

Michael J Sadowsky

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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	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017 , 5, 10	16.6	595
445	Changes in the composition of the human fecal microbiome after bacteriotherapy for recurrent <i>Clostridium difficile</i> -associated diarrhea. <i>Journal of Clinical Gastroenterology</i> , 2010 , 44, 354-60	3	499
444	Standardized frozen preparation for transplantation of fecal microbiota for recurrent <i>Clostridium difficile</i> infection. <i>American Journal of Gastroenterology</i> , 2012 , 107, 761-7	0.7	466
443	Use of repetitive DNA sequences and the PCR To differentiate <i>Escherichia coli</i> isolates from human and animal sources. <i>Applied and Environmental Microbiology</i> , 2000 , 66, 2572-7	4.8	374
442	Presence and growth of naturalized <i>Escherichia coli</i> in temperate soils from Lake Superior watersheds. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 612-21	4.8	372
441	Effect of Fecal Microbiota Transplantation on Recurrence in Multiply Recurrent <i>Clostridium difficile</i> Infection: A Randomized Trial. <i>Annals of Internal Medicine</i> , 2016 , 165, 609-616	8	344
440	Complete nucleotide sequence and organization of the atrazine catabolic plasmid pADP-1 from <i>Pseudomonas</i> sp. strain ADP. <i>Journal of Bacteriology</i> , 2001 , 183, 5684-97	3.5	303
439	<i>Escherichia coli</i> in the Environment: Implications for Water Quality and Human Health. <i>Microbes and Environments</i> , 2008 , 23, 101-8	2.6	298
438	Biodegradation of atrazine and related s-triazine compounds: from enzymes to field studies. <i>Applied Microbiology and Biotechnology</i> , 2002 , 58, 39-45	5.7	265
437	Hydrothermal carbonization of microalgae. <i>Biomass and Bioenergy</i> , 2010 , 34, 875-882	5.3	256
436	Microbiota transplantation restores normal fecal bile acid composition in recurrent <i>Clostridium difficile</i> infection. <i>American Journal of Physiology - Renal Physiology</i> , 2014 , 306, G310-9	5.1	254
435	Understanding the mechanisms of faecal microbiota transplantation. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2016 , 13, 508-16	24.2	245
434	Interaction of gut microbiota with bile acid metabolism and its influence on disease states. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 47-64	5.7	235
433	Environmental <i>Escherichia coli</i> : ecology and public health implications-a review. <i>Journal of Applied Microbiology</i> , 2017 , 123, 570-581	4.7	230
432	High-throughput DNA sequence analysis reveals stable engraftment of gut microbiota following transplantation of previously frozen fecal bacteria. <i>Gut Microbes</i> , 2013 , 4, 125-35	8.8	218
431	Genetics of competition for nodulation of legumes. <i>Annual Review of Microbiology</i> , 1992 , 46, 399-428	17.5	215
430	Proposed Minimal Standards for the Description of New Genera and Species of Root- and Stem-Nodulating Bacteria. <i>International Journal of Systematic Bacteriology</i> , 1991 , 41, 582-587		209

429	The atrazine catabolism genes atzABC are widespread and highly conserved. <i>Journal of Bacteriology</i> , 1998 , 180, 1951-4	3.5	206
428	Atrazine chlorohydrolase from <i>Pseudomonas</i> sp. strain ADP: gene sequence, enzyme purification, and protein characterization. <i>Journal of Bacteriology</i> , 1996 , 178, 4894-900	3.5	197
427	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E864-70	11.5	178
426	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. <i>Cell Host and Microbe</i> , 2018 , 23, 229-240.e5	23.4	177
425	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015 , 3, 10	16.6	175
424	Frequency and distribution of tetracycline resistance genes in genetically diverse, nonselected, and nonclinical <i>Escherichia coli</i> strains isolated from diverse human and animal sources. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 2503-7	4.8	175
423	Molecular basis of a bacterial consortium: interspecies catabolism of atrazine. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 178-84	4.8	167
422	Secrets of soil survival revealed by the genome sequence of <i>Arthrobacter aureus</i> TC1. <i>PLoS Genetics</i> , 2006 , 2, e214	6	166
421	Population structure, persistence, and seasonality of autochthonous <i>Escherichia coli</i> in temperate, coastal forest soil from a Great Lakes watershed. <i>Environmental Microbiology</i> , 2006 , 8, 504-13	5.2	165
420	Growth and survival of <i>Escherichia coli</i> and enterococci populations in the macro-alga <i>Cladophora</i> (Chlorophyta). <i>FEMS Microbiology Ecology</i> , 2003 , 46, 203-11	4.3	165
419	Beach sand and sediments are temporal sinks and sources of <i>Escherichia coli</i> in Lake Superior. <i>Environmental Science & Technology</i> , 2007 , 41, 2203-9	10.3	164
418	<i>Arthrobacter aureus</i> TC1 metabolizes diverse s-triazine ring compounds. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 5973-80	4.8	162
417	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. <i>Journal of Applied Microbiology</i> , 2013 , 115, 1147-58	4.7	156
416	Genetic Diversity in <i>Bradyrhizobium japonicum</i> Serogroup 123 and Its Relation to Genotype-Specific Nodulation of Soybean. <i>Applied and Environmental Microbiology</i> , 1987 , 53, 2624-30	4.8	155
415	Inflammatory Bowel Disease Affects the Outcome of Fecal Microbiota Transplantation for Recurrent <i>Clostridium difficile</i> Infection. <i>Clinical Gastroenterology and Hepatology</i> , 2016 , 14, 1433-8	6.9	149
414	Sample size, library composition, and genotypic diversity among natural populations of <i>Escherichia coli</i> from different animals influence accuracy of determining sources of fecal pollution. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4478-85	4.8	145
413	Transcriptional and physiological responses of <i>Bradyrhizobium japonicum</i> to desiccation-induced stress. <i>Journal of Bacteriology</i> , 2007 , 189, 6751-62	3.5	142
412	AtzC is a new member of the amidohydrolase protein superfamily and is homologous to other atrazine-metabolizing enzymes. <i>Journal of Bacteriology</i> , 1998 , 180, 152-8	3.5	135

