

# Gary L Andersen

## List of Publications by Year in descending order

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157  
papers

49,578  
citations

12322

69  
h-index

6990

154  
g-index

160  
all docs

160  
docs citations

160  
times ranked

53182  
citing authors

#	ARTICLE	IF	CITATIONS
1	Greengenes, a Chimera-Checked 16S rRNA Gene Database and Workbench Compatible with ARB. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5069-5072.	1.4	9,859
2	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
3	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012, 6, 610-618.	4.4	4,581
4	PyNAST: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010, 26, 266-267.	1.8	3,400
5	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
6	Deciphering the Rhizosphere Microbiome for Disease-Suppressive Bacteria. <i>Science</i> , 2011, 332, 1097-1100.	6.0	2,135
7	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	6.0	1,109
8	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.	6.5	918
9	Chronic kidney disease alters intestinal microbial flora. <i>Kidney International</i> , 2013, 83, 308-315.	2.6	828
10	Urban aerosols harbor diverse and dynamic bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 299-304.	3.3	593
11	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. <i>Nucleic Acids Research</i> , 2008, 36, e120-e120.	6.5	508
12	Expansion of Urease- and Uricase-Containing, Indole- and p-Cresol-Forming and Contraction of Short-Chain Fatty Acid-Producing Intestinal Microbiota in ESRD. <i>American Journal of Nephrology</i> , 2014, 39, 230-237.	1.4	478
13	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	6.0	474
14	High-Density Universal 16S rRNA Microarray Analysis Reveals Broader Diversity than Typical Clone Library When Sampling the Environment. <i>Microbial Ecology</i> , 2007, 53, 371-383.	1.4	416
15	Application of a High-Density Oligonucleotide Microarray Approach To Study Bacterial Population Dynamics during Uranium Reduction and Reoxidation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6288-6298.	1.4	404
16	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. <i>PLoS ONE</i> , 2010, 5, e11044.	1.1	395
17	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009, 3, 512-521.	4.4	364
18	Long-Term Sustainability of a High-Energy, Low-Diversity Crustal Biome. <i>Science</i> , 2006, 314, 479-482.	6.0	350

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19	Succession of Hydrocarbon-Degrading Bacteria in the Aftermath of the <i>Deepwater Horizon</i> Oil Spill in the Gulf of Mexico. <i>Environmental Science &amp; Technology</i> , 2013, 47, 10860-10867.	4.6	344
20	Selective progressive response of soil microbial community to wild oat roots. <i>ISME Journal</i> , 2009, 3, 168-178.	4.4	306
21	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. <i>ISME Journal</i> , 2008, 2, 1146-1156.	4.4	299
22	High-Density Microarray of Small-Subunit Ribosomal DNA Probes. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2535-2541.	1.4	277
23	Sequence-specific identification of 18 pathogenic microorganisms using microarray technology. <i>Molecular and Cellular Probes</i> , 2002, 16, 119-127.	0.9	258
24	Oil Impacts on Coastal Wetlands: Implications for the Mississippi River Delta Ecosystem after the Deepwater Horizon Oil Spill. <i>BioScience</i> , 2012, 62, 562-574.	2.2	257
25	Whole-Genome Transcriptional Analysis of Heavy Metal Stresses in <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2005, 187, 8437-8449.	1.0	247
26	Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. <i>ISME Journal</i> , 2009, 3, 738-744.	4.4	228
27	Soil Microbial Community Successional Patterns during Forest Ecosystem Restoration. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6158-6164.	1.4	226
28	PhyloChip hybridization uncovered an enormous bacterial diversity in the rhizosphere of different potato cultivars: many common and few cultivar-dependent taxa. <i>FEMS Microbiology Ecology</i> , 2011, 75, 497-506.	1.3	198
29	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. <i>Nature Microbiology</i> , 2019, 4, 603-613.	5.9	187
30	Bacterial Community Structure in Geographically Distributed Biological Wastewater Treatment Reactors. <i>Environmental Science &amp; Technology</i> , 2010, 44, 7391-7396.	4.6	180
31	Complete Genome Sequence of <i>Yersinia pestis</i> Strains Antiqua and Nepal516: Evidence of Gene Reduction in an Emerging Pathogen. <i>Journal of Bacteriology</i> , 2006, 188, 4453-4463.	1.0	174
32	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 231.	1.2	170
33	Genome Differences That Distinguish <i>Bacillus anthracis</i> from <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 2755-2764.	1.4	167
34	Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 1954-1962.	1.8	166
35	Pyrosequencing Analysis of Bacterial Biofilm Communities in Water Meters of a Drinking Water Distribution System. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5631-5635.	1.4	166
36	Complexity and Variability of Gut Commensal Microbiota in Polyphagous Lepidopteran Larvae. <i>PLoS ONE</i> , 2012, 7, e36978.	1.1	162

