# Gary L Andersen

## List of Publications by Year
## in descending order

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Version: 2024-02-01

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|---|---|---|---|
| 156<br>papers | 49,578<br>citations | 12303<br>69<br>h-index | 7136<br>153<br>g-index |
| 160<br>all docs | 160<br>docs citations | 160<br>times ranked | 53182<br>citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1 | Penicillium oxalicum XD-3.1 removes pharmaceutical compounds from hospital wastewater and outcompetes native bacterial and fungal communities in fluidised batch bioreactors. International Biodeterioration and Biodegradation, 2021, 158, 105179. | 1.9 | 14 |
| 2 | Assessment of bacterial and fungal communities in a full-scale thermophilic sewage sludge composting pile under a semipermeable cover. Bioresource Technology, 2020, 298, 122550. | 4.8 | 46 |
| 3 | 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 |
| 4 | Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613. | 5.9 | 187 |
| 5 | Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. MBio, 2019, 10, . | 1.8 | 43 |
| 6 | A comparison of methods used to unveil the genetic and metabolic pool in the built environment. Microbiome, 2018, 6, 71. | 4.9 | 19 |
| 7 | Attenuating Sulfidogenesis in a Soured Continuous Flow Column System With Perchlorate Treatment. Frontiers in Microbiology, 2018, 9, 1575. | 1.5 | 32 |
| 8 | Investigation of Yersinia pestis and Yersinia pseudotuberculosis strains from Georgia and neighboring countries in the Caucasus by high-density SNP microarray. Archives of Microbiology, 2018, 200, 1345-1355. | 1.0 | 1 |
| 9 | Reply to Delmont and Eren: Strain variants and population structure during the Deepwater Horizon oil spill. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8950-E8952. | 3.3 | 0 |
| 10 | Simulation of <i>Deepwater Horizon</i> 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 |
| 11 | Methane-Oxidizing Bacteria Shunt Carbon to Microbial Mats at a Marine Hydrocarbon Seep. Frontiers in Microbiology, 2017, 8, 186. | 1.5 | 39 |
| 12 | Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. Frontiers in Microbiology, 2017, 8, 1435. | 1.5 | 73 |
| 13 | Bacterial community structure transformed after thermophilically composting human waste in Haiti. PLoS ONE, 2017, 12, e0177626. | 1.1 | 37 |
| 14 | 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 |
| 15 | Microbial source tracking in impaired watersheds using PhyloChip and machine-learning classification. Water Research, 2016, 105, 56-64. | 5.3 | 52 |
| 16 | Biodegradation of dispersed Macondo crude oil by indigenous Gulf of Mexico microbial communities. Science of the Total Environment, 2016, 557-558, 453-468. | 3.9 | 75 |
| 17 | Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. ISME Journal, 2016, 10, 582-595. | 4.4 | 91 |
| 18 | Single-Nucleotide Polymorphisms Reveal Spatial Diversity Among Clones of<i>Yersinia pestis</i>During Plague Outbreaks in Colorado and the Western United States. Vector-Borne and Zoonotic Diseases, 2015, 15, 291-302. | 0.6 | 27 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | Ecogenomics Reveals Metals and Land-Use Pressures on Microbial Communities in the Waterways of a Megacity. Environmental Science &amp; Technology, 2015, 49, 1462-1471. | 4.6 | 53 |
| 20 | Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. Scientific Reports, 2015, 5, 9156. | 1.6 | 52 |
| 21 | Coupling Genetic and Chemical Microbiome Profiling Reveals Heterogeneity of Archaeome and Bacteriome in Subsurface Biofilms That Are Dominated by the Same Archaeal Species. PLoS ONE, 2014, 9, e99801. | 1.1 | 28 |
| 22 | Comparing Bacterial Community Composition of Healthy and Dark Spot-Affected Siderastrea siderea in Florida and the Caribbean. PLoS ONE, 2014, 9, e108767. | 1.1 | 30 |
| 23 | Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs. Frontiers in Microbiology, 2014, 5, 409. | 1.5 | 37 |