4 ¹¹	Cladophora (Chlorophyta) spp. harbor human bacterial pathogens in nearshore water of Lake Michigan. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 4545-53	4.8	131
4 ¹⁰	Environmental fate of two sulfonamide antimicrobial agents in soil. <i>Journal of Agricultural and Food Chemistry</i> , 2007 , 55, 2677-82	5.7	124
4 ⁰⁹	The atzB gene of Pseudomonas sp. strain ADP encodes the second enzyme of a novel atrazine degradation pathway. <i>Applied and Environmental Microbiology</i> , 1997 , 63, 916-23	4.8	124
4 ⁰⁸	Field-scale remediation of atrazine-contaminated soil using recombinant Escherichia coli expressing atrazine chlorohydrolase. <i>Environmental Microbiology</i> , 2000 , 2, 91-8	5.2	122
4 ⁰⁷	The atzABC genes encoding atrazine catabolism are located on a self-transmissible plasmid in Pseudomonas sp. strain ADP. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 2323-6	4.8	122
4 ⁰⁶	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. <i>Journal of Experimental Medicine</i> , 2013 , 210, 2011-24	16.6	121
4 ⁰⁵	Candidate genes and genetic architecture of symbiotic and agronomic traits revealed by whole-genome, sequence-based association genetics in Medicago truncatula. <i>PLoS ONE</i> , 2013 , 8, e65688 ^{3.7}		121
4 ⁰⁴	Genomes of the symbiotic nitrogen-fixing bacteria of legumes. <i>Plant Physiology</i> , 2007 , 144, 615-22	6.6	120
4 ⁰³	The Bradyrhizobium japonicum nola gene and its involvement in the genotype-specific nodulation of soybeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991 , 88, 637-41	11.5	118
4 ⁰²	Hydrothermal carbonization of microalgae II. Fatty acid, char, and algal nutrient products. <i>Applied Energy</i> , 2011 , 88, 3286-3290	10.7	117
4 ⁰¹	Soybean metabolites regulated in root hairs in response to the symbiotic bacterium Bradyrhizobium japonicum. <i>Plant Physiology</i> , 2010 , 153, 1808-22	6.6	116
4 ⁰⁰	Comparative genomics of the core and accessory genomes of 48 Sinorhizobium strains comprising five genospecies. <i>Genome Biology</i> , 2013 , 14, R17	18.3	114
399	Hydrothermal carbonization of distiller's grains. <i>Biomass and Bioenergy</i> , 2011 , 35, 2526-2533	5.3	113
398	Successful Resolution of Recurrent Clostridium difficile Infection using Freeze-Dried, Encapsulated Fecal Microbiota; Pragmatic Cohort Study. <i>American Journal of Gastroenterology</i> , 2017 , 112, 940-947	0.7	109
397	Melamine deaminase and atrazine chlorohydrolase: 98 percent identical but functionally different. <i>Journal of Bacteriology</i> , 2001 , 183, 2405-10	3.5	108
396	Peptide-mediated shape- and size-tunable synthesis of gold nanostructures. <i>Acta Biomaterialia</i> , 2010 , 6, 2681-9	10.8	106
395	Microbial community changes in the rhizospheres of white clover and perennial ryegrass exposed to Free Air Carbon dioxide Enrichment (FACE). <i>Soil Biology and Biochemistry</i> , 1996 , 28, 1717-1724	7.5	105
394	Cloning, characterization, and expression of a gene region from Pseudomonas sp. strain ADP involved in the dechlorination of atrazine. <i>Applied and Environmental Microbiology</i> , 1995 , 61, 3373-8	4.8	104