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37	Environmental microarray analyses of Antarctic soil microbial communities. <i>ISME Journal</i> , 2009, 3, 340-351.	4.4	156
38	Identification by Subtractive Hybridization of Sequences Specific for <i>Salmonella enterica</i> Serovar Enteritidis. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4984-4991.	1.4	152
39	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , 2016, 7, e01669-15.	1.8	151
40	Microbial Community Dynamics of an Urban Drinking Water Distribution System Subjected to Phases of Chloramination and Chlorination Treatments. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7856-7865.	1.4	147
41	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4858-4862.	1.4	146
42	Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. <i>PLoS ONE</i> , 2012, 7, e41305.	1.1	146
43	Bacterial community structure corresponds to performance during cathodic nitrate reduction. <i>ISME Journal</i> , 2010, 4, 1443-1455.	4.4	137
44	Sustainable syntrophic growth of <i>Dehalococcoides ethenogenes</i> strain 195 with <i>Desulfovibrio vulgaris</i> Hildenborough and <i>Methanobacterium congolense</i> : global transcriptomic and proteomic analyses. <i>ISME Journal</i> , 2012, 6, 410-421.	4.4	137
45	Genetic variability of <i>Bacillus anthracis</i> and related species. <i>Journal of Clinical Microbiology</i> , 1995, 33, 1847-1850.	1.8	135
46	Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated $\text{CO}_2$ and warming in an Australian native grassland soil. <i>Environmental Microbiology</i> , 2012, 14, 3081-3096.	1.8	134
47	New perspectives on viable microbial communities in low-biomass cleanroom environments. <i>ISME Journal</i> , 2013, 7, 312-324.	4.4	126
48	Bacterial Diversity Analysis of Huanglongbing Pathogen-Infected Citrus, Using PhyloChip Arrays and 16S rRNA Gene Clone Library Sequencing. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1566-1574.	1.4	125
49	Developing microbe-plant interactions for applications in plant growth promotion and disease control, production of useful compounds, remediation and carbon sequestration. <i>Microbial Biotechnology</i> , 2009, 2, 428-440.	2.0	124
50	The response of marine picoplankton to ocean acidification. <i>Environmental Microbiology</i> , 2012, 14, 2293-2307.	1.8	124
51	Identification of a region of genetic variability among <i>Bacillus anthracis</i> strains and related species. <i>Journal of Bacteriology</i> , 1996, 178, 377-384.	1.0	120
52	Simulation of Deepwater Horizon oil plume reveals substrate specialization within a complex community of hydrocarbon degraders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7432-7437.	3.3	120
53	Identification of Genes Associated with Survival of <i>Salmonella enterica</i> Serovar Enteritidis in Chicken Egg Albumen. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1055-1064.	1.4	119
54	The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. <i>ISME Journal</i> , 2012, 6, 259-272.	4.4	110

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55	Rapid quantification and taxonomic classification of environmental DNA from both prokaryotic and eukaryotic origins using a microarray. <i>FEMS Microbiology Letters</i> , 2005, 245, 271-278.	0.7	103
56	Microbial Diversity in Uranium Mining-Impacted Soils as Revealed by High-Density 16S Microarray and Clone Library. <i>Microbial Ecology</i> , 2010, 59, 94-108.	1.4	102
57	Comprehensive aligned sequence construction for automated design of effective probes (CASCADE-P) using 16S rDNA. <i>Bioinformatics</i> , 2003, 19, 1461-1468.	1.8	101
58	Development of a high-volume aerosol collection system for the identification of air-borne micro-organisms. <i>Letters in Applied Microbiology</i> , 2002, 34, 162-167.	1.0	99
59	Changes of Soil Bacterial Diversity as a Consequence of Agricultural Land Use in a Semi-Arid Ecosystem. <i>PLoS ONE</i> , 2013, 8, e59497.	1.1	95
60	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. <i>ISME Journal</i> , 2016, 10, 582-595.	4.4	91
61	Role of the <i>rapA</i> Gene in Controlling Antibiotic Resistance of <i>Escherichia coli</i> Biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3650-3658.	1.4	90
62	Microbial Response to the MC-252 Oil and Corexit 9500 in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2012, 3, 357.	1.5	86
63	Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6559-6567.	1.4	80
64	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , 2014, 8, 2411-2422.	4.4	80
65	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . <i>ISME Journal</i> , 2014, 8, 6-18.	4.4	80
66	Influence of geogenic factors on microbial communities in metallogenic Australian soils. <i>ISME Journal</i> , 2012, 6, 2107-2118.	4.4	79
67	Biodegradation of dispersed Macondo crude oil by indigenous Gulf of Mexico microbial communities. <i>Science of the Total Environment</i> , 2016, 557-558, 453-468.	3.9	75
68	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6313-6322.	1.4	74
69	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	73
70	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1435.	1.5	73
71	Temporal Transcriptomic Microarray Analysis of <i>Dehalococcoides ethenogenes</i> Strain 195 during the Transition into Stationary Phase. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2864-2872.	1.4	72
72	Occurrence and Properties of Copper-Tolerant Strains of <i>Pseudomonas syringae</i> isolated from Fruit Trees in California. <i>Phytopathology</i> , 1991, 81, 648.	1.1	71

