Michael J Sadowsky

List of Publications by Year in Descending Order

446 papers	20,439 citations	74 h-index	123 g-index
476 ext. papers	23,928 ext. citations	6.1 avg, IF	7.03 L-index

#	Paper	IF	Citations
446	Composition and Potential Functions of Rhizobacterial Communities in a Pioneer Plant from Andean Altiplano. *Diversity*, **2022**, 14, 14	2.5	2
445	Erosion and deposition divergently affect the structure of soil bacterial communities and functionality. *Catena*, **2022**, 209, 105805	5.8	0
444	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. *Science of the Total Environment*, **2022**, 805, 149877	10.2	36
443	Differential hydrogen sulfide production by a human cohort in response to animal- and plant-based diet interventions.. *Clinical Nutrition*, **2022**, 41, 1153-1162	5.9	0
442	Halophytes increase rhizosphere microbial diversity, network complexity and function in inland saline ecosystem.. *Science of the Total Environment*, **2022**, 154944	10.2	2
441	Probable role of Cutibacterium acnes in the gut of the polychaete Capitella teleta. *Science of the Total Environment*, **2021**, 809, 151127	10.2	
440	Methanogen Abundance Thresholds Capable of Differentiating In Vitro Methane Production in Human Stool Samples. *Digestive Diseases and Sciences*, **2021**, 66, 3822-3830	4	2
439	Erosion reduces soil microbial diversity, network complexity and multifunctionality. *ISME Journal*, **2021**, 15, 2474-2489	11.9	38
438	Comparative genomic analysis of diverse rhizobia and effective nitrogen-fixing clover-nodulating Rhizobium strains adapted to Egyptian dry ecosystems. *Symbiosis*, **2021**, 84, 39-47	3	1
437	Impacts of cover crops and nitrogen fertilization on agricultural soil fungal and bacterial communities. *Plant and Soil*, **2021**, 466, 139-150	4.2	3
436	Rhizobacteria from 'flowering desert' events contribute to the mitigation of water scarcity stress during tomato seedling germination and growth. *Scientific Reports*, **2021**, 11, 13745	4.9	5
435	Comparative decay of culturable faecal indicator bacteria, microbial source tracking marker genes, and enteric pathogens in laboratory microcosms that mimic a sub-tropical environment. *Science of the Total Environment*, **2021**, 751, 141475	10.2	6
434	Influence of Environmental Stressors on the Microbiota of Zebra Mussels (Dreissena polymorpha). *Microbial Ecology*, **2021**, 81, 1042-1053	4.4	3
433	Influence of seasonality on the aerosol microbiome of the Amazon rainforest. *Science of the Total Environment*, **2021**, 760, 144092	10.2	1
432	Bioturbation by the marine polychaete Capitella teleta alters the sediment microbial community by ingestion and defecation of sediment particles. *Science of the Total Environment*, **2021**, 752, 142239	10.2	2
431	Composition and predicted functions of the bacterial community in spouting pool sediments from the El Tatio Geyser field in Chile. *Archives of Microbiology*, **2021**, 203, 389-397	3	1
430	Faecal microbiota transplantation for Clostridioides difficile: mechanisms and pharmacology. *Nature Reviews Gastroenterology and Hepatology*, **2021**, 18, 67-80	24.2	31

429	Structural modifications that increase gut restriction of bile acid derivatives. *RSC Medicinal Chemistry*, **2021**, 12, 394-405	3.5	1
428	Lower endoscopic delivery of freeze-dried intestinal microbiota results in more rapid and efficient engraftment than oral administration. *Scientific Reports*, **2021**, 11, 4519	4.9	3
427	Microbial source tracking using metagenomics and other new technologies. *Journal of Microbiology*, **2021**, 59, 259-269	3	1
426	Bioaugmentation with As-transforming bacteria improves arsenic availability and uptake by the hyperaccumulator plant (L). *International Journal of Phytoremediation*, **2021**, 1-9	3.9	2
425	A Combined Digital PCR and Next Generation DNA-Sequencing Based Approach for Tracking Nearshore Pollutant Dynamics Along the Southwest United States/Mexico Border. *Frontiers in Microbiology*, **2021**, 12, 674214	5.7	3
424	Biodegradation of azo dyes by bacterial or fungal consortium and identification of the biodegradation products. *Egyptian Journal of Aquatic Research*, **2021**, 47, 269-276	3.1	5
423	Gut Microbiota Associated With Different Sea Lamprey () Life Stages. *Frontiers in Microbiology*, **2021**, 12, 706683	5.7	0
422	Engineering Multigenerational Host-Modulated Microbiota against Soilborne Pathogens in Response to Global Climate Change. *Biology*, **2021**, 10,	4.9	4
421	Temperature alters dicyandiamide (DCD) efficacy for multiple reactive nitrogen species in urea-amended soils: Experiments and modeling. *Soil Biology and Biochemistry*, **2021**, 160, 108341	7.5	1
420	A hybrid DNA sequencing approach is needed to properly link genotype to phenotype in multi-drug resistant bacteria. *Environmental Pollution*, **2021**, 289, 117856	9.3	
419	Inoculation of Mimosa Pudica with Paraburkholderia phymatum Results in Changes to the Rhizoplane Microbial Community Structure. *Microbes and Environments*, **2021**, 36,	2.6	2
418	Niche Differentiation in the Composition, Predicted Function, and Co-occurrence Networks in Bacterial Communities Associated With Antarctic Vascular Plants. *Frontiers in Microbiology*, **2020**, 11, 1036	5.7	10
417	Indigenous soil bacteria and the hyperaccumulator Pteris vittata mediate phytoremediation of soil contaminated with arsenic species. *Ecotoxicology and Environmental Safety*, **2020**, 195, 110458	7	14
416	Environmental and Adaptive Changes Necessitate a Paradigm Shift for Indicators of Fecal Contamination. *Microbiology Spectrum*, **2020**, 8,	8.9	5
415	Lack of evidence for the role of gut microbiota in PAH biodegradation by the polychaete Capitella teleta. *Science of the Total Environment*, **2020**, 725, 138356	10.2	2
414	Composition, Predicted Functions and Co-occurrence Networks of Rhizobacterial Communities Impacting Flowering Desert Events in the Atacama Desert, Chile. *Frontiers in Microbiology*, **2020**, 11, 571	5.7	12
413	Do shared traits create the same fates? Examining the link between morphological type and the biogeography of fungal and bacterial communities. *Fungal Ecology*, **2020**, 46, 100948	4.1	10
412	Structuring biofilm communities living in pesticide contaminated water. *Heliyon*, **2020**, 6, e03996	3.6	7

411	Herbicide bioremediation: from strains to bacterial communities. *Heliyon*, **2020**, 6, e05767	3.6	18
410	Source-Associated Gastroenteritis Risk from Swimming Exposure to Aging Fecal Pathogens. *Environmental Science & Technology*, **2020**, 54, 921-929	10.3	7
409	Water and sediment act as reservoirs for microbial taxa associated with invasive dreissenid mussels. *Science of the Total Environment*, **2020**, 703, 134915	10.2	6
408	Convenient Protocol for Production and Purification of Spores for Germination Studies. *STAR Protocols*, **2020**, 1, 100071	1.4	1
407	Sequence-enabled community-based microbial source tracking in surface waters using machine learning classification: A review. *Journal of Microbiological Methods*, **2020**, 177, 106050	2.8	7
406	Bacterial community composition in agricultural soils under long-term organic and conventional management **2020**, 3, e20063		3
405	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. *Scientific Reports*, **2020**, 10, 20340	4.9	3
404	Randomised clinical study: oral aspirin 325 mg daily vs placebo alters gut microbial composition and bacterial taxa associated with colorectal cancer risk. *Alimentary Pharmacology and Therapeutics*, **2020**, 52, 976-987	6.1	13
403	Impact of Atrazine Exposure on the Microbial Community Structure in a Brazilian Tropical Latosol Soil. *Microbes and Environments*, **2020**, 35,	2.6	11
402	Letter to the Editor. *Clinical Infectious Diseases*, **2019**, 69, 2232-2233	11.6	1
401	Dietary Factors in Sulfur Metabolism and Pathogenesis of Ulcerative Colitis. *Nutrients*, **2019**, 11,	6.7	19
400	Endophytic Bacterial Communities Associated with Roots and Leaves of Plants Growing in Chilean Extreme Environments. *Scientific Reports*, **2019**, 9, 4950	4.9	44
399	Breastmilk and NICU surfaces are potential sources of fungi for infant mycobiomes. *Fungal Genetics and Biology*, **2019**, 128, 29-35	3.9	20
398	Impacts of Sampling Design on Estimates of Microbial Community Diversity and Composition in Agricultural Soils. *Microbial Ecology*, **2019**, 78, 753-763	4.4	8
397	Response of dry bean (Phaseolus vulgaris L.) to inoculation with indigenous and commercial Rhizobium strains under organic farming systems in Minnesota. *Symbiosis*, **2019**, 78, 125-134	3	4
396	Influence of short-term changes in dietary sulfur on the relative abundances of intestinal sulfate-reducing bacteria. *Gut Microbes*, **2019**, 10, 447-457	8.8	15
395	The deposit feeder Capitella teleta has a unique and relatively complex microbiome likely supporting its ability to degrade pollutants. *Science of the Total Environment*, **2019**, 670, 547-554	10.2	10
394	A microfluidic platform for the simultaneous quantification of methanogen populations in anaerobic digestion processes. *Environmental Microbiology*, **2019**, 21, 1798-1808	5.2	7