| 24 | Effects of TiO<sub>2</sub> and Ag Nanoparticles on Polyhydroxybutyrate Biosynthesis By Activated Sludge Bacteria. Environmental Science &amp; Technology, 2014, 48, 14712-14720. | 4.6 | 19 |
| 25 | Microbial Community Responses to Organophosphate Substrate Additions in Contaminated Subsurface Sediments. PLoS ONE, 2014, 9, e100383. | 1.1 | 28 |
| 26 | 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 |
| 27 | Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. Applied Microbiology and Biotechnology, 2014, 98, 4723-4736. | 1.7 | 51 |
| 28 | Microbial Community Structures of Novel Icelandic Hot Spring Systems Revealed by PhyloChip G3 Analysis. Astrobiology, 2014, 14, 229-240. | 1.5 | 16 |
| 29 | Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i>. ISME Journal, 2014, 8, 2411-2422. | 4.4 | 80 |
| 30 | Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i>. ISME Journal, 2014, 8, 6-18. | 4.4 | 80 |
| 31 | Analysis of Gut Microbiome and Diet Modification in Patients with Crohnâ€™s Disease. SOJ Microbiology & Infectious Diseases, 2014, 2, 1-13. | 0.7 | 65 |
| 32 | Bacterial communities in commercial aircraft high-efficiency particulate air (HEPA) filters assessed by PhyloChip analysis. Indoor Air, 2013, 23, 50-61. | 2.0 | 43 |
| 33 | The Influence of In Situ Chemical Oxidation on Microbial Community Composition in Groundwater Contaminated with Chlorinated Solvents. Microbial Ecology, 2013, 65, 39-49. | 1.4 | 20 |
| 34 | Evaluation of molecular community analysis methods for discerning fecal sources and human waste. Water Research, 2013, 47, 6862-6872. | 5.3 | 50 |
| 35 | Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. FEMS Microbiology Ecology, 2013, 86, 277-287. | 1.3 | 41 |
| 36 | New perspectives on viable microbial communities in low-biomass cleanroom environments. ISME Journal, 2013, 7, 312-324. | 4.4 | 126 |

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|---|---|---|---|
| 37 | Succession of Hydrocarbon-Degrading Bacteria in the Aftermath of the <i>Deepwater Horizon</i> Oil Spill in the Gulf of Mexico. Environmental Science &amp; Technology, 2013, 47, 10860-10867. | 4.6 | 344 |
| 38 | Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. ISME Journal, 2013, 7, 635-651. | 4.4 | 57 |
| 39 | Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. Soil Biology and Biochemistry, 2013, 57, 675-682. | 4.2 | 28 |
| 40 | Biogeography of bacterioplankton in the tropical seawaters of Singapore. FEMS Microbiology Ecology, 2013, 84, 259-269. | 1.3 | 19 |
| 41 | Chronic kidney disease alters intestinal microbial flora. Kidney International, 2013, 83, 308-315. | 2.6 | 828 |
| 42 | Truffle BrÃ»lÃ©s Have an Impact on the Diversity of Soil Bacterial Communities. PLoS ONE, 2013, 8, e61945. | 1.1 | 55 |
| 43 | Changes of Soil Bacterial Diversity as a Consequence of Agricultural Land Use in a Semi-Arid Ecosystem. PLoS ONE, 2013, 8, e59497. | 1.1 | 95 |
| 44 | Comparing Bacterial Community Composition between Healthy and White Plague-Like Disease States in Orbicella annularis Using PhyloChipâ„¢ G3 Microarrays. PLoS ONE, 2013, 8, e79801. | 1.1 | 32 |
| 45 | Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e41305. | 1.1 | 146 |
| 46 | 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 |
| 47 | Global Transcriptomic and Proteomic Responses of Dehalococcoides ethenogenes Strain 195 to Fixed Nitrogen Limitation. Applied and Environmental Microbiology, 2012, 78, 1424-1436. | 1.4 | 24 |
| 48 | Annual grassland resource pools and fluxes: sensitivity to precipitation and dry periods on two contrasting soils. Ecosphere, 2012, 3, art70-art70. | 1.0 | 5 |
| 49 | Evaluation of Methods for the Extraction of DNA from Drinking Water Distribution System Biofilms. Microbes and Environments, 2012, 27, 9-18. | 0.7 | 43 |
| 50 | Effect of Rainfall-Induced Soil Geochemistry Dynamics on Grassland Soil Microbial Communities. Applied and Environmental Microbiology, 2012, 78, 7587-7595. | 1.4 | 55 |