393	Biogenic formation of photoactive arsenic-sulfide nanotubes by <i>Shewanella</i> sp. strain HN-41. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 20410-5	11.5	100
392	Secretion systems and signal exchange between nitrogen-fixing rhizobia and legumes. <i>Frontiers in Plant Science</i> , 2015 , 6, 491	6.2	99
391	Microbes in Beach Sands: Integrating Environment, Ecology and Public Health. <i>Reviews in Environmental Science and Biotechnology</i> , 2014 , 13, 329-368	13.9	98
390	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. <i>Science of the Total Environment</i> , 2015 , 505, 435-45	10.2	97
389	Use of barcoded pyrosequencing and shared OTUs to determine sources of fecal bacteria in watersheds. <i>Environmental Science & Technology</i> , 2010 , 44, 7777-82	10.3	95
388	Applications of the rep-PCR DNA fingerprinting technique to study microbial diversity, ecology and evolution. <i>Environmental Microbiology</i> , 2009 , 11, 733-40	5.2	95
387	Use of repetitive sequences and the polymerase chain reaction technique to classify genetically related <i>Bradyrhizobium japonicum</i> serocluster 123 strains. <i>Applied and Environmental Microbiology</i> , 1993 , 59, 1702-8	4.8	94
386	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016 , 4, 44	16.6	90
385	Relationship between phylogenetic groups, genotypic clusters, and virulence gene profiles of <i>Escherichia coli</i> strains from diverse human and animal sources. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 5703-10	4.8	90
384	Changes in Colonic Bile Acid Composition following Fecal Microbiota Transplantation Are Sufficient to Control <i>Clostridium difficile</i> Germination and Growth. <i>PLoS ONE</i> , 2016 , 11, e0147210	3.7	90
383	Ammonium sorption and ammonia inhibition of nitrite-oxidizing bacteria explain contrasting soil N ₂ O production. <i>Scientific Reports</i> , 2015 , 5, 12153	4.9	89
382	Metabolism of polyhalogenated compounds by a genetically engineered bacterium. <i>Nature</i> , 1994 , 368, 627-9	50.4	89
381	Fate of antibiotic resistance genes and class 1 integrons in soil microcosms following the application of treated residual municipal wastewater solids. <i>Environmental Science & Technology</i> , 2014 , 48, 5620-7	10.3	88
380	<i>Arthrobacter aureus</i> TC1 atrazine catabolism genes <i>trzN</i> , <i>atzB</i> , and <i>atzC</i> are linked on a 160-kilobase region and are functional in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4402-7	4.8	87
379	Evolution of catabolic pathways: Genomic insights into microbial s-triazine metabolism. <i>Journal of Bacteriology</i> , 2007 , 189, 674-82	3.5	84
378	A manganese-dependent dioxygenase from <i>Arthrobacter globiformis</i> CM-2 belongs to the major extradiol dioxygenase family. <i>Journal of Bacteriology</i> , 1995 , 177, 1225-32	3.5	84
377	Presence and sources of fecal coliform bacteria in epilithic periphyton communities of Lake Superior. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 3771-8	4.8	83
376	Biodegradation of atrazine in transgenic plants expressing a modified bacterial atrazine chlorohydrolase (<i>atzA</i>) gene. <i>Plant Biotechnology Journal</i> , 2005 , 3, 475-86	11.6	78