393	Signal Disruption Leads to Changes in Bacterial Community Population. *Frontiers in Microbiology*, **2019**, 10, 611	5.7	13
392	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. *Frontiers in Microbiology*, **2019**, 10, 635	5.7	18
391	Intermittent flooding of organic-rich soil promotes the formation of denitrification hot moments and hot spots. *Ecosphere*, **2019**, 10, e02549	3.1	17
390	A pilot study of fecal bile acid and microbiota profiles in inflammatory bowel disease and primary sclerosing cholangitis. *Clinical and Experimental Gastroenterology*, **2019**, 12, 9-19	3.1	33
389	Role of Rhizobacteria in Phytoremediation of Metal-Impacted Sites **2019**, 299-328		7
388	Synergy between quantitative microbial source tracking (qMST) and quantitative microbial risk assessment (QMRA): A review and prospectus. *Environment International*, **2019**, 130, 104703	12.9	36
387	Impacts of a changing earth on microbial dynamics and human health risks in the continuum between beach water and sand. *Water Research*, **2019**, 162, 456-470	12.5	28
386	Durable Long-Term Bacterial Engraftment following Encapsulated Fecal Microbiota Transplantation To Treat Clostridium difficile Infection. *MBio*, **2019**, 10,	7.8	36
385	7-Methylation of Chenodeoxycholic Acid Derivatives Yields a Substantial Increase in TGR5 Receptor Potency. *Journal of Medicinal Chemistry*, **2019**, 62, 6824-6830	8.3	8
384	Microbiota transplant therapy and autism: lessons for the clinic. *Expert Review of Gastroenterology and Hepatology*, **2019**, 13, 1033-1037	4.2	12
383	An Alkane Sulfonate Monooxygenase Is Required for Symbiotic Nitrogen Fixation by (syn. Bradyrhizobium japonicum) USDA110. *Applied and Environmental Microbiology*, **2019**, 85,	4.8	4
382	Compositional and temporal stability of fecal taxon libraries for use with SourceTracker in sub-tropical catchments. *Water Research*, **2019**, 165, 114967	12.5	8
381	Influence of Library Composition on SourceTracker Predictions for Community-Based Microbial Source Tracking. *Environmental Science & Technology*, **2019**, 53, 60-68	10.3	20
380	Impact of long-term grazing exclusion on soil microbial community composition and nutrient availability. *Biology and Fertility of Soils*, **2019**, 55, 121-134	6.1	32
379	Comparative decay of sewage-associated marker genes in beach water and sediment in a subtropical region. *Water Research*, **2019**, 149, 511-521	12.5	39
378	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. *Applied Microbiology and Biotechnology*, **2019**, 103, 1973-1987	5.7	9
377	Association between submerged aquatic vegetation and elevated levels of Escherichia coli and potential bacterial pathogens in freshwater lakes. *Science of the Total Environment*, **2019**, 657, 319-324	10.2	13
376	Antibiotic-induced Disruption of Intestinal Microbiota Contributes to Failure of Vertical Sleeve Gastrectomy. *Annals of Surgery*, **2019**, 269, 1092-1100	7.8	19

375	Application of SourceTracker for Accurate Identification of Fecal Pollution in Recreational Freshwater: A Double-Blinded Study. *Environmental Science & Technology*, **2018**, 52, 4207-4217	10.3	42
374	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. *Journal of Microbiology*, **2018**, 56, 189-198	3	63
373	Comparisons of bacterial and archaeal communities in the rumen and a dual-flow continuous culture fermentation system using amplicon sequencing. *Journal of Animal Science*, **2018**, 96, 1059-1072	0.7	8
372	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. *Scientific Reports*, **2018**, 8, 6219	4.9	61
371	The Effects of Turbulence and Carbon Amendments on Nitrate Uptake and Microbial Gene Abundances in Stream Sediment. *Journal of Geophysical Research G: Biogeosciences*, **2018**, 123, 1289-1301	3.7	11
370	Seasonal metabolic analysis of marine sediments collected from Moreton Bay in South East Queensland, Australia, using a multi-omics-based approach. *Science of the Total Environment*, **2018**, 631-632, 1328-1341	10.2	18
369	Select and resequence reveals relative fitness of bacteria in symbiotic and free-living environments. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 2425-2430	11.5	45
368	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. *Cell Host and Microbe*, **2018**, 23, 229-240.e5	23.4	177
367	Widespread occurrence of Sinorhizobium meliloti strains with a type IV secretion system. *Symbiosis*, **2018**, 75, 81-91	3	2
366	Bacillus megaterium strains derived from water and soil exhibit differential responses to the herbicide mesotrione. *PLoS ONE*, **2018**, 13, e0196166	3.7	11
365	Urea Amendment Decreases Microbial Diversity and Selects for Specific Nitrifying Strains in Eight Contrasting Agricultural Soils. *Frontiers in Microbiology*, **2018**, 9, 634	5.7	23
364	CLOUD: a non-parametric detection test for microbiome outliers. *Microbiome*, **2018**, 6, 137	16.6	3
363	Decay of sewage-associated bacterial communities in fresh and marine environmental waters and sediment. *Applied Microbiology and Biotechnology*, **2018**, 102, 7159-7170	5.7	9
362	The complete replicons of 16 Ensifer meliloti strains offer insights into intra- and inter-replicon gene transfer, transposon-associated loci, and repeat elements. *Microbial Genomics*, **2018**, 4,	4.4	8
361	Genome-Wide Association Analyses in the Model Rhizobium. *MSphere*, **2018**, 3,	5	17
360	Complete Genome Sequence of Sinorhizobium meliloti Bacteriophage HMSP1-Susan. *Genome Announcements*, **2018**, 6,		1
359	Practical considerations for sampling and data analysis in contemporary metagenomics-based environmental studies. *Journal of Microbiological Methods*, **2018**, 154, 14-18	2.8	6
358	Comprehensive Functional Analysis of the Enterococcus faecalis Core Genome Using an Ordered, Sequence-Defined Collection of Insertional Mutations in Strain OG1RF. *MSystems*, **2018**, 3,	7.6	28

357	Putative Nitrogen-Fixing Bacteria Associated With the Rhizosphere and Root Endosphere of Wheat Plants Grown in an Andisol From Southern Chile. *Frontiers in Microbiology*, **2018**, 9, 2710	5.7	36
356	Influence of Physicochemical Factors on Bacterial Communities Along the Lower Mekong River Assessed by Illumina Next-Generation Sequencing. *Water, Air, and Soil Pollution*, **2018**, 229, 1	2.6	5
355	Predicting recurrence of Clostridium difficile infection following encapsulated fecal microbiota transplantation. *Microbiome*, **2018**, 6, 166	16.6	49
354	Spatial and temporal characterization of epiphytic microbial communities associated with Eurasian watermilfoil: a highly invasive macrophyte in North America. *FEMS Microbiology Ecology*, **2018**, 94,	4.3	3
353	Fecal pollution: new trends and challenges in microbial source tracking using next-generation sequencing. *Environmental Microbiology*, **2018**, 20, 3132-3140	5.2	30
352	Quantitative microbial risk assessment of microbial source tracking markers in recreational water contaminated with fresh untreated and secondary treated sewage. *Environment International*, **2018** , 117, 243-249	12.9	57
351	Precipitation influences pathogenic bacteria and antibiotic resistance gene abundance in storm drain outfalls in coastal sub-tropical waters. *Environment International*, **2018**, 116, 308-318	12.9	61
350	Sleeve gastrectomy drives persistent shifts in the gut microbiome. *Surgery for Obesity and Related Diseases*, **2017**, 13, 916-924	3	32
349	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. *Microbiome*, **2017**, 5, 10	16.6	595
348	Complete Genome Sequence of the Triclosan- and Multidrug-Resistant Pseudomonas aeruginosa Strain B10W Isolated from Municipal Wastewater. *Genome Announcements*, **2017**, 5,		1
347	Community dynamics drive punctuated engraftment of the fecal microbiome following transplantation using freeze-dried, encapsulated fecal microbiota. *Gut Microbes*, **2017**, 8, 276-288	8.8	25
346	Metabolic Interference of sod gene mutations on catalase activity in Escherichia coli exposed to Gramoxone (paraquat) herbicide. *Ecotoxicology and Environmental Safety*, **2017**, 139, 89-96	7	10
345	Successful Resolution of Recurrent Clostridium difficile Infection using Freeze-Dried, Encapsulated Fecal Microbiota; Pragmatic Cohort Study. *American Journal of Gastroenterology*, **2017**, 112, 940-947	0.7	109
344	Synthesis and Biological Evaluation of Bile Acid Analogues Inhibitory to Clostridium difficile Spore Germination. *Journal of Medicinal Chemistry*, **2017**, 60, 3451-3471	8.3	25
343	Nitrification gene ratio and free ammonia explain nitrite and nitrous oxide production in urea-amended soils. *Soil Biology and Biochemistry*, **2017**, 111, 143-153	7.5	51
342	The Diet and Gut Microbial Communities of Two Closely Related Combtooth Blennies,Chasmodes saburraeandScartella cristata. *Copeia*, **2017**, 105, 249-256	1.1	5
341	Factors influencing the Salmonella internalization into seedpods and whole plants of Arachis hypogaea (L.). *Food Microbiology*, **2017**, 66, 184-189	6	3
340	Novel Microbial Assemblages Dominate Weathered Sulfide-Bearing Rock from Copper-Nickel Deposits in the Duluth Complex, Minnesota, USA. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	23

