

Gary L Andersen

List of Publications by Year in descending order

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156
papers

49,578
citations

12303

69
h-index

7136

153
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. Applied and Environmental Microbiology, 2006, 72, 5069-5072.	1.4	9,859
2	Structure, function and diversity of the healthy human microbiome. Nature, 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. ISME Journal, 2012, 6, 610-618.	4.4	4,581
4	PyNAST: a flexible tool for aligning sequences to a template alignment. Bioinformatics, 2010, 26, 266-267.	1.8	3,400
5	A framework for human microbiome research. Nature, 2012, 486, 215-221.	13.7	2,249
6	Deciphering the Rhizosphere Microbiome for Disease-Suppressive Bacteria. Science, 2011, 332, 1097-1100.	6.0	2,135
7	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. Science, 2010, 330, 204-208.	6.0	1,109
8	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. Nucleic Acids Research, 2006, 34, W394-W399.	6.5	918
9	Chronic kidney disease alters intestinal microbial flora. Kidney International, 2013, 83, 308-315.	2.6	828
10	Urban aerosols harbor diverse and dynamic bacterial populations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 299-304.	3.3	593
11	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. Nucleic Acids Research, 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. American Journal of Nephrology, 2014, 39, 230-237.	1.4	478
13	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. Science, 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. Microbial Ecology, 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. Applied and Environmental Microbiology, 2006, 72, 6288-6298.	1.4	404
16	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. PLoS ONE, 2010, 5, e11044.	1.1	395
17	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . ISME Journal, 2009, 3, 512-521.	4.4	364
18	Long-Term Sustainability of a High-Energy, Low-Diversity Crustal Biome. Science, 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 & 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 & 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. ISME Journal, 2009, 3, 340-351.	4.4	156
38	Identification by Subtractive Hybridization of Sequences Specific for Salmonella enterica Serovar Enteritidis. Applied and Environmental Microbiology, 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. MBio, 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. Applied and Environmental Microbiology, 2012, 78, 7856-7865.	1.4	147
41	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. Applied and Environmental Microbiology, 2010, 76, 4858-4862.	1.4	146
42	Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e41305.	1.1	146
43	Bacterial community structure corresponds to performance during cathodic nitrate reduction. ISME Journal, 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. ISME Journal, 2012, 6, 410-421.	4.4	137
45	Genetic variability of Bacillus anthracis and related species. Journal of Clinical Microbiology, 1995, 33, 1847-1850.	1.8	135
46	Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated CO_2 and warming in an Australian native grassland soil. Environmental Microbiology, 2012, 14, 3081-3096.	1.8	134
47	New perspectives on viable microbial communities in low-biomass cleanroom environments. ISME Journal, 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. Applied and Environmental Microbiology, 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. Microbial Biotechnology, 2009, 2, 428-440.	2.0	124
50	The response of marine picoplankton to ocean acidification. Environmental Microbiology, 2012, 14, 2293-2307.	1.8	124
51	Identification of a region of genetic variability among Bacillus anthracis strains and related species. Journal of Bacteriology, 1996, 178, 377-384.	1.0	120
52	Simulation of Deepwater Horizon oil plume reveals substrate specialization within a complex community of hydrocarbon degraders. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7432-7437.	3.3	120
53	Identification of Genes Associated with Survival of Salmonella enterica Serovar Enteritidis in Chicken Egg Albumen. Applied and Environmental Microbiology, 2006, 72, 1055-1064.	1.4	119
54	The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. ISME Journal, 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 & 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 & 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 & 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 & 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 ₂ 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 ₂ and Ag Nanoparticles on Polyhydroxybutyrate Biosynthesis By Activated Sludge Bacteria. <i>Environmental Science & 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
147	Establishment of uncharacterized plasmids in Escherichia coli by in vitro transposition. FEMS Microbiology Letters, 2002, 217, 249-254.	0.7	8
148	A data analysis and coordination center for the human microbiome project. Genome Biology, 2010, 11, O13.	13.9	8
149	Community Analysis-Based Methods. , 2011, , 251-282.		8
150	Annual grassland resource pools and fluxes: sensitivity to precipitation and dry periods on two contrasting soils. Ecosphere, 2012, 3, art70-art70.	1.0	5
151	Microcomputer Measurements of Pathogen Injury to Weeds. Weed Science, 1986, 34, 38-42.	0.8	3
152	Bone haemangio-sarcoma in a young Belgian malinois. Journal of Small Animal Practice, 1990, 31, 349-352.	0.5	2
153	Culture-Independent Bacterial Population Analysis – Clinical Implications for Respiratory and Other Infections. Current Respiratory Medicine Reviews, 2008, 4, 35-39.	0.1	1
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