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73	Microbial and Mineralogical Characterizations of Soils Collected from the Deep Biosphere of the Former Homestake Gold Mine, South Dakota. <i>Microbial Ecology</i> , 2010, 60, 539-550.	1.4	70
74	Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. <i>FEMS Microbiology Ecology</i> , 2012, 79, 298-311.	1.3	69
75	Genome plasticity in <i>Yersinia pestis</i> The GenBank accession numbers for the sequences reported in this paper can be found in Table 1 T1 ; the GenBank accession number for DFR4 is AF426171.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1687-1698.	0.7	67
76	Bacterial Diversity of Weathered Terrestrial Icelandic Volcanic Glasses. <i>Microbial Ecology</i> , 2010, 60, 740-752.	1.4	66
77	Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. <i>PLoS ONE</i> , 2010, 5, e11285.	1.1	66
78	Analysis of Gut Microbiome and Diet Modification in Patients with Crohn's Disease. <i>SOJ Microbiology &amp; Infectious Diseases</i> , 2014, 2, 1-13.	0.7	65
79	<i>Caulobacter crescentus</i> as a Whole-Cell Uranium Biosensor. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7615-7621.	1.4	62
80	Intestinal Microbiota as Novel Biomarkers of Prior Radiation Exposure. <i>Radiation Research</i> , 2012, 177, 573.	0.7	61
81	Functional Biogeography as Evidence of Gene Transfer in Hypersaline Microbial Communities. <i>PLoS ONE</i> , 2010, 5, e12919.	1.1	57
82	Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. <i>ISME Journal</i> , 2013, 7, 635-651.	4.4	57
83	Characteristics of Insertional Mutants of <i>Pseudomonas syringae</i> with Reduced Epiphytic Fitness. <i>Applied and Environmental Microbiology</i> , 1993, 59, 1593-1601.	1.4	57
84	Environmental Determinants of and Impact on Childhood Asthma by the Bacterial Community in Household Dust. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2663-2667.	1.4	56
85	Effect of Rainfall-Induced Soil Geochemistry Dynamics on Grassland Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7587-7595.	1.4	55
86	Truffle BrÃ©s Have an Impact on the Diversity of Soil Bacterial Communities. <i>PLoS ONE</i> , 2013, 8, e61945.	1.1	55
87	Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. <i>ISME Journal</i> , 2011, 5, 1014-1024.	4.4	54
88	Comparative Genomics of <i>Dehalococcoides ethenogenes</i> 195 and an Enrichment Culture Containing Unsequenced <i>Dehalococcoides</i> Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3533-3540.	1.4	53
89	Application of Phylogenetic Microarray Analysis to Discriminate Sources of Fecal Pollution. <i>Environmental Science &amp; Technology</i> , 2012, 46, 4340-4347.	4.6	53
90	Ecogenomics Reveals Metals and Land-Use Pressures on Microbial Communities in the Waterways of a Megacity. <i>Environmental Science &amp; Technology</i> , 2015, 49, 1462-1471.	4.6	53