339	Environmental Escherichia coli: ecology and public health implications-a review. *Journal of Applied Microbiology*, **2017**, 123, 570-581	4.7	230
338	Differential Impacts of Land-Based Sources of Pollution on the Microbiota of Southeast Florida Coral Reefs. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	31
337	Gut-sparing treatment of urinary tract infection in patients at high risk of Clostridium difficile infection. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 522-528	5.1	6
336	Type IV Effector Proteins Involved in the Medicago-Sinorhizobium Symbiosis. *Molecular Plant-Microbe Interactions*, **2017**, 30, 28-34	3.6	14
335	Analysis of gut microbiota - An ever changing landscape. *Gut Microbes*, **2017**, 8, 268-275	8.8	18
334	Phylogenetic Backgrounds and Virulence-Associated Traits of Escherichia coli Isolates from Surface Waters and Diverse Animals in Minnesota and Wisconsin. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	10
333	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. *Microbiome*, **2017**, 5, 87	16.6	77
332	Optimization of conditions for decolorization of azo-based textile dyes by multiple fungal species. *Journal of Biotechnology*, **2017**, 260, 11-17	3.7	36
331	Influence of heavy metals on rhizosphere microbial communities of Siam weed (Chromolaena odorata (L.)) using a 16S rRNA gene amplicon sequencing approach. *Agriculture and Natural Resources*, **2017**, 51, 137-141	1.3	3
330	Environmental drivers of denitrification rates and denitrifying gene abundances in channels and riparian areas. *Water Resources Research*, **2017**, 53, 6523-6538	5.4	26
329	A multi-omics based ecological analysis of coastal marine sediments from Gladstone, in Australia's Central Queensland, and Heron Island, a nearby fringing platform reef. *Science of the Total Environment*, **2017**, 609, 842-853	10.2	19
328	Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. *Molecular Ecology*, **2017**, 26, 6122-6135	5.7	23
327	Competition between introduced Bradyrhizobium japonicum strains and indigenous bradyrhizobia in Minnesota organic farming systems. *Symbiosis*, **2017**, 73, 155-163	3	11
326	Contemporary Applications of Fecal Microbiota Transplantation to Treat Intestinal Diseases in Humans. *Archives of Medical Research*, **2017**, 48, 766-773	6.6	20
325	Effect of Different Treatment Technologies on the Fate of Antibiotic Resistance Genes and Class 1 Integrons when Residual Municipal Wastewater Solids are Applied to Soil. *Environmental Science & Technology*, **2017**, 51, 14225-14232	10.3	45
324	A High-Throughput DNA-Sequencing Approach for Determining Sources of Fecal Bacteria in a Lake Superior Estuary. *Environmental Science & Technology*, **2017**, 51, 8263-8271	10.3	40
323	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. *Microbiome*, **2017**, 5, 65	16.6	30
322	Virulence and biodegradation potential of dynamic microbial communities associated with decaying Cladophora in Great Lakes. *Science of the Total Environment*, **2017**, 574, 872-880	10.2	11

321	Amplicon-based taxonomic characterization of bacteria in urban and peri-urban roof-harvested rainwater stored in tanks. *Science of the Total Environment*, **2017**, 576, 326-334	10.2	29
320	Recent changes to the classification of symbiotic, nitrogen-fixing, legume-associating bacteria: a review. *Symbiosis*, **2017**, 71, 91-109	3	42
319	Interaction of gut microbiota with bile acid metabolism and its influence on disease states. *Applied Microbiology and Biotechnology*, **2017**, 101, 47-64	5.7	235
318	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, Medicago truncatula. *BMC Genomics*, **2017**, 18, 578	4.5	41
317	Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. *Genes*, **2017**, 8,	4.2	29
316	A Community Multi-Omics Approach towards the Assessment of Surface Water Quality in an Urban River System. *International Journal of Environmental Research and Public Health*, **2017**, 14,	4.6	36
315	Increased Denitrification Rates Associated with Shifts in Prokaryotic Community Composition Caused by Varying Hydrologic Connectivity. *Frontiers in Microbiology*, **2017**, 8, 2304	5.7	16
314	Effect of Fecal Microbiota Transplantation on Recurrence in Multiply Recurrent Clostridium difficile Infection: A Randomized Trial. *Annals of Internal Medicine*, **2016**, 165, 609-616	8	344
313	Environment shapes the fecal microbiome of invasive carp species. *Microbiome*, **2016**, 4, 44	16.6	90
312	Faecal microbiota transplantation is promising but not a panacea. *Nature Microbiology*, **2016**, 1, 16015	26.6	20
311	GST activity and membrane lipid saturation prevents mesotrione-induced cellular damage in Pantoea ananatis. *AMB Express*, **2016**, 6, 70	4.1	12
310	Ursodeoxycholic Acid Inhibits Clostridium difficile Spore Germination and Vegetative Growth, and Prevents the Recurrence of Ileal Pouchitis Associated With the Infection. *Journal of Clinical Gastroenterology*, **2016**, 50, 624-30	3	69
309	Understanding the mechanisms of faecal microbiota transplantation. *Nature Reviews Gastroenterology and Hepatology*, **2016**, 13, 508-16	24.2	245
308	The symbiovar trifolii of Rhizobium bangladeshense and Rhizobium aegyptiacum sp. nov. nodulate Trifolium alexandrinum in Egypt. *Systematic and Applied Microbiology*, **2016**, 39, 275-279	4.2	29
307	Associations between soil bacterial community structure and nutrient cycling functions in long-term organic farm soils following cover crop and organic fertilizer amendment. *Science of the Total Environment*, **2016**, 566-567, 949-959	10.2	69
306	Modeling the fate of antibiotic resistance genes and class 1 integrons during thermophilic anaerobic digestion of municipal wastewater solids. *Applied Microbiology and Biotechnology*, **2016**, 100, 1437-1444	5.7	31
305	Sediments and Soils Act as Reservoirs for Taxonomic and Functional Bacterial Diversity in the Upper Mississippi River. *Microbial Ecology*, **2016**, 71, 814-24	4.4	20
304	Inflammatory Bowel Disease Affects the Outcome of Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection. *Clinical Gastroenterology and Hepatology*, **2016**, 14, 1433-8	6.9	149

303	Regional Similarities and Consistent Patterns of Local Variation in Beach Sand Bacterial Communities throughout the Northern Hemisphere. *Applied and Environmental Microbiology*, **2016**, 82, 2751-2762	4.8	20
302	Changes in Colonic Bile Acid Composition following Fecal Microbiota Transplantation Are Sufficient to Control Clostridium difficile Germination and Growth. *PLoS ONE*, **2016**, 11, e0147210	3.7	90
301	Bacterial biogeography influenced by shelf-basin exchange in the Arctic surface sediment at the Chukchi Borderland. *Environmental Microbiology*, **2016**, 18, 668-78	5.2	1
300	Complete Microbiota Engraftment Is Not Essential for Recovery from Recurrent Clostridium difficile Infection following Fecal Microbiota Transplantation. *MBio*, **2016**, 7,	7.8	66
299	Application of metagenomics to assess microbial communities in water and other environmental matrices. *Journal of the Marine Biological Association of the United Kingdom*, **2016**, 96, 121-129	1.1	19
298	Draft Genome Sequences of Four Novel Thermal- and Alkaline-Tolerant Egyptian Rhizobium Strains Nodulating Berseem Clover. *Genome Announcements*, **2016**, 4,		2
297	Beach sand and the potential for infectious disease transmission: observations and recommendations. *Journal of the Marine Biological Association of the United Kingdom*, **2016**, 96, 101-120	1.1	53
296	Environmental Contamination in Households of Patients with Recurrent Clostridium difficile Infection. *Applied and Environmental Microbiology*, **2016**, 82, 2686-2692	4.8	23
295	Correlations between pathogen concentration and fecal indicator marker genes in beach environments. *Science of the Total Environment*, **2016**, 573, 826-830	10.2	31
294	Structure of bacterial communities in soil following cover crop and organic fertilizer incorporation. *Applied Microbiology and Biotechnology*, **2016**, 100, 9331-9341	5.7	50
293	Survival and Competitiveness of Bradyrhizobium japonicum Strains 20 Years after Introduction into Field Locations in Poland. *Applied and Environmental Microbiology*, **2015**, 81, 5552-9	4.8	29
292	Toolbox Approaches Using Molecular Markers and 16S rRNA Gene Amplicon Data Sets for Identification of Fecal Pollution in Surface Water. *Applied and Environmental Microbiology*, **2015**, 81, 7067-77	4.8	55
291	Influence of seawater intrusion on microbial communities in groundwater. *Science of the Total Environment*, **2015**, 532, 337-43	10.2	28
290	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. *Journal of Dairy Science*, **2015**, 98, 3568-76	4	41
289	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. *Microbiome*, **2015**, 3, 10	16.6	175
288	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. *Journal of Microbiological Methods*, **2015**, 114, 43-50	2.8	31
287	Influence of Hyphal Inoculum potential on the Competitive Success of Fungi Colonizing Wood. *Microbial Ecology*, **2015**, 69, 758-67	4.4	23
286	Isolation and Characterization of a Novel Imidacloprid-Degrading Mycobacterium sp. Strain MK6 from an Egyptian Soil. *Journal of Agricultural and Food Chemistry*, **2015**, 63, 4721-7	5.7	36