| 51 | Influence of geogenic factors on microbial communities in metallogenic Australian soils. ISME Journal, 2012, 6, 2107-2118. | 4.4 | 79 |
| 52 | Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214. | 13.7 | 9,614 |
| 53 | Application of Phylogenetic Microarray Analysis to Discriminate Sources of Fecal Pollution. Environmental Science &amp; Technology, 2012, 46, 4340-4347. | 4.6 | 53 |
| 54 | A framework for human microbiome research. Nature, 2012, 486, 215-221. | 13.7 | 2,249 |

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|---|---|---|---|
| 55 | Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. Environmental Science &amp; Technology, 2012, 46, 1044-1054. | 4.6 | 36 |
| 56 | 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 |
| 57 | PhyloChipâ„¢ microarray comparison of sampling methods used for coral microbial ecology. Journal of Microbiological Methods, 2012, 88, 103-109. | 0.7 | 19 |
| 58 | Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated <scp><scp>CO<sub>2</sub></scp></scp> and warming in an <scp>A</scp>ustralian native grassland soil. Environmental Microbiology, 2012, 14, 3081-3096. | 1.8 | 134 |
| 59 | Intestinal Microbiota as Novel Biomarkers of Prior Radiation Exposure. Radiation Research, 2012, 177, 573. | 0.7 | 61 |
| 60 | Oil Impacts on Coastal Wetlands: Implications for the Mississippi River Delta Ecosystem after the Deepwater Horizon Oil Spill. BioScience, 2012, 62, 562-574. | 2.2 | 257 |
| 61 | 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 |
| 62 | Novel Plasmids and Resistance Phenotypes in Yersinia pestis: Unique Plasmid Inventory of Strain Java 9 Mediates High Levels of Arsenic Resistance. PLoS ONE, 2012, 7, e32911. | 1.1 | 16 |
| 63 | Complexity and Variability of Gut Commensal Microbiota in Polyphagous Lepidopteran Larvae. PLoS ONE, 2012, 7, e36978. | 1.1 | 162 |
| 64 | Microbial Response to the MC-252 Oil and Corexit 9500 in the Gulf of Mexico. Frontiers in Microbiology, 2012, 3, 357. | 1.5 | 86 |
| 65 | Comparison of the Fecal Microbiota in Feral and Domestic Goats. Genes, 2012, 3, 1-18. | 1.0 | 19 |
| 66 | 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 |
| 67 | Bacterial Diversity in the Cecum of the Worldâ€™s Largest Living Rodent (Hydrochoerus hydrochaeris). Microbial Ecology, 2012, 63, 719-725. | 1.4 | 16 |
| 68 | Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. FEMS Microbiology Ecology, 2012, 79, 298-311. | 1.3 | 69 |
| 69 | High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. FEMS Microbiology Ecology, 2012, 81, 188-204. | 1.3 | 43 |
| 70 | The response of marine picoplankton to ocean acidification. Environmental Microbiology, 2012, 14, 2293-2307. | 1.8 | 124 |
| 71 | Olive-Mill Wastewater Bacterial Communities Display a Cultivar Specific Profile. Current Microbiology, 2012, 64, 197-203. | 1.0 | 34 |
| 72 | Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness. Applied and Environmental Microbiology, 2011, 77, 5438-5444. | 1.4 | 27 |

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|---|---|---|---|
| 73 | PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. Applied and Environmental Microbiology, 2011, 77, 6313-6322. | 1.4 | 74 |
| 74 | Changes in Fecal Microbiota of Gulf War Veterans With Irritable Bowel Syndrome. Gastroenterology, 2011, 140, S-532. | 0.6 | 0 |
| 75 | Bacterial and Archaeal Community Structure of Two Adjacent Calcite Speleothems in Kartchner Caverns, Arizona, USA. Geomicrobiology Journal, 2011, 28, 99-117. | 1.0 | 45 |
| 76 | Community Analysis-Based Methods. , 2011, , 251-282. | | 8 |
| 77 | Deciphering the Rhizosphere Microbiome for Disease-Suppressive Bacteria. Science, 2011, 332, 1097-1100. | 6.0 | 2,135 |
| 78 | PhyloChip microarray analysis reveals altered gastrointestinal microbial communities in a rat model of colonic hypersensitivity. Neurogastroenterology and Motility, 2011, 23, 169-e42. | 1.6 | 36 |
