

# Gary L Andersen

## List of Publications by Year in Descending Order

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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.

156  
papers

38,051  
citations

64  
h-index

159  
g-index

159  
ext. papers

45,967  
ext. citations

7.4  
avg, IF

8.04  
L-index

#	Paper	IF	Citations
156	Penicillium oxalicum 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> , <b>2021</b> , 158, 105179	4.8	5
155	Bacterial community and environmental factors associated to rivers runoff and their possible impacts on coral reef conservation. <i>Marine Pollution Bulletin</i> , <b>2020</b> , 156, 111233	6.7	3
154	Assessment of bacterial and fungal communities in a full-scale thermophilic sewage sludge composting pile under a semipermeable cover. <i>Bioresource Technology</i> , <b>2020</b> , 298, 122550	11	27
153	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. <i>Nature Microbiology</i> , <b>2019</b> , 4, 603-613	26.6	84
152	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , <b>2019</b> , 10,	7.8	19
151	Unusual metabolism and hypervariation in the genome of a Gracilibacteria (BD1-5) from an oil degrading community <b>2019</b> ,		4
150	A comparison of methods used to unveil the genetic and metabolic pool in the built environment. <i>Microbiome</i> , <b>2018</b> , 6, 71	16.6	11
149	Attenuating Sulfidogenesis in a Soured Continuous Flow Column System With Perchlorate Treatment. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1575	5.7	10
148	Investigation of Yersinia pestis and Yersinia pseudotuberculosis strains from Georgia and neighboring countries in the Caucasus by high-density SNP microarray. <i>Archives of Microbiology</i> , <b>2018</b> , 200, 1345-1355	3	1
147	Reply to Delmont and Eren: Strain variants and population structure during the oil spill. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E8950-E8952	11.5	
146	Bacterial community structure transformed after thermophilically composting human waste in Haiti. <i>PLoS ONE</i> , <b>2017</b> , 12, e0177626	3.7	24
145	Simulation of 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> , <b>2017</b> , 114, 7432-7437	11.5	82
144	Methane-Oxidizing Bacteria Shunt Carbon to Microbial Mats at a Marine Hydrocarbon Seep. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 186	5.7	28
143	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> , <b>2017</b> , 8, 1435	5.7	51
142	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. <i>ISME Journal</i> , <b>2016</b> , 10, 582-95	11.9	73
141	Microbial source tracking in impaired watersheds using PhyloChip and machine-learning classification. <i>Water Research</i> , <b>2016</b> , 105, 56-64	12.5	32
140	Biodegradation of dispersed Macondo crude oil by indigenous Gulf of Mexico microbial communities. <i>Science of the Total Environment</i> , <b>2016</b> , 557-558, 453-68	10.2	61

139	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , <b>2016</b> , 7, e01669-15	7.8	100
138	Ecogenomics reveals metals and land-use pressures on microbial communities in the waterways of a megacity. <i>Environmental Science &amp; Technology</i> , <b>2015</b> , 49, 1462-71	10.3	36
137	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , <b>2015</b> , 5, 9156	4.9	31
136	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> , <b>2015</b> , 15, 291-302	2.4	16
135	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. <i>Applied Microbiology and Biotechnology</i> , <b>2014</b> , 98, 4723-36	5.7	39
134	Microbial community structures of novel Icelandic hot spring systems revealed by PhyloChip G3 analysis. <i>Astrobiology</i> , <b>2014</b> , 14, 229-40	3.7	11
133	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , <b>2014</b> , 8, 2411-22	11.9	63
132	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . <i>ISME Journal</i> , <b>2014</b> , 8, 6-18	11.9	49
131	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> , <b>2014</b> , 9, e99801	3.7	22
130	Comparing bacterial community composition of healthy and dark spot-affected <i>Siderastrea siderea</i> in Florida and the Caribbean. <i>PLoS ONE</i> , <b>2014</b> , 9, e108767	3.7	18
129	Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 409	5.7	21
128	Effects of TiO <sub>2</sub> and Ag nanoparticles on polyhydroxybutyrate biosynthesis by activated sludge bacteria. <i>Environmental Science &amp; Technology</i> , <b>2014</b> , 48, 14712-20	10.3	18
127	Microbial community responses to organophosphate substrate additions in contaminated subsurface sediments. <i>PLoS ONE</i> , <b>2014</b> , 9, e100383	3.7	24
126	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> , <b>2014</b> , 39, 230-237	4.6	331
125	Analysis of Gut Microbiome and Diet Modification in Patients with Crohn's Disease. <i>SOJ Microbiology &amp; Infectious Diseases</i> , <b>2014</b> , 2, 1-13	0.5	47
124	Bacterial communities in commercial aircraft high-efficiency particulate air (HEPA) filters assessed by PhyloChip analysis. <i>Indoor Air</i> , <b>2013</b> , 23, 50-61	5.4	33
123	The influence of in situ chemical oxidation on microbial community composition in groundwater contaminated with chlorinated solvents. <i>Microbial Ecology</i> , <b>2013</b> , 65, 39-49	4.4	18
122	Evaluation of molecular community analysis methods for discerning fecal sources and human waste. <i>Water Research</i> , <b>2013</b> , 47, 6862-72	12.5	48

