2013</b> , 37, 793-829	15.1	75
55	Temporal bacterial community dynamics vary among ulcerative colitis patients after fecal microbiota transplantation. <i>American Journal of Gastroenterology</i> , <b>2013</b> , 108, 1620-30	0.7	254
54	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> , <b>2013</b> , 110, 4720-5	11.5	147
53	Dispersal of thermophilic <i>Desulfotomaculum</i> endospores into Baltic Sea sediments over thousands of years. <i>ISME Journal</i> , <b>2013</b> , 7, 72-84	11.9	58
52	Intestinal bacteria modify lymphoma incidence and latency by affecting systemic inflammatory state, oxidative stress, and leukocyte genotoxicity. <i>Cancer Research</i> , <b>2013</b> , 73, 4222-32	10.1	48
51	amoA-based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of amoA genes from soils of four different geographic regions. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 525-39	5.2	402
50	Three manganese oxide-rich marine sediments harbor similar communities of acetate-oxidizing manganese-reducing bacteria. <i>ISME Journal</i> , <b>2012</b> , 6, 2078-90	11.9	72
49	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <i>ISME Journal</i> , <b>2012</b> , 6, 2091-106	11.9	208
48	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6300-1	3.5	46
47	Barcoded Primers Used in Multiplex Amplicon Pyrosequencing Bias Amplification. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 612-612	4.8	20
46	Sulfate-reducing microorganisms in wetlands - fameless actors in carbon cycling and climate change. <i>Frontiers in Microbiology</i> , <b>2012</b> , 3, 72	5.7	174
45	Modeling formamide denaturation of probe-target hybrids for improved microarray probe design in microbial diagnostics. <i>PLoS ONE</i> , <b>2012</b> , 7, e43862	3.7	10
44	Barcoded primers used in multiplex amplicon pyrosequencing bias amplification. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 7846-9	4.8	377
43	Systematic spatial bias in DNA microarray hybridization is caused by probe spot position-dependent variability in lateral diffusion. <i>PLoS ONE</i> , <b>2011</b> , 6, e23727	3.7	16
42	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> , <b>2011</b> , 77, 1231-42	4.8	35
41	Paracatenula, an ancient symbiosis between thiotrophic Alphaproteobacteria and catenulid flatworms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 12078-83	11.5	57
40	Phylogenetic microarrays for cultivation-independent identification and metabolic characterization of microorganisms in complex samples. <i>Methods in Molecular Biology</i> , <b>2011</b> , 688, 187-206	1.4	5

39	A rare biosphere microorganism contributes to sulfate reduction in a peatland. <i>ISME Journal</i> , <b>2010</b> , 4, 1591-602	11.9	208
38	Thermophilic anaerobes in Arctic marine sediments induced to mineralize complex organic matter at high temperature. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 1089-104	5.2	45
37	Geomicrobiology: Molecular and Environmental Perspective <b>2010</b> ,		5
36	Probing Identity and Physiology of Uncultured Microorganisms with Isotope Labeling Techniques <b>2010</b> , 127-145		4
35	Isotope array analysis of Rhodocyclales uncovers functional redundancy and versatility in an activated sludge. <i>ISME Journal</i> , <b>2009</b> , 3, 1349-64	11.9	74
34	High genetic similarity between two geographically distinct strains of the sulfur-oxidizing symbiont <i>Candidatus Thiobios zoothamnicoli</i> <i>FEMS Microbiology Ecology</i> , <b>2009</b> , 67, 229-41	4.3	16
33	Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 289-99	5.2	111
32	16S rRNA gene-based phylogenetic microarray for simultaneous identification of members of the genus <i>Burkholderia</i> . <i>Environmental Microbiology</i> , <b>2009</b> , 11, 779-800	5.2	21
31	A constant flux of diverse thermophilic bacteria into the cold Arctic seabed. <i>Science</i> , <b>2009</b> , 325, 1541-4	33.3	145
30	probeCheck--a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2894-8	5.2	154
29	Multiple bacterial symbionts in two species of co-occurring gutless oligochaete worms from Mediterranean sea grass sediments. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 3404-16	5.2	46
28	Biogeography of sulfate-reducing prokaryotes in river floodplains. <i>FEMS Microbiology Ecology</i> , <b>2008</b> , 64, 395-406	4.3	31
27	Evolution and Ecology of Microbes Dissimilating Sulfur Compounds: Insights from Siroheme Sulfite Reductases <b>2008</b> , 46-59		15
26	Diversity and abundance of sulfate-reducing microorganisms in the sulfate and methane zones of a marine sediment, Black Sea. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 131-42	5.2	193
25	Diversity of sulfate-reducing bacteria from an extreme hypersaline sediment, Great Salt Lake (Utah). <i>FEMS Microbiology Ecology</i> , <b>2007</b> , 60, 287-98	4.3	97
24	Unravelling microbial communities with DNA-microarrays: challenges and future directions. <i>Microbial Ecology</i> , <b>2007</b> , 53, 498-506	4.4	86
23	probeBase--an online resource for rRNA-targeted oligonucleotide probes: new features 2007. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D800-4	20.1	373
22	Improved 16S rRNA-targeted probe set for analysis of sulfate-reducing bacteria by fluorescence in situ hybridization. <i>Journal of Microbiological Methods</i> , <b>2007</b> , 69, 523-8	2.8	87