| 79 | Linking leaf transcript levels to whole plant analyses provides mechanistic insights to the impact of warming and altered water availability in an annual grass. Global Change Biology, 2011, 17, 1577-1594. | 4.2 | 16 |
| 80 | PhyloChip hybridization uncovered an enormous bacterial diversity in the rhizosphere of different potato cultivars: many common and few cultivar-dependent taxa. FEMS Microbiology Ecology, 2011, 75, 497-506. | 1.3 | 198 |
| 81 | Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. ISME Journal, 2011, 5, 1014-1024. | 4.4 | 54 |
| 82 | Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. Microbial Ecology, 2011, 62, 69-79. | 1.4 | 51 |
| 83 | Simrank: Rapid and sensitive general-purpose k-mer search tool. BMC Ecology, 2011, 11, 11. | 3.0 | 24 |
| 84 | Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231. | 1.2 | 170 |
| 85 | Analysis of Leaf and Root Transcriptomes of Soil-Grown Avena barbata Plants. Plant and Cell Physiology, 2011, 52, 317-332. | 1.5 | 34 |
| 86 | Soil Microbial Community Successional Patterns during Forest Ecosystem Restoration. Applied and Environmental Microbiology, 2011, 77, 6158-6164. | 1.4 | 226 |
| 87 | Humic Acid-Oxidizing, Nitrate-Reducing Bacteria in Agricultural Soils. MBio, 2011, 2, e00044-11. | 1.8 | 45 |
| 88 | Microbial Diversity in Uranium Mining-Impacted Soils as Revealed by High-Density 16S Microarray and Clone Library. Microbial Ecology, 2010, 59, 94-108. | 1.4 | 102 |
| 89 | Microbial and Mineralogical Characterizations of Soils Collected from the Deep Biosphere of the Former Homestake Gold Mine, South Dakota. Microbial Ecology, 2010, 60, 539-550. | 1.4 | 70 |
| 90 | Bacterial Diversity of Weathered Terrestrial Icelandic Volcanic Glasses. Microbial Ecology, 2010, 60, 740-752. | 1.4 | 66 |

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|---|---|---|---|
| 91 | Microbial secondary succession in a chronosequence of chalk grasslands. ISME Journal, 2010, 4, 711-715. | 4.4 | 73 |
| 92 | Bacterial community structure corresponds to performance during cathodic nitrate reduction. ISME Journal, 2010, 4, 1443-1455. | 4.4 | 137 |
| 93 | Environmental Determinants of and Impact on Childhood Asthma by the Bacterial Community in Household Dust. Applied and Environmental Microbiology, 2010, 76, 2663-2667. | 1.4 | 56 |
| 94 | Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. Applied and Environmental Microbiology, 2010, 76, 5636-5638. | 1.4 | 24 |
| 95 | Functional Biogeography as Evidence of Gene Transfer in Hypersaline Microbial Communities. PLoS ONE, 2010, 5, e12919. | 1.1 | 57 |
| 96 | Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms. Applied and Environmental Microbiology, 2010, 76, 2837-2845. | 1.4 | 50 |
| 97 | High-Density 16S Microarray and Clone Libraryâ€“Based Microbial Community Composition of the Phoenix Spacecraft Assembly Clean Room. Astrobiology, 2010, 10, 499-508. | 1.5 | 37 |
| 98 | Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. Applied and Environmental Microbiology, 2010, 76, 4858-4862. | 1.4 | 146 |
| 99 | Bacterial Community Structure in Geographically Distributed Biological Wastewater Treatment Reactors. Environmental Science &amp; Technology, 2010, 44, 7391-7396. | 4.6 | 180 |
| 100 | Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. Science, 2010, 330, 204-208. | 6.0 | 1,109 |
| 101 | Pyrosequencing Analysis of Bacterial Biofilm Communities in Water Meters of a Drinking Water Distribution System. Applied and Environmental Microbiology, 2010, 76, 5631-5635. | 1.4 | 166 |
| 102 | PyNAST: a flexible tool for aligning sequences to a template alignment. Bioinformatics, 2010, 26, 266-267. | 1.8 | 3,400 |
| 103 | A data analysis and coordination center for the human microbiome project. Genome Biology, 2010, 11, O13. | 13.9 | 8 |
| 104 | Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. PLoS ONE, 2010, 5, e11044. | 1.1 | 395 |