121	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , <b>2013</b> , 86, 277-87	4.3	33
120	New perspectives on viable microbial communities in low-biomass cleanroom environments. <i>ISME Journal</i> , <b>2013</b> , 7, 312-24	11.9	94
119	Succession of hydrocarbon-degrading bacteria in the aftermath of the deepwater horizon oil spill in the gulf of Mexico. <i>Environmental Science &amp; Technology</i> , <b>2013</b> , 47, 10860-7	10.3	245
118	Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. <i>ISME Journal</i> , <b>2013</b> , 7, 635-51	11.9	51
117	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> , <b>2013</b> , 57, 675-682	7.5	19
116	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , <b>2013</b> , 84, 259-69	4.3	9
115	Chronic kidney disease alters intestinal microbial flora. <i>Kidney International</i> , <b>2013</b> , 83, 308-15	9.9	581
114	Truffle brñ have an impact on the diversity of soil bacterial communities. <i>PLoS ONE</i> , <b>2013</b> , 8, e61945	3.7	39
113	Changes of soil bacterial diversity as a consequence of agricultural land use in a semi-arid ecosystem. <i>PLoS ONE</i> , <b>2013</b> , 8, e59497	3.7	72
112	Comparing bacterial community composition between healthy and white plague-like disease states in <i>Orbicella annularis</i> using PhyloChipG3 microarrays. <i>PLoS ONE</i> , <b>2013</b> , 8, e79801	3.7	26
111	High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. <i>FEMS Microbiology Ecology</i> , <b>2012</b> , 81, 188-204	4.3	42
110	The response of marine picoplankton to ocean acidification. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 2293-307	5.07	83
109	Olive-mill wastewater bacterial communities display a cultivar specific profile. <i>Current Microbiology</i> , <b>2012</b> , 64, 197-203	2.4	30
108	Evaluation of methods for the extraction of DNA from drinking water distribution system biofilms. <i>Microbes and Environments</i> , <b>2012</b> , 27, 9-18	2.6	38
107	Effect of rainfall-induced soil geochemistry dynamics on grassland soil microbial communities. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 7587-95	4.8	41
106	Influence of geogenic factors on microbial communities in metallogenic Australian soils. <i>ISME Journal</i> , <b>2012</b> , 6, 2107-18	11.9	54
105	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
104	Application of phylogenetic microarray analysis to discriminate sources of fecal pollution. <i>Environmental Science &amp; Technology</i> , <b>2012</b> , 46, 4340-7	10.3	44

103	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
102	Phylogenetic microarray analysis of a microbial community performing reductive dechlorination at a TCE-contaminated site. <i>Environmental Science &amp; Technology</i> , <b>2012</b> , 46, 1044-54	10.3	28
101	Sustainable syntrophic growth of Dehalococcoides ethenogenes strain 195 with Desulfovibrio vulgaris Hildenborough and Methanobacterium congolense: global transcriptomic and proteomic analyses. <i>ISME Journal</i> , <b>2012</b> , 6, 410-21	11.9	100
100	PhyloChip microarray comparison of sampling methods used for coral microbial ecology. <i>Journal of Microbiological Methods</i> , <b>2012</b> , 88, 103-9	2.8	17
99	Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated CO <sub>2</sub> and warming in an Australian native grassland soil. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 3081-96	5.2	101
98	Intestinal microbiota as novel biomarkers of prior radiation exposure. <i>Radiation Research</i> , <b>2012</b> , 177, 573-83	3.1	47
97	Oil Impacts on Coastal Wetlands: Implications for the Mississippi River Delta Ecosystem after the Deepwater Horizon Oil Spill. <i>BioScience</i> , <b>2012</b> , 62, 562-574	5.7	204
96	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , <b>2012</b> , 6, 610-8	11.9	3287
95	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> , <b>2012</b> , 7, e32911	3.7	15
94	Complexity and variability of gut commensal microbiota in polyphagous lepidopteran larvae. <i>PLoS ONE</i> , <b>2012</b> , 7, e36978	3.7	111
93	Microbial Response to the MC-252 Oil and Corexit 9500 in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , <b>2012</b> , 3, 357	5.7	72
92	The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. <i>ISME Journal</i> , <b>2012</b> , 6, 259-72	11.9	95
91	Bacterial diversity in the cecum of the world's largest living rodent ( <i>Hydrochoerus hydrochaeris</i> ). <i>Microbial Ecology</i> , <b>2012</b> , 63, 719-25	4.4	11
90	Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. <i>FEMS Microbiology Ecology</i> , <b>2012</b> , 79, 298-311	4.3	46
89	Microbial community analysis of a coastal salt marsh affected by the Deepwater Horizon oil spill. <i>PLoS ONE</i> , <b>2012</b> , 7, e41305	3.7	119
88	Microbial community dynamics of an urban drinking water distribution system subjected to phases of chloramination and chlorination treatments. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 7856-65	4.8	105
87	Global transcriptomic and proteomic responses of <i>Dehalococcoides ethenogenes</i> strain 195 to fixed nitrogen limitation. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 1424-36	4.8	21
86	Annual grassland resource pools and fluxes: sensitivity to precipitation and dry periods on two contrasting soils. <i>Ecosphere</i> , <b>2012</b> , 3, art70-art70	3.1	4