285	Rapid method using two microbial enzymes for detection of L-abrine in food as a marker for the toxic protein abrin. *Applied and Environmental Microbiology*, **2015**, 81, 1610-5	4.8	2
284	Geographic isolation of Escherichia coli genotypes in sediments and water of the Seven Mile Creek - A constructed riverine watershed. *Science of the Total Environment*, **2015**, 538, 78-85	10.2	14
283	Site-specific distribution and competitive ability of indigenous bean-nodulating rhizobia isolated from organic fields in Minnesota. *Journal of Biotechnology*, **2015**, 214, 158-68	3.7	3
282	Development of fecal microbiota transplantation suitable for mainstream medicine. *Clinical Gastroenterology and Hepatology*, **2015**, 13, 246-50	6.9	32
281	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. *Science of the Total Environment*, **2015**, 505, 435-45	10.2	97
280	Ammonium sorption and ammonia inhibition of nitrite-oxidizing bacteria explain contrasting soil N2O production. *Scientific Reports*, **2015**, 5, 12153	4.9	89
279	An Alternative Approach to "Identification of Unknowns": Designing a Protocol to Verify the Identities of Nitrogen Fixing Bacteria. *Journal of Microbiology and Biology Education*, **2015**, 16, 247-53	1.3	4
278	High-throughput functional screening reveals low frequency of antibiotic resistance genes in DNA recovered from the Upper Mississippi River. *Journal of Water and Health*, **2015**, 13, 693-703	2.2	9
277	Characterization of a Functional Role of the Bradyrhizobium japonicum Isocitrate Lyase in Desiccation Tolerance. *International Journal of Molecular Sciences*, **2015**, 16, 16695-709	6.3	9
276	Secretion systems and signal exchange between nitrogen-fixing rhizobia and legumes. *Frontiers in Plant Science*, **2015**, 6, 491	6.2	99
275	Transformation of tetracycline by TetX and its subsequent degradation in a heterologous host. *FEMS Microbiology Ecology*, **2015**, 91,	4.3	17
274	A novel microbial source tracking microarray for pathogen detection and fecal source identification in environmental systems. *Environmental Science & Technology*, **2015**, 49, 7319-29	10.3	33
273	Dynamic changes in the population structure of Escherichia coli in the Yeongsan River basin of South Korea. *FEMS Microbiology Ecology*, **2015**, 91,	4.3	5
272	Frequencies of heavy metal resistance are associated with land cover type in the Upper Mississippi River. *Science of the Total Environment*, **2015**, 511, 461-8	10.2	15
271	Biodegradation of atrazine by three transgenic grasses and alfalfa expressing a modified bacterial atrazine chlorohydrolase gene. *Transgenic Research*, **2015**, 24, 475-88	3.3	11
270	Predominant populations of indigenous soybean-nodulating Bradyrhizobium japonicum strains obtained from organic farming systems in Minnesota. *Journal of Applied Microbiology*, **2015**, 118, 1152-64	4.7	11
269	Prevalence of toxin-producing Clostridium botulinum associated with the macroalga Cladophora in three Great Lakes: growth and management. *Science of the Total Environment*, **2015**, 511, 523-9	10.2	9
268	Complementary amplicon-based genomic approaches for the study of fungal communities in humans. *PLoS ONE*, **2015**, 10, e0116705	3.7	37

267	Microscale measurements reveal contrasting effects of photosynthesis and epiphytes on frictional drag on the surfaces of filamentous algae. *Freshwater Biology*, **2014**, 59, 312-324	3.1	6
266	Shift of bacterial community structure in two Thai soil series affected by silver nanoparticles using ARISA. *World Journal of Microbiology and Biotechnology*, **2014**, 30, 2119-24	4.4	14
265	Environmental and animal-associated enterococci. *Advances in Applied Microbiology*, **2014**, 87, 147-86	4.9	31
264	Enhanced nodulation and nodule development by nolR mutants of Sinorhizobium medicae on specific Medicago host genotypes. *Molecular Plant-Microbe Interactions*, **2014**, 27, 328-35	3.6	13
263	Quantitative PCR for measuring biomass of decomposer fungi in planta. *Fungal Ecology*, **2014**, 7, 39-46	4.1	18
262	Microbiota transplantation restores normal fecal bile acid composition in recurrent Clostridium difficile infection. *American Journal of Physiology - Renal Physiology*, **2014**, 306, G310-9	5.1	254
261	Biodegradation in Waters from Hydraulic Fracturing: Chemistry, Microbiology, and Engineering. *Journal of Environmental Engineering, ASCE*, **2014**, 140,	2	54
260	Fate of antibiotic resistance genes and class 1 integrons in soil microcosms following the application of treated residual municipal wastewater solids. *Environmental Science & Technology*, **2014**, 48, 5620-7	10.3	88
259	Species and genus level resolution analysis of gut microbiota in Clostridium difficile patients following fecal microbiota transplantation. *Microbiome*, **2014**, 2, 13	16.6	77
258	Microbes in Beach Sands: Integrating Environment, Ecology and Public Health. *Reviews in Environmental Science and Biotechnology*, **2014**, 13, 329-368	13.9	98
257	Decay of genetic markers for fecal bacterial indicators and pathogens in sand from Lake Superior. *Water Research*, **2014**, 59, 99-111	12.5	35
256	Enteric pathogen-plant interactions: molecular connections leading to colonization and growth and implications for food safety. *Microbes and Environments*, **2014**, 29, 123-35	2.6	52
255	Mechanisms of tolerance and high degradation capacity of the herbicide mesotrione by Escherichia coli strain DH5-□*PLoS ONE*, **2014**, 9, e99960	3.7	25
254	Measurement and Modeling of Denitrification in Sand-Bed Streams under Various Land Uses. *Journal of Environmental Quality*, **2014**, 43, 1013-23	3.4	8
253	Selection on horizontally transferred and duplicated genes in sinorhizobium (ensifer), the root-nodule symbionts of medicago. *Genome Biology and Evolution*, **2014**, 6, 1199-209	3.9	14
252	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. *Frontiers in Microbiology*, **2014**, 5, 414	5.7	64
251	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. *Frontiers in Microbiology*, **2014**, 5, 524	5.7	61
250	Draft Genome Sequence of Sphingobacterium sp. Strain PM2-P1-29, a Tetracycline-Degrading TetX-Expressing Aerobic Bacterium Isolated from Agricultural Soil. *Genome Announcements*, **2014**, 2,		4

249	Genome-scale metabolic network validation of Shewanella oneidensis using transposon insertion frequency analysis. *PLoS Computational Biology*, **2014**, 10, e1003848	5	20
248	Near-full length sequencing of 16S rDNA and RFLP indicates that Rhizobium etli is the dominant species nodulating Egyptian winter Berseem clover (Trifolium alexandrinum L.). *Systematic and Applied Microbiology*, **2014**, 37, 121-8	4.2	14
247	Notable decomposition products of senescing Lake Michigan Cladophora glomerata. *Journal of Great Lakes Research*, **2014**, 40, 800-806	3	7
246	Immune mediated shaping of microflora community composition depends on barrier site. *PLoS ONE* , **2014**, 9, e84019	3.7	27
245	Seasonal and genotypic changes in escherichia coli phylogenetic groups in the Yeongsan River basin of South Korea. *PLoS ONE*, **2014**, 9, e100585	3.7	13
244	Measurement and Modeling of Denitrification in Sand-Bed Streams under Various Land Uses **2014**, 43, 1013		0
243	Comparative genomics of the core and accessory genomes of 48 Sinorhizobium strains comprising five genospecies. *Genome Biology*, **2013**, 14, R17	18.3	114
242	Evaluation of molecular community analysis methods for discerning fecal sources and human waste. *Water Research*, **2013**, 47, 6862-72	12.5	48
241	Amino acid substitutions in naphthalene dioxygenase from Pseudomonas sp. strain NCIB 9816-4 result in regio- and stereo-specific hydroxylation of flavanone and isoflavanone. *Applied Microbiology and Biotechnology*, **2013**, 97, 693-704	5.7	10
240	Air-drying beds reduce the quantities of antibiotic resistance genes and class 1 integrons in residual municipal wastewater solids. *Environmental Science & Technology*, **2013**, 47, 9965-71	10.3	38
239	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. *Journal of Applied Microbiology*, **2013**, 115, 1147-58	4.7	156
238	Methanogenesis facilitated by geobiochemical iron cycle in a novel syntrophic methanogenic microbial community. *Environmental Science & Technology*, **2013**, 47, 10078-84	10.3	66
237	Characterization of an isoeugenol monooxygenase (Iem) from Pseudomonas nitroreducens Jin1 that transforms isoeugenol to vanillin. *Bioscience, Biotechnology and Biochemistry*, **2013**, 77, 289-94	2.1	20
236	Photosynthetic Bradyrhizobium sp. strain ORS285 is capable of forming nitrogen-fixing root nodules on soybeans (Glycine max). *Applied and Environmental Microbiology*, **2013**, 79, 2459-62	4.8	11
235	Evaluation of the repeatability and reproducibility of a suite of qPCR-based microbial source tracking methods. *Water Research*, **2013**, 47, 6839-48	12.5	48
234	Multi-laboratory evaluations of the performance of Catellicoccus marimammalium PCR assays developed to target gull fecal sources. *Water Research*, **2013**, 47, 6883-96	12.5	46
233	The establishment of the nuisance cyanobacteria Lyngbya wollei in Lake St. Clair and its potential to harbor fecal indicator bacteria. *Journal of Great Lakes Research*, **2013**, 39, 560-568	3	21
232	Root and Stem Nodule Bacteria of Legumes **2013**, 401-425		5