| 105 | Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. PLoS ONE, 2010, 5, e11285. | 1.1 | 66 |
| 106 | Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods. Applied and Environmental Microbiology, 2009, 75, 6559-6567. | 1.4 | 80 |
| 107 | Developing microbeâ€“plant interactions for applications in plantâ€growth promotion and disease control, production of useful compounds, remediation and carbon sequestration. Microbial Biotechnology, 2009, 2, 428-440. | 2.0 | 124 |
| 108 | Influence of trace erythromycin and erythromycin-H2O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). Applied Microbiology and Biotechnology, 2009, 85, 185-195. | 1.7 | 21 |

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|---|---|---|---|
| 109 | Selective progressive response of soil microbial community to wild oat roots. ISME Journal, 2009, 3, 168-178. | 4.4 | 306 |
| 110 | Environmental microarray analyses of Antarctic soil microbial communities. ISME Journal, 2009, 3, 340-351. | 4.4 | 156 |
| 111 | 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 |
| 112 | Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. ISME Journal, 2009, 3, 738-744. | 4.4 | 228 |
| 113 | Transcriptomic microarray analysis of corrinoid responsive genes in<i>Dehalococcoides ethenogenes</i>strain 195. FEMS Microbiology Letters, 2009, 294, 198-206. | 0.7 | 47 |
| 114 | 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 |
| 115 | Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. Science, 2008, 322, 275-278. | 6.0 | 474 |
| 116 | A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. ISME Journal, 2008, 2, 1146-1156. | 4.4 | 299 |
| 117 | Prokaryotic community profiles at different operational stages of a Greek solar saltern. Research in Microbiology, 2008, 159, 609-627. | 1.0 | 52 |
| 118 | Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. Nucleic Acids Research, 2008, 36, e120-e120. | 6.5 | 508 |
| 119 | Comparative Genomics of â€œ <i>Dehalococcoides ethenogenes</i> â€•195 and an Enrichment Culture Containing Unsequenced â€œ <i>Dehalococcoides</i> â€•Strains. Applied and Environmental Microbiology, 2008, 74, 3533-3540. | 1.4 | 53 |
| 120 | Temporal Transcriptomic Microarray Analysis of â€œ <i>Dehalococcoides ethenogenes</i> â€•Strain 195 during the Transition into Stationary Phase. Applied and Environmental Microbiology, 2008, 74, 2864-2872. | 1.4 | 72 |
| 121 | Culture-Independent Bacterial Population Analysis â€“ Clinical Implications for Respiratory and Other Infections. Current Respiratory Medicine Reviews, 2008, 4, 35-39. | 0.1 | 1 |
| 122 | Assays for the rapid and specific identification of North American <i>Yersinia pestis</i> and the common laboratory strain CO92. BioTechniques, 2008, 44, 201-207. | 0.8 | 18 |
| 123 | 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 |
| 124 | Caulobacter crescentus as a Whole-Cell Uranium Biosensor. Applied and Environmental Microbiology, 2007, 73, 7615-7621. | 1.4 | 62 |
| 125 | Role of the <i>rapA</i> Gene in Controlling Antibiotic Resistance of <i>Escherichia coli</i> Biofilms. Antimicrobial Agents and Chemotherapy, 2007, 51, 3650-3658. | 1.4 | 90 |
| 126 | Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with Pseudomonas aeruginosa. Journal of Clinical Microbiology, 2007, 45, 1954-1962. | 1.8 | 166 |

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|---|---|---|---|
| 127 | Automated group assignment in large phylogenetic trees using GRUNT: GRouping, Ungrouping, Naming Tool. BMC Bioinformatics, 2007, 8, 402. | 1.2 | 9 |
| 128 | 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 |
| 129 | Mortality, Recruitment and Change of Desert Tree Populations in a Hyper-Arid Environment. PLoS ONE, 2007, 2, e208. | 1.1 | 38 |
| 130 | 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 |
| 131 | Long-Term Sustainability of a High-Energy, Low-Diversity Crustal Biome. Science, 2006, 314, 479-482. | 6.0 | 350 |