85	Comparison of the fecal microbiota in feral and domestic goats. <i>Genes</i> , <b>2011</b> , 3, 1-18	4.2	15
84	Bacterial and Archaeal Community Structure of Two Adjacent Calcite Speleothems in Kartchner Caverns, Arizona, USA. <i>Geomicrobiology Journal</i> , <b>2011</b> , 28, 99-117	2.5	29
83	Community Analysis-Based Methods <b>2011</b> , 251-282		6
82	Deciphering the rhizosphere microbiome for disease-suppressive bacteria. <i>Science</i> , <b>2011</b> , 332, 1097-1100	33.3	1516
81	PhyloChip microarray analysis reveals altered gastrointestinal microbial communities in a rat model of colonic hypersensitivity. <i>Neurogastroenterology and Motility</i> , <b>2011</b> , 23, 169-77, e41-2	4	26
80	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> , <b>2011</b> , 17, 1577-1594	11.4	14
79	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> , <b>2011</b> , 75, 497-506	4.3	154
78	Comparative genomics of two newly isolated Dehalococcoides strains and an enrichment using a genus microarray. <i>ISME Journal</i> , <b>2011</b> , 5, 1014-24	11.9	49
77	Bacterial diversity of terrestrial crystalline volcanic rocks, Iceland. <i>Microbial Ecology</i> , <b>2011</b> , 62, 69-79	4.4	38
76	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , <b>2011</b> , 11, 11	2.7	21
75	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 231	3.6	126
74	Comparison of innovative molecular approaches and standard spore assays for assessment of surface cleanliness. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 5438-44	4.8	25
73	PCR amplification-independent methods for detection of microbial communities by the high-density microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 6313-22	4.8	62
72	Analysis of leaf and root transcriptomes of soil-grown Avena barbata plants. <i>Plant and Cell Physiology</i> , <b>2011</b> , 52, 317-32	4.9	33
71	Soil microbial community successional patterns during forest ecosystem restoration. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 6158-64	4.8	162
70	Humic acid-oxidizing, nitrate-reducing bacteria in agricultural soils. <i>MBio</i> , <b>2011</b> , 2, e00044-11	7.8	38
69	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , <b>2010</b> , 4, 711-5	11.9	55
68	Bacterial community structure corresponds to performance during cathodic nitrate reduction. <i>ISME Journal</i> , <b>2010</b> , 4, 1443-55	11.9	114