231	Incidence of naturally internalized bacteria in lettuce leaves. *International Journal of Food Microbiology*, **2013**, 162, 260-5	5.8	28
230	Transcriptional and functional responses of Escherichia coli O157:H7 growing in the lettuce rhizoplane. *Food Microbiology*, **2013**, 35, 136-42	6	17
229	Antimicrobial peptides targeting Gram-negative pathogens, produced and delivered by lactic acid bacteria. *ACS Synthetic Biology*, **2013**, 2, 643-50	5.7	50
228	Pathogenic Escherichia coli strains producing extended-spectrum β-lactamases in the Yeongsan River basin of South Korea. *Environmental Science & Technology*, **2013**, 47, 1128-36	10.3	29
227	Distribution of genetic markers of fecal pollution on a freshwater sandy shoreline in proximity to wastewater effluent. *Environmental Science & Technology*, **2013**, 47, 3395-402	10.3	24
226	Association of toxin-producing Clostridium botulinum with the macroalga Cladophora in the Great Lakes. *Environmental Science & Technology*, **2013**, 47, 2587-94	10.3	34
225	Complete Genome Sequence of the Sesbania Symbiont and Rice Growth-Promoting Endophyte Rhizobium sp. Strain IRBG74. *Genome Announcements*, **2013**, 1,		28
224	Resolution of severe Clostridium difficile infection following sequential fecal microbiota transplantation. *Journal of Clinical Gastroenterology*, **2013**, 47, 735-7	3	71
223	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. *Journal of Experimental Medicine*, **2013**, 210, 2011-24	16.6	121
222	High-throughput DNA sequence analysis reveals stable engraftment of gut microbiota following transplantation of previously frozen fecal bacteria. *Gut Microbes*, **2013**, 4, 125-35	8.8	218
221	Occurrence, genetic diversity, and persistence of enterococci in a Lake Superior watershed. *Applied and Environmental Microbiology*, **2013**, 79, 3067-75	4.8	22
220	Influence of elevated atmospheric carbon dioxide on transcriptional responses of Bradyrhizobium japonicum in the soybean rhizoplane. *Microbes and Environments*, **2013**, 28, 217-27	2.6	13
219	Characterization of a self-sufficient trans-anethole oxygenase from Pseudomonas putida JYR-1. *PLoS ONE*, **2013**, 8, e73350	3.7	4
218	Candidate genes and genetic architecture of symbiotic and agronomic traits revealed by whole-genome, sequence-based association genetics in Medicago truncatula. *PLoS ONE*, **2013**, 8, e65688	3.7	121
217	Aerobic digestion reduces the quantity of antibiotic resistance genes in residual municipal wastewater solids. *Frontiers in Microbiology*, **2013**, 4, 17	5.7	58
216	The population structure of Escherichia coli isolated from subtropical and temperate soils. *Science of the Total Environment*, **2012**, 417-418, 273-9	10.2	40
215	Gene expression profiling of Escherichia coli in response to interactions with the lettuce rhizosphere. *Journal of Applied Microbiology*, **2012**, 113, 1076-86	4.7	18
214	Integrated online system for a pyrosequencing-based microbial source tracking method that targets Bacteroidetes 16S rDNA. *Environmental Science & Technology*, **2012**, 46, 93-8	10.3	33

213	A model laboratory system to study the synergistic interaction and growth of environmental Escherichia coli with macrophytic green algae. *Journal of Great Lakes Research*, **2012**, 38, 390-395	3	3
212	Silica gel-encapsulated AtzA biocatalyst for atrazine biodegradation. *Applied Microbiology and Biotechnology*, **2012**, 96, 231-40	5.7	29
211	Standardized frozen preparation for transplantation of fecal microbiota for recurrent Clostridium difficile infection. *American Journal of Gastroenterology*, **2012**, 107, 761-7	0.7	466
210	LegumeMicrobe Symbioses **2012**, 73-88		
209	Phylogenetic and phenotypic analyses of arsenic-reducing bacteria isolated from an old tin mine area in Thailand. *World Journal of Microbiology and Biotechnology*, **2012**, 28, 2287-92	4.4	4
208	Competition between two wood-degrading fungi with distinct influences on residues. *FEMS Microbiology Ecology*, **2012**, 79, 109-17	4.3	27
207	Isolation of mesotrione-degrading bacteria from aquatic environments in Brazil. *Chemosphere*, **2012** , 86, 1127-32	8.4	34
206	Plasmid localization and organization of melamine degradation genes in Rhodococcus sp. strain Mel. *Applied and Environmental Microbiology*, **2012**, 78, 1397-403	4.8	21
205	Transcriptional responses of Escherichia coli K-12 and O157:H7 associated with lettuce leaves. *Applied and Environmental Microbiology*, **2012**, 78, 1752-64	4.8	73
204	Transcriptional control of the isoeugenol monooxygenase of Pseudomonas nitroreducens Jin1 in Escherichia coli. *Bioscience, Biotechnology and Biochemistry*, **2012**, 76, 1891-6	2.1	10
203	Transcriptional Responses of Escherichia coli K-12 and O157:H7 Associated with Lettuce Leaves. *Applied and Environmental Microbiology*, **2012**, 78, 3783-3783	4.8	1
202	Defining sequence space and reaction products within the cyanuric acid hydrolase (AtzD)/barbiturase protein family. *Journal of Bacteriology*, **2012**, 194, 4579-88	3.5	25
201	Population genomics of the facultatively mutualistic bacteria Sinorhizobium meliloti and S. medicae. *PLoS Genetics*, **2012**, 8, e1002868	6	56
200	Simultaneous synthesis of temperature-tunable peptide and gold nanoparticle hybrid spheres. *Biomacromolecules*, **2011**, 12, 2518-23	6.9	24
199	Multi-scale temporal and spatial variation in genotypic composition of Cladophora-borne Escherichia coli populations in Lake Michigan. *Water Research*, **2011**, 45, 721-31	12.5	21
198	E. coli histidine triad nucleotide binding protein 1 (ecHinT) is a catalytic regulator of D-alanine dehydrogenase (DadA) activity in vivo. *PLoS ONE*, **2011**, 6, e20897	3.7	12
197	Expression and functional roles of Bradyrhizobium japonicum genes involved in the utilization of inorganic and organic sulfur compounds in free-living and symbiotic conditions. *Molecular Plant-Microbe Interactions*, **2011**, 24, 451-7	3.6	10
196	Waterfowl abundance does not predict the dominant avian source of beach Escherichia coli. *Journal of Environmental Quality*, **2011**, 40, 1924-31	3.4	7

195	Genotypic and phenotypic trends in antibiotic resistant pathogenic Escherichia coli isolated from humans and farm animals in South Korea. *Microbes and Environments*, **2011**, 26, 198-204	2.6	10
194	Prevalence of season-specific Escherichia coli strains in the Yeongsan River Basin of South Korea. *Environmental Microbiology*, **2011**, 13, 3103-13	5.2	14
193	Soil nitrogen transformations under elevated atmospheric CO and O during the soybean growing season. *Environmental Pollution*, **2011**, 159, 401-7	9.3	20
192	The occurrence of virulence traits among high-level aminoglycosides resistant Enterococcus isolates obtained from feces of humans, animals, and birds in South Korea. *International Journal of Food Microbiology*, **2011**, 144, 387-92	5.8	40
191	Hydrothermal carbonization of microalgae II. Fatty acid, char, and algal nutrient products. *Applied Energy*, **2011**, 88, 3286-3290	10.7	117
190	Synthesis of chalcogenide ternary and quaternary nanotubes through directed compositional alterations of bacterial As nanotubes. *Journal of Materials Chemistry*, **2011**, 21, 10277		7
189	Bacterial formation of extracellular U(VI) nanowires. *Chemical Communications*, **2011**, 47, 8076-8	5.8	15
188	Biodegradation and mineralization of metolachlor and alachlor by Candida xestobii. *Journal of Agricultural and Food Chemistry*, **2011**, 59, 619-27	5.7	39
187	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume Medicago truncatula. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E864-70	11.5	178
186	A New Family of Biuret Hydrolases Involved in S-Triazine Ring Metabolism. *ACS Catalysis*, **2011**, 2011, 1075-1082	13.1	19
185	Hydrothermal carbonization of distillers grains. *Biomass and Bioenergy*, **2011**, 35, 2526-2533	5.3	113
184	Therapeutic transplantation of the distal gut microbiota. *Mucosal Immunology*, **2011**, 4, 4-7	9.2	66
183	Identification of a Brevibacterium marker gene specific to poultry litter and development of a quantitative PCR assay. *Journal of Applied Microbiology*, **2010**, 109, 334-47	4.7	53
182	Functional role of Bradyrhizobium japonicum trehalose biosynthesis and metabolism genes during physiological stress and nodulation. *Applied and Environmental Microbiology*, **2010**, 76, 1071-81	4.8	67
181	Bacterial ammeline metabolism via guanine deaminase. *Journal of Bacteriology*, **2010**, 192, 1106-12	3.5	27
180	X-ray structure and mutational analysis of the atrazine Chlorohydrolase TrzN. *Journal of Biological Chemistry*, **2010**, 285, 30606-14	5.4	24
179	Soybean metabolites regulated in root hairs in response to the symbiotic bacterium Bradyrhizobium japonicum. *Plant Physiology*, **2010**, 153, 1808-22	6.6	116
178	Use of barcoded pyrosequencing and shared OTUs to determine sources of fecal bacteria in watersheds. *Environmental Science & Technology*, **2010**, 44, 7777-82	10.3	95