| 132 | Comparison of fecal biota from specific pathogen free and feral mice. Anaerobe, 2006, 12, 249-253. | 1.0 | 31 |
| 133 | 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 |
| 134 | NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. Nucleic Acids Research, 2006, 34, W394-W399. | 6.5 | 918 |
| 135 | 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 |
| 136 | Complete Genome Sequence of Yersinia pestis Strains Antiqua and Nepal516: Evidence of Gene Reduction in an Emerging Pathogen. Journal of Bacteriology, 2006, 188, 4453-4463. | 1.0 | 174 |
| 137 | Rapid quantification and taxonomic classification of environmental DNA from both prokaryotic and eukaryotic origins using a microarray. FEMS Microbiology Letters, 2005, 245, 271-278. | 0.7 | 103 |
| 138 | Whole-Genome Transcriptional Analysis of Heavy Metal Stresses in Caulobacter crescentus. Journal of Bacteriology, 2005, 187, 8437-8449. | 1.0 | 247 |
| 139 | Genome Differences That Distinguish Bacillus anthracis from Bacillus cereus and Bacillus thuringiensis. Applied and Environmental Microbiology, 2003, 69, 2755-2764. | 1.4 | 167 |
| 140 | Comprehensive aligned sequence construction for automated design of effective probes (CASCADE-P) using 16S rDNA. Bioinformatics, 2003, 19, 1461-1468. | 1.8 | 101 |
| 141 | Sequence-specific identification of 18 pathogenic microorganisms using microarray technology. Molecular and Cellular Probes, 2002, 16, 119-127. | 0.9 | 258 |
| 142 | High-Density Microarray of Small-Subunit Ribosomal DNA Probes. Applied and Environmental Microbiology, 2002, 68, 2535-2541. | 1.4 | 277 |
| 143 | Development of a high-volume aerosol collection system for the identification of air-borne micro-organisms. Letters in Applied Microbiology, 2002, 34, 162-167. | 1.0 | 99 |
| 144 | Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. FEMS Microbiology Letters, 2002, 211, 175-182. | 0.7 | 49 |

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|---|---|---|---|
| 145 | Establishment of uncharacterized plasmids inEscherichia coliby in vitro transposition. FEMS Microbiology Letters, 2002, 217, 249-254. | 0.7 | 8 |
| 146 | Genome plasticity in Yersinia pestis 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.. Microbiology (United Kingdom), 2002, 148, 1687-1698. | 0.7 | 67 |
| 147 | Identification by Subtractive Hybridization of Sequences Specific for Salmonella enterica Serovar Enteritidis. Applied and Environmental Microbiology, 2001, 67, 4984-4991. | 1.4 | 152 |
| 148 | Identification of Nucleotide Sequences for the Specific and Rapid Detection of Yersinia pestis. Applied and Environmental Microbiology, 2001, 67, 3759-3762. | 1.4 | 51 |
| 149 | Identification and localization of differences between Escherichia coli and Salmonella typhimurium genomes by suppressive subtractive hybridization. Molecular Genetics and Genomics, 1999, 262, 721-729. | 2.4 | 38 |
| 150 | Molecular Characterization and Sequence of a Methionine Biosynthetic Locus from Pseudomonas syringae. Journal of Bacteriology, 1998, 180, 4497-4507. | 1.0 | 36 |
| 151 | Identification of a region of genetic variability among Bacillus anthracis strains and related species. Journal of Bacteriology, 1996, 178, 377-384. | 1.0 | 120 |
| 152 | Genetic variability of Bacillus anthracis and related species. Journal of Clinical Microbiology, 1995, 33, 1847-1850. | 1.8 | 135 |
| 153 | Characteristics of Insertional Mutants of Pseudomonas syringae with Reduced Epiphytic Fitness. Applied and Environmental Microbiology, 1993, 59, 1593-1601. | 1.4 | 57 |
| 154 | Occurrence and Properties of Copper-Tolerant Strains ofPseudomonas syringaeIsolated from Fruit Trees in California. Phytopathology, 1991, 81, 648. | 1.1 | 71 |
| 155 | Bone haemangio-sarcoma in a young Belgian malinois. Journal of Small Animal Practice, 1990, 31, 349-352. | 0.5 | 2 |
| 156 | Microcomputer Measurements of Pathogen Injury to Weeds. Weed Science, 1986, 34, 38-42. | 0.8 | 3 |