67	Environmental determinants of and impact on childhood asthma by the bacterial community in household dust. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 2663-7	4.8	50
66	Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5636-8	4.8	21
65	Functional biogeography as evidence of gene transfer in hypersaline microbial communities. <i>PLoS ONE</i> , <b>2010</b> , 5, e12919	3.7	49
64	Diversity of anaerobic microbes in spacecraft assembly clean rooms. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 2837-45	4.8	45
63	High-density 16S microarray and clone library-based microbial community composition of the Phoenix spacecraft assembly clean room. <i>Astrobiology</i> , <b>2010</b> , 10, 499-508	3.7	36
62	Animal-to-animal variation in fecal microbial diversity among beef cattle. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 4858-62	4.8	118
61	Bacterial community structure in geographically distributed biological wastewater treatment reactors. <i>Environmental Science &amp; Technology</i> , <b>2010</b> , 44, 7391-6	10.3	162
60	Deep-sea oil plume enriches indigenous oil-degrading bacteria. <i>Science</i> , <b>2010</b> , 330, 204-8	33.3	906
59	Pyrosequencing analysis of bacterial biofilm communities in water meters of a drinking water distribution system. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5631-5	4.8	157
58	PyNASt: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , <b>2010</b> , 26, 266-7	7.2	2728
57	A data analysis and coordination center for the human microbiome project <b>2010</b> , 11, O13		6
56	Microbial diversity in uranium mining-impacted soils as revealed by high-density 16S microarray and clone library. <i>Microbial Ecology</i> , <b>2010</b> , 59, 94-108	4.4	89
55	Microbial and mineralogical characterizations of soils collected from the deep biosphere of the former Homestake gold mine, South Dakota. <i>Microbial Ecology</i> , <b>2010</b> , 60, 539-50	4.4	58
54	Bacterial diversity of weathered terrestrial Icelandic volcanic glasses. <i>Microbial Ecology</i> , <b>2010</b> , 60, 740-52	4.4	48
53	Airway microbiota and pathogen abundance in age-stratified cystic fibrosis patients. <i>PLoS ONE</i> , <b>2010</b> , 5, e11044	3.7	331
52	Characterization of coastal urban watershed bacterial communities leads to alternative community-based indicators. <i>PLoS ONE</i> , <b>2010</b> , 5, e11285	3.7	58
51	Comprehensive census of bacteria in clean rooms by using DNA microarray and cloning methods. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 6559-67	4.8	74
50	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> , <b>2009</b> , 2, 428-40	6.3	94

49	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> , <b>2009</b> , 85, 185-95	5.7	20
48	Selective progressive response of soil microbial community to wild oat roots. <i>ISME Journal</i> , <b>2009</b> , 3, 168-78	11.9	251
47	Environmental microarray analyses of Antarctic soil microbial communities. <i>ISME Journal</i> , <b>2009</b> , 3, 340-51	11.9	130
46	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , <b>2009</b> , 3, 512-21	11.9	287
45	Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. <i>ISME Journal</i> , <b>2009</b> , 3, 738-44	11.9	194
44	Transcriptomic microarray analysis of corrinoid responsive genes in <i>Dehalococcoides ethenogenes</i> strain 195. <i>FEMS Microbiology Letters</i> , <b>2009</b> , 294, 198-206	2.9	45
43	Bacterial diversity analysis of Huanglongbing pathogen-infected citrus, using PhyloChip arrays and 16S rRNA gene clone library sequencing. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 1566-74	4.8	106
42	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. <i>ISME Journal</i> , <b>2008</b> , 2, 1146-56	11.9	266
41	Prokaryotic community profiles at different operational stages of a Greek solar saltern. <i>Research in Microbiology</i> , <b>2008</b> , 159, 609-27	4	42
40	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, e120	20.1	423
39	Comparative genomics of " <i>Dehalococcoides ethenogenes</i> " 195 and an enrichment culture containing unsequenced " <i>Dehalococcoides</i> " strains. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 3533-40	4.8	52
38	Temporal transcriptomic microarray analysis of " <i>Dehalococcoides ethenogenes</i> " strain 195 during the transition into stationary phase. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 2864-72	4.8	67
37	Culture-Independent Bacterial Population Analysis [Clinical Implications for Respiratory and Other Infections]. <i>Current Respiratory Medicine Reviews</i> , <b>2008</b> , 4, 35-39	0.3	1
36	Assays for the rapid and specific identification of North American <i>Yersinia pestis</i> and the common laboratory strain CO92. <i>BioTechniques</i> , <b>2008</b> , 44, 201, 203-4, 207	2.5	16
35	Environmental genomics reveals a single-species ecosystem deep within Earth. <i>Science</i> , <b>2008</b> , 322, 275-83	33.3	344
34	Loss of bacterial diversity during antibiotic treatment of intubated patients colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , <b>2007</b> , 45, 1954-62	9.7	143
33	Automated group assignment in large phylogenetic trees using GRUNT: GRouping, Ungrouping, Naming Tool. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 402	3.6	9
32	High-density universal 16S rRNA microarray analysis reveals broader diversity than typical clone library when sampling the environment. <i>Microbial Ecology</i> , <b>2007</b> , 53, 371-83	4.4	387