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91	Prokaryotic community profiles at different operational stages of a Greek solar saltern. <i>Research in Microbiology</i> , 2008, 159, 609-627.	1.0	52
92	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , 2015, 5, 9156.	1.6	52
93	Microbial source tracking in impaired watersheds using PhyloChip and machine-learning classification. <i>Water Research</i> , 2016, 105, 56-64.	5.3	52
94	Identification of Nucleotide Sequences for the Specific and Rapid Detection of <i>Yersinia pestis</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 3759-3762.	1.4	51
95	Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. <i>Microbial Ecology</i> , 2011, 62, 69-79.	1.4	51
96	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4723-4736.	1.7	51
97	Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2837-2845.	1.4	50
98	Evaluation of molecular community analysis methods for discerning fecal sources and human waste. <i>Water Research</i> , 2013, 47, 6862-6872.	5.3	50
99	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. <i>FEMS Microbiology Letters</i> , 2002, 211, 175-182.	0.7	49
100	Transcriptomic microarray analysis of corrinoid responsive genes in <i>Dehalococcoides ethenogenes</i> strain 195. <i>FEMS Microbiology Letters</i> , 2009, 294, 198-206.	0.7	47
101	Assessment of bacterial and fungal communities in a full-scale thermophilic sewage sludge composting pile under a semipermeable cover. <i>Bioresource Technology</i> , 2020, 298, 122550.	4.8	46
102	Bacterial and Archaeal Community Structure of Two Adjacent Calcite Speleothems in Kartchner Caverns, Arizona, USA. <i>Geomicrobiology Journal</i> , 2011, 28, 99-117.	1.0	45
103	Humic Acid-Oxidizing, Nitrate-Reducing Bacteria in Agricultural Soils. <i>MBio</i> , 2011, 2, e00044-11.	1.8	45
104	Evaluation of Methods for the Extraction of DNA from Drinking Water Distribution System Biofilms. <i>Microbes and Environments</i> , 2012, 27, 9-18.	0.7	43
105	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
106	Bacterial communities in commercial aircraft high-efficiency particulate air (HEPA) filters assessed by PhyloChip analysis. <i>Indoor Air</i> , 2013, 23, 50-61.	2.0	43
107	Unusual Metabolism and Hypervariation in the Genome of a <i>Gracilibacterium</i> (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , 2019, 10, .	1.8	43
108	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , 2013, 86, 277-287.	1.3	41

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109	Methane-Oxidizing Bacteria Shunt Carbon to Microbial Mats at a Marine Hydrocarbon Seep. <i>Frontiers in Microbiology</i> , 2017, 8, 186.	1.5	39
110	Identification and localization of differences between <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> genomes by suppressive subtractive hybridization. <i>Molecular Genetics and Genomics</i> , 1999, 262, 721-729.	2.4	38
111	Mortality, Recruitment and Change of Desert Tree Populations in a Hyper-Arid Environment. <i>PLoS ONE</i> , 2007, 2, e208.	1.1	38
112	High-Density 16S Microarray and Clone Library-Based Microbial Community Composition of the Phoenix Spacecraft Assembly Clean Room. <i>Astrobiology</i> , 2010, 10, 499-508.	1.5	37
113	Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs. <i>Frontiers in Microbiology</i> , 2014, 5, 409.	1.5	37
114	Bacterial community structure transformed after thermophilically composting human waste in Haiti. <i>PLoS ONE</i> , 2017, 12, e0177626.	1.1	37
115	PhyloChip microarray analysis reveals altered gastrointestinal microbial communities in a rat model of colonic hypersensitivity. <i>Neurogastroenterology and Motility</i> , 2011, 23, 169-e42.	1.6	36
116	Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. <i>Environmental Science &amp; Technology</i> , 2012, 46, 1044-1054.	4.6	36
117	Molecular Characterization and Sequence of a Methionine Biosynthetic Locus from <i>Pseudomonas syringae</i> . <i>Journal of Bacteriology</i> , 1998, 180, 4497-4507.	1.0	36
118	Analysis of Leaf and Root Transcriptomes of Soil-Grown <i>Avena barbata</i> Plants. <i>Plant and Cell Physiology</i> , 2011, 52, 317-332.	1.5	34
119	Olive-Mill Wastewater Bacterial Communities Display a Cultivar Specific Profile. <i>Current Microbiology</i> , 2012, 64, 197-203.	1.0	34
120	Attenuating Sulfidogenesis in a Soured Continuous Flow Column System With Perchlorate Treatment. <i>Frontiers in Microbiology</i> , 2018, 9, 1575.	1.5	32
121	Comparing Bacterial Community Composition between Healthy and White Plague-Like Disease States in <i>Orbicella annularis</i> Using PhyloChip and G3 Microarrays. <i>PLoS ONE</i> , 2013, 8, e79801.	1.1	32
122	Comparison of fecal biota from specific pathogen free and feral mice. <i>Anaerobe</i> , 2006, 12, 249-253.	1.0	31
123	Comparing Bacterial Community Composition of Healthy and Dark Spot-Affected <i>Siderastrea siderea</i> in Florida and the Caribbean. <i>PLoS ONE</i> , 2014, 9, e108767.	1.1	30
124	Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. <i>Soil Biology and Biochemistry</i> , 2013, 57, 675-682.	4.2	28
125	Coupling Genetic and Chemical Microbiome Profiling Reveals Heterogeneity of Archaeome and Bacteriome in Subsurface Biofilms That Are Dominated by the Same Archaeal Species. <i>PLoS ONE</i> , 2014, 9, e99801.	1.1	28
126	Microbial Community Responses to Organophosphate Substrate Additions in Contaminated Subsurface Sediments. <i>PLoS ONE</i> , 2014, 9, e100383.	1.1	28