21	Highly parallel microbial diagnostics using oligonucleotide microarrays. <i>Clinica Chimica Acta</i> , <b>2006</b> , 363, 106-19	6.2	115
20	Linking microbial community structure with function: fluorescence in situ hybridization-microautoradiography and isotope arrays. <i>Current Opinion in Biotechnology</i> , <b>2006</b> , 17, 83-91	11.4	146
19	Non-sulfate-reducing, syntrophic bacteria affiliated with desulfotomaculum cluster I are widely distributed in methanogenic environments. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 2080-91	4.8	147
18	16S rRNA gene-based oligonucleotide microarray for environmental monitoring of the betaproteobacterial order "Rhodocyclales". <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 1373-86	4.8	209
17	Functional marker genes for identification of sulfate-reducing prokaryotes. <i>Methods in Enzymology</i> , <b>2005</b> , 397, 469-89	1.7	74
16	Oligonucleotide microarray for identification of Enterococcus species. <i>FEMS Microbiology Letters</i> , <b>2005</b> , 246, 133-42	2.9	45
15	New insights into metabolic properties of marine bacteria encoding proteorhodopsins. <i>PLoS Biology</i> , <b>2005</b> , 3, e273	9.7	180
14	Lateral gene transfer of dissimilatory (bi)sulfite reductase revisited. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 2203-8	3.5	132
13	Diversity of bacteria growing in natural mineral water after bottling. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 3624-32	4.8	68
12	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> , <b>2004</b> , 70, 6998-7009	4.8	164
11	probeBase: an online resource for rRNA-targeted oligonucleotide probes. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 514-6	20.1	302
10	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> , <b>2002</b> , 25, 84-99	4.2	310
9	Bacterial community composition and function in sewage treatment systems. <i>Current Opinion in Biotechnology</i> , <b>2002</b> , 13, 218-27	11.4	435
8	Microbial community composition and function in wastewater treatment plants. <i>Antonie Van Leeuwenhoek</i> , <b>2002</b> , 81, 665-80	2.1	287
7	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> , <b>2002</b> , 68, 5064-81	4.8	541
6	Molecular strategies for studies of natural populations of sulphate-reducing microorganisms	39-116	11
5	Ecogenomics and biogeochemical impacts of uncultivated globally abundant ocean viruses		5
4	Novel taxa of Acidobacteriota involved in seafloor sulfur cycling		5

3	Growth arrest in the active rare biosphere	2
2	DNA-foraging bacteria in the seafloor	4
1	Activated Sludge and Biofilms: Molecular Techniques for Determining Community Composition	3