177	Large scale analysis of virulence genes in Escherichia coli strains isolated from Avalon Bay, CA. *Water Research*, **2010**, 44, 5463-73	12.5	48
176	Bioavailability of organoclay formulations of atrazine in soil. *Journal of Agricultural and Food Chemistry*, **2010**, 58, 11857-63	5.7	13
175	Shewanella-mediated synthesis of selenium nanowires and nanoribbons. *Journal of Materials Chemistry*, **2010**, 20, 5899		29
174	Factors controlling long-term survival and growth of naturalized Escherichia coli populations in temperate field soils. *Microbes and Environments*, **2010**, 25, 8-14	2.6	43
173	Changes in the composition of the human fecal microbiome after bacteriotherapy for recurrent Clostridium difficile-associated diarrhea. *Journal of Clinical Gastroenterology*, **2010**, 44, 354-60	3	499
172	Laser imaging for rapid Microbial Source Tracking. *International Journal of Computational Biology and Drug Design*, **2010**, 3, 177-86	0.4	3
171	DNA Profiling in Ecology **2010**,		1
170	Isoeugenol monooxygenase and its putative regulatory gene are located in the eugenol metabolic gene cluster in Pseudomonas nitroreducens Jin1. *Archives of Microbiology*, **2010**, 192, 201-9	3	16
169	High diversity and abundance of antibiotic-resistant Escherichia coli isolated from humans and farm animal hosts in Jeonnam Province, South Korea. *Science of the Total Environment*, **2010**, 408, 3499-506	10.2	20
168	Peptide-mediated shape- and size-tunable synthesis of gold nanostructures. *Acta Biomaterialia*, **2010**, 6, 2681-9	10.8	106
167	Hydrothermal carbonization of microalgae. *Biomass and Bioenergy*, **2010**, 34, 875-882	5.3	256
166	Structure and Diversity of Arsenic Resistant Bacteria in an Old Tin Mine Area of Thailand. *Journal of Microbiology and Biotechnology*, **2010**, 20, 169-178	3.3	18
165	Structure and diversity of arsenic resistant bacteria in an old tin mine area of Thailand. *Journal of Microbiology and Biotechnology*, **2010**, 20, 169-78	3.3	4
164	Arthrobacter sp. strain KU001 isolated from a Thai soil degrades atrazine in the presence of inorganic nitrogen sources. *Journal of Microbiology and Biotechnology*, **2010**, 20, 602-8	3.3	11
163	Escherichia coli populations in Great Lakes waterfowl exhibit spatial stability and temporal shifting. *Applied and Environmental Microbiology*, **2009**, 75, 1546-51	4.8	16
162	Absence of Escherichia coli phylogenetic group B2 strains in humans and domesticated animals from Jeonnam Province, Republic of Korea. *Applied and Environmental Microbiology*, **2009**, 75, 5659-66	4.8	39
161	Thermostable cyanuric acid hydrolase from Moorella thermoacetica ATCC 39073. *Applied and Environmental Microbiology*, **2009**, 75, 6986-91	4.8	14
160	Rapid identification and discrimination among Egyptian genotypes of Rhizobium leguminosarum bv. viciae and Sinorhizobium meliloti nodulating faba bean (Vicia faba L.) by analysis of nodC, ARDRA, and rDNA sequence analysis. *Soil Biology and Biochemistry*, **2009**, 41, 45-53	7.5	26

159	Sphingobacterium sp. strain PM2-P1-29 harbours a functional tet(X) gene encoding for the degradation of tetracycline. *Journal of Applied Microbiology*, **2009**, 106, 1336-42	4.7	77
158	Applications of the rep-PCR DNA fingerprinting technique to study microbial diversity, ecology and evolution. *Environmental Microbiology*, **2009**, 11, 733-40	5.2	95
157	Rapid and complete degradation of the herbicide picloram by Lipomyces kononenkoae. *Journal of Agricultural and Food Chemistry*, **2009**, 57, 4878-82	5.7	12
156	Biogenic formation of As-S nanotubes by diverse Shewanella strains. *Applied and Environmental Microbiology*, **2009**, 75, 6896-9	4.8	46
155	Seasonal stability of Cladophora-associated Salmonella in Lake Michigan watersheds. *Water Research*, **2009**, 43, 806-14	12.5	68
154	Identification of a Brevibacterium marker gene specific to poultry litter and development of a quantitative PCR assay. *Journal of Applied Microbiology*, **2009**, 109, 334	4.7	2
153	Insights learned from pBTAi1, a 229-kb accessory plasmid from Bradyrhizobium sp. strain BTAi1 and prevalence of accessory plasmids in other Bradyrhizobium sp. strains. *ISME Journal*, **2008**, 2, 158-70	11.9	20
152	Sources and Sinks of Escherichia coli in Benthic and Pelagic Fish. *Journal of Great Lakes Research*, **2008**, 34, 228-234	3	16
151	Mineralization of the Bacillus thuringiensis Cry1Ac endotoxin in soil. *Journal of Agricultural and Food Chemistry*, **2008**, 56, 1025-8	5.7	18
150	Microbial Degradation of s-Triazine Herbicides **2008**, 301-328		13
149	Availability of triazine herbicides in aged soils amended with olive oil mill waste. *Journal of Agricultural and Food Chemistry*, **2008**, 56, 4112-9	5.7	31
148	Nodulation gene regulation and quorum sensing control density-dependent suppression and restriction of nodulation in the Bradyrhizobium japonicum-soybean symbiosis. *Applied and Environmental Microbiology*, **2008**, 74, 3749-56	4.8	33
147	Whole-genome transcriptional profiling of Bradyrhizobium japonicum during chemoautotrophic growth. *Journal of Bacteriology*, **2008**, 190, 6697-705	3.5	35
146	Escherichia coli in the Environment: Implications for Water Quality and Human Health. *Microbes and Environments*, **2008**, 23, 101-8	2.6	298
145	Beach sand and sediments are temporal sinks and sources of Escherichia coli in Lake Superior. *Environmental Science & Technology*, **2007**, 41, 2203-9	10.3	164
144	Environmental fate of two sulfonamide antimicrobial agents in soil. *Journal of Agricultural and Food Chemistry*, **2007**, 55, 2677-82	5.7	124
143	Biogenic formation of photoactive arsenic-sulfide nanotubes by Shewanella sp. strain HN-41. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20410-5	11.5	100
142	High-throughput and quantitative procedure for determining sources of Escherichia coli in waterways by using host-specific DNA marker genes. *Applied and Environmental Microbiology*, **2007**, 73, 890-6	4.8	22

141	Presence and sources of fecal coliform bacteria in epilithic periphyton communities of Lake Superior. *Applied and Environmental Microbiology*, **2007**, 73, 3771-8	4.8	83
140	Relationship between phylogenetic groups, genotypic clusters, and virulence gene profiles of Escherichia coli strains from diverse human and animal sources. *Applied and Environmental Microbiology*, **2007**, 73, 5703-10	4.8	90
139	Genomes of the symbiotic nitrogen-fixing bacteria of legumes. *Plant Physiology*, **2007**, 144, 615-22	6.6	120
138	Hydroxyatrazine N-ethylaminohydrolase (AtzB): an amidohydrolase superfamily enzyme catalyzing deamination and dechlorination. *Journal of Bacteriology*, **2007**, 189, 6989-97	3.5	23
137	Evolution of catabolic pathways: Genomic insights into microbial s-triazine metabolism. *Journal of Bacteriology*, **2007**, 189, 674-82	3.5	84
136	Transcriptional and Physiological Responses of Bradyrhizobium japonicum to Desiccation-Induced Stress. *Journal of Bacteriology*, **2007**, 189, 9150-9150	3.5	4
135	An oligonucleotide microarray resource for transcriptional profiling of Bradyrhizobium japonicum. *Molecular Plant-Microbe Interactions*, **2007**, 20, 1298-307	3.6	69
134	Population structure of Cladophora-borne Escherichia coli in nearshore water of Lake Michigan. *Water Research*, **2007**, 41, 3649-54	12.5	47
133	Determining sources of fecal bacteria in waterways. *Environmental Monitoring and Assessment*, **2007**, 129, 97-106	3.1	31
132	Transcriptional and physiological responses of Bradyrhizobium japonicum to desiccation-induced stress. *Journal of Bacteriology*, **2007**, 189, 6751-62	3.5	142
131	Secrets of soil survival revealed by the genome sequence of Arthrobacter aurescens TC1. *PLoS Genetics*, **2006**, 2, e214	6	166
130	TrzN from Arthrobacter aurescens TC1 Is a zinc amidohydrolase. *Journal of Bacteriology*, **2006**, 188, 5859-64	3.5	42
129	Purification and characterization of TrzF: biuret hydrolysis by allophanate hydrolase supports growth. *Applied and Environmental Microbiology*, **2006**, 72, 2491-5	4.8	26
128	Development of goose- and duck-specific DNA markers to determine sources of Escherichia coli in waterways. *Applied and Environmental Microbiology*, **2006**, 72, 4012-9	4.8	44
127	Cladophora (Chlorophyta) spp. harbor human bacterial pathogens in nearshore water of Lake Michigan. *Applied and Environmental Microbiology*, **2006**, 72, 4545-53	4.8	131
126	Presence and growth of naturalized Escherichia coli in temperate soils from Lake Superior watersheds. *Applied and Environmental Microbiology*, **2006**, 72, 612-21	4.8	372
125	Root and Stem Nodule Bacteria of Legumes **2006**, 818-841		3
124	Influence of soil aging on sorption and bioavailability of simazine. *Journal of Agricultural and Food Chemistry*, **2006**, 54, 1373-9	5.7	54