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127	Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5438-5444.	1.4	27
128	Single-Nucleotide Polymorphisms Reveal Spatial Diversity Among Clones of <i>Yersinia pestis</i> During Plague Outbreaks in Colorado and the Western United States. <i>Vector-Borne and Zoonotic Diseases</i> , 2015, 15, 291-302.	0.6	27
129	Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5636-5638.	1.4	24
130	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , 2011, 11, 11.	3.0	24
131	Global Transcriptomic and Proteomic Responses of <i>Dehalococcoides ethenogenes</i> Strain 195 to Fixed Nitrogen Limitation. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1424-1436.	1.4	24
132	Influence of trace erythromycin and erythromycin-H <sub>2</sub> O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 185-195.	1.7	21
133	The Influence of In Situ Chemical Oxidation on Microbial Community Composition in Groundwater Contaminated with Chlorinated Solvents. <i>Microbial Ecology</i> , 2013, 65, 39-49.	1.4	20
134	PhyloChip microarray comparison of sampling methods used for coral microbial ecology. <i>Journal of Microbiological Methods</i> , 2012, 88, 103-109.	0.7	19
135	Comparison of the Fecal Microbiota in Feral and Domestic Goats. <i>Genes</i> , 2012, 3, 1-18.	1.0	19
136	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	1.3	19
137	Effects of TiO <sub>2</sub> and Ag Nanoparticles on Polyhydroxybutyrate Biosynthesis By Activated Sludge Bacteria. <i>Environmental Science &amp; Technology</i> , 2014, 48, 14712-14720.	4.6	19
138	A comparison of methods used to unveil the genetic and metabolic pool in the built environment. <i>Microbiome</i> , 2018, 6, 71.	4.9	19
139	Assays for the rapid and specific identification of North American <i>Yersinia pestis</i> and the common laboratory strain CO92. <i>BioTechniques</i> , 2008, 44, 201-207.	0.8	18
140	Linking leaf transcript levels to whole plant analyses provides mechanistic insights to the impact of warming and altered water availability in an annual grass. <i>Global Change Biology</i> , 2011, 17, 1577-1594.	4.2	16
141	Novel Plasmids and Resistance Phenotypes in <i>Yersinia pestis</i> : Unique Plasmid Inventory of Strain Java 9 Mediates High Levels of Arsenic Resistance. <i>PLoS ONE</i> , 2012, 7, e32911.	1.1	16
142	Bacterial Diversity in the Cecum of the World's Largest Living Rodent ( <i>Hydrochoerus hydrochaeris</i> ). <i>Microbial Ecology</i> , 2012, 63, 719-725.	1.4	16
143	Microbial Community Structures of Novel Icelandic Hot Spring Systems Revealed by PhyloChip G3 Analysis. <i>Astrobiology</i> , 2014, 14, 229-240.	1.5	16
144	<i>Penicillium oxalicum</i> XD-3.1 removes pharmaceutical compounds from hospital wastewater and outcompetes native bacterial and fungal communities in fluidised batch bioreactors. <i>International Biodeterioration and Biodegradation</i> , 2021, 158, 105179.	1.9	14

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145	Automated group assignment in large phylogenetic trees using GRUNT: GRouping, Ungrouping, Naming Tool. BMC Bioinformatics, 2007, 8, 402.	1.2	9
146	Bacterial community and environmental factors associated to rivers runoff and their possible impacts on coral reef conservation. Marine Pollution Bulletin, 2020, 156, 111233.	2.3	9
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