31	Urban aerosols harbor diverse and dynamic bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 299-304	11.5	512
30	<i>Caulobacter crescentus</i> as a whole-cell uranium biosensor. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 7615-21	4.8	52
29	Role of the rapA gene in controlling antibiotic resistance of <i>Escherichia coli</i> biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2007</b> , 51, 3650-8	5.9	78
28	Mortality, recruitment and change of desert tree populations in a hyper-arid environment. <i>PLoS ONE</i> , <b>2007</b> , 2, e208	3.7	27
27	Comparison of fecal biota from specific pathogen free and feral mice. <i>Anaerobe</i> , <b>2006</b> , 12, 249-53	2.8	29
26	Identification of genes associated with survival of <i>Salmonella enterica</i> serovar Enteritidis in chicken egg albumen. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 1055-64	4.8	104
25	NASt: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W394-9	20.1	810
24	Application of a high-density oligonucleotide microarray approach to study bacterial population dynamics during uranium reduction and reoxidation. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 6288-98	4.8	387
23	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> , <b>2006</b> , 188, 4453-63	3.5	153
22	Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 5069-72	4.8	7556
21	Long-term sustainability of a high-energy, low-diversity crustal biome. <i>Science</i> , <b>2006</b> , 314, 479-82	33.3	283
20	Rapid quantification and taxonomic classification of environmental DNA from both prokaryotic and eukaryotic origins using a microarray. <i>FEMS Microbiology Letters</i> , <b>2005</b> , 245, 271-8	2.9	96
19	Whole-genome transcriptional analysis of heavy metal stresses in <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 8437-49	3.5	204
18	Comprehensive aligned sequence construction for automated design of effective probes (CASCADE-P) using 16S rDNA. <i>Bioinformatics</i> , <b>2003</b> , 19, 1461-8	7.2	91
17	Genome differences that distinguish <i>Bacillus anthracis</i> from <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> . <i>Applied and Environmental Microbiology</i> , <b>2003</b> , 69, 2755-64	4.8	153
16	Development of a high-volume aerosol collection system for the identification of air-borne micro-organisms. <i>Letters in Applied Microbiology</i> , <b>2002</b> , 34, 162-7	2.9	81
15	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. <i>FEMS Microbiology Letters</i> , <b>2002</b> , 211, 175-82	2.9	46
14	Establishment of uncharacterized plasmids in <i>Escherichia coli</i> by in vitro transposition. <i>FEMS Microbiology Letters</i> , <b>2002</b> , 217, 249-54	2.9	8

13	Sequence-specific identification of 18 pathogenic microorganisms using microarray technology. <i>Molecular and Cellular Probes</i> , <b>2002</b> , 16, 119-27	3.3	230
12	High-density microarray of small-subunit ribosomal DNA probes. <i>Applied and Environmental Microbiology</i> , <b>2002</b> , 68, 2535-41	4.8	256
11	Genome plasticity in <i>Yersinia pestis</i> . <i>Microbiology (United Kingdom)</i> , <b>2002</b> , 148, 1687-1698	2.9	59
10	Identification of nucleotide sequences for the specific and rapid detection of <i>Yersinia pestis</i> . <i>Applied and Environmental Microbiology</i> , <b>2001</b> , 67, 3759-62	4.8	44
9	Identification by subtractive hybridization of sequences specific for <i>Salmonella enterica</i> serovar enteritidis. <i>Applied and Environmental Microbiology</i> , <b>2001</b> , 67, 4984-91	4.8	127
8	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> , <b>1999</b> , 262, 721-9		29
7	Molecular characterization and sequence of a methionine biosynthetic locus from <i>Pseudomonas syringae</i> . <i>Journal of Bacteriology</i> , <b>1998</b> , 180, 4497-507	3.5	31
6	Identification of a region of genetic variability among <i>Bacillus anthracis</i> strains and related species. <i>Journal of Bacteriology</i> , <b>1996</b> , 178, 377-84	3.5	106
5	Genetic variability of <i>Bacillus anthracis</i> and related species. <i>Journal of Clinical Microbiology</i> , <b>1995</b> , 33, 1847-50	9.7	119
4	Characteristics of Insertional Mutants of <i>Pseudomonas syringae</i> with Reduced Epiphytic Fitness. <i>Applied and Environmental Microbiology</i> , <b>1993</b> , 59, 1593-601	4.8	44
3	Occurrence and Properties of Copper-Tolerant Strains of <i>Pseudomonas syringae</i> isolated from Fruit Trees in California. <i>Phytopathology</i> , <b>1991</b> , 81, 648	3.8	52
2	Bone haemangio-sarcoma in a young Belgian malinois. <i>Journal of Small Animal Practice</i> , <b>1990</b> , 31, 349-352.6		2
1	Microcomputer Measurements of Pathogen Injury to Weeds. <i>Weed Science</i> , <b>1986</b> , 34, 38-42	2	2