123	Influence of Cry1Ac toxin on mineralization and bioavailability of glyphosate in soil. *Journal of Agricultural and Food Chemistry*, **2006**, 54, 164-9	5.7	4
122	The argRB of Escherichia coli is rare in isolates obtained from natural sources. *Gene*, **2006**, 376, 240-7	3.8	3
121	Automated Robotic Assay of Phosphomonoesterase Activity in Soils. *Soil Science Society of America Journal*, **2006**, 70, 378-381	2.5	5
120	Population structure, persistence, and seasonality of autochthonous Escherichia coli in temperate, coastal forest soil from a Great Lakes watershed. *Environmental Microbiology*, **2006**, 8, 504-13	5.2	165
119	Biological Nitrogen Fixation: A Key Process for the Response of Grassland Ecosystems to Elevated Atmospheric [CO2]. *Ecological Studies*, **2006**, 325-336	1.1	5
118	Effects of incorporated corn residues on glyphosate mineralization and sorption in soil. *Journal of Agricultural and Food Chemistry*, **2005**, 53, 4110-7	5.7	43
117	Soil Stress Factors Influencing Symbiotic Nitrogen Fixation **2005**, 89-112		23
116	Biodegradation of atrazine in transgenic plants expressing a modified bacterial atrazine chlorohydrolase (atzA) gene. *Plant Biotechnology Journal*, **2005**, 3, 475-86	11.6	78
115	Detection of homoserine lactone-like quorum sensing molecules in bradyrhizobium strains. *Current Microbiology*, **2005**, 51, 250-4	2.4	27
114	The role of histidine 200 in MndD, the Mn(II)-dependent 3,4-dihydroxyphenylacetate 2,3-dioxygenase from Arthrobacter globiformis CM-2, a site-directed mutagenesis study. *Journal of Biological Inorganic Chemistry*, **2005**, 10, 751-60	3.7	27
113	Allophanate hydrolase, not urease, functions in bacterial cyanuric acid metabolism. *Applied and Environmental Microbiology*, **2005**, 71, 4437-45	4.8	54
112	Purification and characterization of allophanate hydrolase (AtzF) from Pseudomonas sp. strain ADP. *Journal of Bacteriology*, **2005**, 187, 3731-8	3.5	43
111	Substrate specificity and colorimetric assay for recombinant TrzN derived from Arthrobacter aurescens TC1. *Applied and Environmental Microbiology*, **2005**, 71, 2214-20	4.8	48
110	Arsenic Availability from Chromated Copper Arsenate (CCA)-treated Wood. *Journal of Environmental Quality*, **2004**, 33, 173	3.4	4
109	Arthrobacter aurescens TC1 atrazine catabolism genes trzN, atzB, and atzC are linked on a 160-kilobase region and are functional in Escherichia coli. *Applied and Environmental Microbiology*, **2004**, 70, 4402-7	4.8	87
108	Frequency and distribution of tetracycline resistance genes in genetically diverse, nonselected, and nonclinical Escherichia coli strains isolated from diverse human and animal sources. *Applied and Environmental Microbiology*, **2004**, 70, 2503-7	4.8	175
107	Sample size, library composition, and genotypic diversity among natural populations of Escherichia coli from different animals influence accuracy of determining sources of fecal pollution. *Applied and Environmental Microbiology*, **2004**, 70, 4478-85	4.8	145
106	Solvent extraction characterization of bioavailability of atrazine residues in soils. *Journal of Agricultural and Food Chemistry*, **2004**, 52, 6552-6	5.7	60

105	Comparison of genotypic-based microbial source tracking methods requiring a host origin database. *Journal of Water and Health*, **2003**, 1, 167-180	2.2	54
104	Phylogeny and distribution of extra-slow-growing Bradyrhizobium japonicum harboring high copy numbers of RSalpha, RSbeta and IS1631. *FEMS Microbiology Ecology*, **2003**, 44, 191-202	4.3	31
103	Growth and survival of Escherichia coli and enterococci populations in the macro-alga Cladophora (Chlorophyta). *FEMS Microbiology Ecology*, **2003**, 46, 203-11	4.3	165
102	On the origins of cyanuric acid hydrolase: purification, substrates, and prevalence of AtzD from Pseudomonas sp. strain ADP. *Applied and Environmental Microbiology*, **2003**, 69, 3653-7	4.8	58
101	Biodegradation of atrazine and related s-triazine compounds: from enzymes to field studies. *Applied Microbiology and Biotechnology*, **2002**, 58, 39-45	5.7	265
100	Changes in microbial activity and composition in a pasture ecosystem exposed to elevated atmospheric carbon dioxide. *Plant and Soil*, **2002**, 243, 197-207	4.2	71
99	Purification, substrate range, and metal center of AtzC: the N-isopropylammelide aminohydrolase involved in bacterial atrazine metabolism. *Journal of Bacteriology*, **2002**, 184, 5376-84	3.5	45
98	Novel psbA1 gene from a naturally occurring atrazine-resistant cyanobacterial isolate. *Applied and Environmental Microbiology*, **2002**, 68, 1358-66	4.8	15
97	Enzymatic degradation of chlorodiamino-s-triazine. *Applied and Environmental Microbiology*, **2002**, 68, 4672-5	4.8	26
96	Arthrobacter aurescens TC1 metabolizes diverse s-triazine ring compounds. *Applied and Environmental Microbiology*, **2002**, 68, 5973-80	4.8	162
95	Atrazine chlorohydrolase from Pseudomonas sp. strain ADP is a metalloenzyme. *Biochemistry*, **2002** , 41, 14430-7	3.2	51
94	Agricultural microbes genome 2. *Comparative and Functional Genomics*, **2001**, 2, 10-3		
93	A marker-dense physical map of the Bradyrhizobium japonicum genome. *Genome Research*, **2001**, 11, 1434-40	9.7	10
92	Melamine deaminase and atrazine chlorohydrolase: 98 percent identical but functionally different. *Journal of Bacteriology*, **2001**, 183, 2405-10	3.5	108
91	Complete nucleotide sequence and organization of the atrazine catabolic plasmid pADP-1 from Pseudomonas sp. strain ADP. *Journal of Bacteriology*, **2001**, 183, 5684-97	3.5	303
90	Field-scale remediation of atrazine-contaminated soil using recombinant Escherichia coli expressing atrazine chlorohydrolase. *Environmental Microbiology*, **2000**, 2, 91-8	5.2	122
89	Elevated atmospheric CO2 alters microbial population structure in a pasture ecosystem. *Global Change Biology*, **2000**, 6, 475-482	11.4	60
88	Substrate specificity of atrazine chlorohydrolase and atrazine-catabolizing bacteria. *Applied and Environmental Microbiology*, **2000**, 66, 4247-52	4.8	59

87	Molecular Basis of a Bacterial Consortium: Interspecies Catabolism of Atrazine. *Applied and Environmental Microbiology*, **2000**, 66, 1252-1252	4.8	2
86	Genetics of Atrazine and s-Triazine Degradation by Psedomonas sp. Strain ADP and Other Bacteria. *ACS Symposium Series*, **2000**, 268-282	0.4	3
85	Use of repetitive DNA sequences and the PCR To differentiate Escherichia coli isolates from human and animal sources. *Applied and Environmental Microbiology*, **2000**, 66, 2572-7	4.8	374
84	The Bradyrhizobium japonicum nolA gene encodes three functionally distinct proteins. *Journal of Bacteriology*, **1999**, 181, 1544-54	3.5	27
83	Atrazine Chlorohydrolase from Pseudomonas sp. Strain ADP: Gene Sequence, Enzyme Purification, and Protein Characterization. *Journal of Bacteriology*, **1999**, 181, 695-695	3.5	
82	Genetics of Atrazine Degradation in Pseudomonas sp. Strain ADP. *ACS Symposium Series*, **1998**, 88-94	0.4	
81	Soil Biology of the Rhizobiaceae **1998**, 155-172		25
80	Use of Endogenous Repeated Sequences to Fingerprint Bacterial Genomic DNA **1998**, 399-413		7
79	The Bradyrhizobium japonicum noeD gene: a negatively acting, genotype-specific nodulation gene for soybean. *Molecular Plant-Microbe Interactions*, **1998**, 11, 476-88	3.6	11
78	The atrazine catabolism genes atzABC are widespread and highly conserved. *Journal of Bacteriology*, **1998**, 180, 1951-4	3.5	206
77	Molecular basis of a bacterial consortium: interspecies catabolism of atrazine. *Applied and Environmental Microbiology*, **1998**, 64, 178-84	4.8	167
76	The atzABC genes encoding atrazine catabolism are located on a self-transmissible plasmid in Pseudomonas sp. strain ADP. *Applied and Environmental Microbiology*, **1998**, 64, 2323-6	4.8	122
75	AtzC is a new member of the amidohydrolase protein superfamily and is homologous to other atrazine-metabolizing enzymes. *Journal of Bacteriology*, **1998**, 180, 152-8	3.5	135
74	A Host-Controlled, Serogroup-Specific, Ineffective-Nodulation System in the Bradyrhizobium-Soybean (Glycine max) Symbiosis. *Molecular Plant-Microbe Interactions*, **1997**, 10, 994-1001	3.6	8
73	Manganese(II) active site mutants of 3,4-dihydroxyphenylacetate 2,3-dioxygenase from Arthrobacter globiformis strain CM-2. *Biochemistry*, **1997**, 36, 2147-53	3.2	33
72	Relationship between root length density and soil microorganisms in the rhizospheres of white clover and perennial ryegrass. *Communications in Soil Science and Plant Analysis*, **1997**, 28, 1675-1682	1.5	9
71	Plasmid Transfer between Spatially Separated Donor and Recipient Bacteria in Earthworm-Containing Soil Microcosms. *Applied and Environmental Microbiology*, **1997**, 63, 679-86	4.8	33
70	The atzB gene of Pseudomonas sp. strain ADP encodes the second enzyme of a novel atrazine degradation pathway. *Applied and Environmental Microbiology*, **1997**, 63, 916-23	4.8	124

69	Host-Controlled Restriction of Nodulation by Bradyrhizobium Japonicum Strain USDA 110 and Characterization of a Gene Regulating Nodulation **1997**, 137-141		
68	Microbial community changes in the rhizospheres of white clover and perennial ryegrass exposed to Free Air Carbon dioxide Enrichment (FACE). *Soil Biology and Biochemistry*, **1996**, 28, 1717-1724	7.5	105
67	Inheritance of Host-Controlled Restriction of Nodulation by Bradyrhizobium japonicum Strain USDA 110. *Crop Science*, **1996**, 36, 1271-1276	2.4	25
66	Atrazine chlorohydrolase from Pseudomonas sp. strain ADP: gene sequence, enzyme purification, and protein characterization. *Journal of Bacteriology*, **1996**, 178, 4894-900	3.5	197
65	Influence of earthworm activity on gene transfer from Pseudomonas fluorescens to indigenous soil bacteria. *Applied and Environmental Microbiology*, **1996**, 62, 515-21	4.8	55
64	Use of repetitive intergenic DNA sequences to classify pathogenic and disease-suppressive Streptomyces strains. *Applied and Environmental Microbiology*, **1996**, 62, 3489-93	4.8	37
63	A manganese-dependent dioxygenase from Arthrobacter globiformis CM-2 belongs to the major extradiol dioxygenase family. *Journal of Bacteriology*, **1995**, 177, 1225-32	3.5	84
62	Differences among strains of Bradyrhizobium in fatty acid methyl ester analysis. *Canadian Journal of Microbiology*, **1995**, 41, 1038-1042	3.2	22
61	Native prairie grasses and microbial community responses to reclamation of taconite iron ore tailing. *Canadian Journal of Botany*, **1995**, 73, 1645-1654		14
60	Restriction of Nodulation by Bradyrhizobium japonicum Is Mediated by Factors Present in the Roots of Glycine max. *Applied and Environmental Microbiology*, **1995**, 61, 832-6	4.8	19
59	Diversity among Field Populations of Bradyrhizobium japonicum in Poland. *Applied and Environmental Microbiology*, **1995**, 61, 1194-200	4.8	41
58	Host-Controlled Restriction of Nodulation by Bradyrhizobium japonicum Strains in Serogroup 110. *Applied and Environmental Microbiology*, **1995**, 61, 2378-83	4.8	20
57	Cloning, characterization, and expression of a gene region from Pseudomonas sp. strain ADP involved in the dechlorination of atrazine. *Applied and Environmental Microbiology*, **1995**, 61, 3373-8	4.8	104
56	Metabolism of polyhalogenated compounds by a genetically engineered bacterium. *Nature*, **1994**, 368, 627-9	50.4	89
55	Metabolism of chlorofluorocarbons and polybrominated compounds by Pseudomonas putida G786(pHG-2) via an engineered metabolic pathway. *Applied and Environmental Microbiology*, **1994**, 60, 4148-54	4.8	17
54	A Selective Medium for the Isolation and Quantification of Bradyrhizobium japonicum and Bradyrhizobium elkanii Strains from Soils and Inoculants. *Applied and Environmental Microbiology*, **1994**, 60, 581-6	4.8	49
53	Tellurium and Selenium Resistance in Rhizobia and Its Potential Use for Direct Isolation of Rhizobium meliloti from Soil. *Applied and Environmental Microbiology*, **1994**, 60, 1674-7	4.8	43
52	Isolation of aBradyrhizobium japonicumserogroup 123 mutant which has an extended host range for nodulation-restricting soybean genotypes. *FEMS Microbiology Letters*, **1993**, 106, 205-209	2.9	8

51	The Bradyrhizobium japonicum serocluster 123 hyperreiterated DNA region, HRS1, has DNA and amino acid sequence homology to IS1380, an insertion sequence from Acetobacter pasteurianus. *Applied and Environmental Microbiology*, **1993**, 59, 1656-61	4.8	9
50	Use of repetitive sequences and the polymerase chain reaction technique to classify genetically related Bradyrhizobium japonicum serocluster 123 strains. *Applied and Environmental Microbiology*, **1993**, 59, 1702-8	4.8	94
49	Plasmids pJP4 and r68.45 Can Be Transferred between Populations of Bradyrhizobia in Nonsterile Soil. *Applied and Environmental Microbiology*, **1993**, 59, 1762-6	4.8	45
48	Genetics of competition for nodulation of legumes. *Annual Review of Microbiology*, **1992**, 46, 399-428	17.5	215
47	Lysogeny in Bradyrhizobium japonicum and Its Effect on Soybean Nodulation. *Applied and Environmental Microbiology*, **1992**, 58, 3360-6	4.8	15
46	The Soybean Rj4 Allele Restricts Nodulation by Bradyrhizobium japonicum Serogroup 123 Strains. *Applied and Environmental Microbiology*, **1992**, 58, 720-3	4.8	26
45	Hyperreiterated DNA regions are conserved among Bradyrhizobium japonicum serocluster 123 strains. *Applied and Environmental Microbiology*, **1992**, 58, 1878-85	4.8	11
44	The Bradyrhizobium japonicum nolA gene and its involvement in the genotype-specific nodulation of soybeans. *Proceedings of the National Academy of Sciences of the United States of America*, **1991**, 88, 637-41	11.5	118
43	Proposed Minimal Standards for the Description of New Genera and Species of Root- and Stem-Nodulating Bacteria. *International Journal of Systematic Bacteriology*, **1991**, 41, 582-587		209
42	Characterization of cytochromes c550 and c555 from Bradyrhizobium japonicum: cloning, mutagenesis, and sequencing of the c555 gene (cycC). *Journal of Bacteriology*, **1991**, 173, 7887-95	3.5	19
41	Gene-for-gene interaction in the legume-Rhizobium symbiosis **1991**, 163-171		2
40	Microbial influence on gene-for-gene interactions in legume-Rhizobium symbioses **1991**, 173-180		0
39	Microbial influence on gene-for-gene interactions in legume-Rhizobium symbioses. *Plant and Soil*, **1990**, 129, 53-60	4.2	15
38	DNA Hybridization Probe for Use in Determining Restricted Nodulation among Bradyrhizobium japonicum Serocluster 123 Field Isolates. *Applied and Environmental Microbiology*, **1990**, 56, 1768-74	4.8	20
37	Genome analysis of Bradyrhizobium japonicum serocluster 123 field isolates by using field inversion gel electrophoresis. *Applied and Environmental Microbiology*, **1990**, 56, 1949-53	4.8	18
36	Cytochrome mutants of bradyrhizobium induced by transposon tn5. *Plant Physiology*, **1989**, 90, 553-9	6.6	27
35	Host Plant Effects on Nodulation and Competitiveness of the Bradyrhizobium japonicum Serotype Strains Constituting Serocluster 123. *Applied and Environmental Microbiology*, **1989**, 55, 2532-6	4.8	38
34	Influence of soil variables on in situ plasmid transfer from Escherichia coli to Rhizobium fredii. *Applied and Environmental Microbiology*, **1989**, 55, 1730-4	4.8	73

33	Soybean Genotype Restricting Nodulation of a Previously Unrestricted Serocluster 123 Bradyrhizobia. *Crop Science*, **1989**, 29, 307	2.4	44
32	Two host-inducible genes of Rhizobium fredii and characterization of the inducing compound. *Journal of Bacteriology*, **1988**, 170, 171-8	3.5	63
31	Nodulation and Nitrogen Fixation Efficacy of Rhizobium fredii with Phaseolus vulgaris Genotypes. *Applied and Environmental Microbiology*, **1988**, 54, 1907-10	4.8	21
30	Genetic Diversity in Bradyrhizobium japonicum Serogroup 123 and Its Relation to Genotype-Specific Nodulation of Soybean. *Applied and Environmental Microbiology*, **1987**, 53, 2624-30	4.8	155
29	Serological Relatedness of Rhizobium fredii to Other Rhizobia and to the Bradyrhizobia. *Applied and Environmental Microbiology*, **1987**, 53, 1785-9	4.8	26
28	Symbiotically defective histidine auxotrophs of Bradyrhizobium japonicum. *Archives of Microbiology* , **1986**, 144, 334-339	3	23
27	Rapid Colored-Nodule Assay for Assessing Root Exudate-Enhanced Competitiveness of Bradyrhizobium japonicum. *Applied and Environmental Microbiology*, **1986**, 52, 847-51	4.8	7
26	Growth of fast- and slow-growing rhizobia on ethanol. *Applied and Environmental Microbiology*, **1986**, 52, 951-3	4.8	9
25	Identification of Genes Involved in the Rhizobium-Legume Symbiosis by Mu-dI (Kan, lac)-Generated Transcription Fusions. *Bio/technology*, **1985**, 3, 143-149		28
24	Biochemical Characterization of Fast- and Slow-Growing Rhizobia That Nodulate Soybeans. *International Journal of Systematic Bacteriology*, **1983**, 33, 716-722		65
23	Competition of Rhizobium japonicum Strains in Early Stages of Soybean Nodulation. *Applied and Environmental Microbiology*, **1983**, 46, 870-3	4.8	47
22	Possible involvement of a megaplasmid in nodulation of soybeans by fast-growing rhizobia from china. *Applied and Environmental Microbiology*, **1983**, 46, 906-11	4.8	22
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