375	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017 , 5, 87	16.6	77
374	Species and genus level resolution analysis of gut microbiota in <i>Clostridium difficile</i> patients following fecal microbiota transplantation. <i>Microbiome</i> , 2014 , 2, 13	16.6	77
373	<i>Sphingobacterium</i> sp. strain PM2-P1-29 harbours a functional tet(X) gene encoding for the degradation of tetracycline. <i>Journal of Applied Microbiology</i> , 2009 , 106, 1336-42	4.7	77
372	Transcriptional responses of <i>Escherichia coli</i> K-12 and O157:H7 associated with lettuce leaves. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1752-64	4.8	73
371	Influence of soil variables on in situ plasmid transfer from <i>Escherichia coli</i> to <i>Rhizobium fredii</i> . <i>Applied and Environmental Microbiology</i> , 1989 , 55, 1730-4	4.8	73
370	Resolution of severe <i>Clostridium difficile</i> infection following sequential fecal microbiota transplantation. <i>Journal of Clinical Gastroenterology</i> , 2013 , 47, 735-7	3	71
369	Changes in microbial activity and composition in a pasture ecosystem exposed to elevated atmospheric carbon dioxide. <i>Plant and Soil</i> , 2002 , 243, 197-207	4.2	71
368	Ursodeoxycholic Acid Inhibits <i>Clostridium difficile</i> Spore Germination and Vegetative Growth, and Prevents the Recurrence of Ileal Pouchitis Associated With the Infection. <i>Journal of Clinical Gastroenterology</i> , 2016 , 50, 624-30	3	69
367	Associations between soil bacterial community structure and nutrient cycling functions in long-term organic farm soils following cover crop and organic fertilizer amendment. <i>Science of the Total Environment</i> , 2016 , 566-567, 949-959	10.2	69
366	An oligonucleotide microarray resource for transcriptional profiling of <i>Bradyrhizobium japonicum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2007 , 20, 1298-307	3.6	69
365	Seasonal stability of <i>Cladophora</i> -associated <i>Salmonella</i> in Lake Michigan watersheds. <i>Water Research</i> , 2009 , 43, 806-14	12.5	68
364	Functional role of <i>Bradyrhizobium japonicum</i> trehalose biosynthesis and metabolism genes during physiological stress and nodulation. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 1071-81	4.8	67
363	Methanogenesis facilitated by geobiochemical iron cycle in a novel syntrophic methanogenic microbial community. <i>Environmental Science & Technology</i> , 2013 , 47, 10078-84	10.3	66
362	Therapeutic transplantation of the distal gut microbiota. <i>Mucosal Immunology</i> , 2011 , 4, 4-7	9.2	66
361	Complete Microbiota Engraftment Is Not Essential for Recovery from Recurrent <i>Clostridium difficile</i> Infection following Fecal Microbiota Transplantation. <i>MBio</i> , 2016 , 7,	7.8	66
360	Biochemical Characterization of Fast- and Slow-Growing Rhizobia That Nodulate Soybeans. <i>International Journal of Systematic Bacteriology</i> , 1983 , 33, 716-722		65
359	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. <i>Frontiers in Microbiology</i> , 2014 , 5, 414	5.7	64
358	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. <i>Journal of Microbiology</i> , 2018 , 56, 189-198	3	63

357	Two host-inducible genes of <i>Rhizobium fredii</i> and characterization of the inducing compound. <i>Journal of Bacteriology</i> , 1988 , 170, 171-8	3.5	63
356	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018 , 8, 6219	4.9	61
355	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014 , 5, 524	5.7	61
354	Precipitation influences pathogenic bacteria and antibiotic resistance gene abundance in storm drain outfalls in coastal sub-tropical waters. <i>Environment International</i> , 2018 , 116, 308-318	12.9	61
353	Solvent extraction characterization of bioavailability of atrazine residues in soils. <i>Journal of Agricultural and Food Chemistry</i> , 2004 , 52, 6552-6	5.7	60
352	Elevated atmospheric CO ₂ alters microbial population structure in a pasture ecosystem. <i>Global Change Biology</i> , 2000 , 6, 475-482	11.4	60
351	Substrate specificity of atrazine chlorohydrolase and atrazine-catabolizing bacteria. <i>Applied and Environmental Microbiology</i> , 2000 , 66, 4247-52	4.8	59
350	Aerobic digestion reduces the quantity of antibiotic resistance genes in residual municipal wastewater solids. <i>Frontiers in Microbiology</i> , 2013 , 4, 17	5.7	58
349	On the origins of cyanuric acid hydrolase: purification, substrates, and prevalence of AtzD from <i>Pseudomonas</i> sp. strain ADP. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 3653-7	4.8	58
348	Quantitative microbial risk assessment of microbial source tracking markers in recreational water contaminated with fresh untreated and secondary treated sewage. <i>Environment International</i> , 2018 , 117, 243-249	12.9	57
347	Population genomics of the facultatively mutualistic bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , 2012 , 8, e1002868	6	56
346	Toolbox Approaches Using Molecular Markers and 16S rRNA Gene Amplicon Data Sets for Identification of Fecal Pollution in Surface Water. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7064-77	4.8	55
345	Influence of earthworm activity on gene transfer from <i>Pseudomonas fluorescens</i> to indigenous soil bacteria. <i>Applied and Environmental Microbiology</i> , 1996 , 62, 515-21	4.8	55
344	Biodegradation in Waters from Hydraulic Fracturing: Chemistry, Microbiology, and Engineering. <i>Journal of Environmental Engineering, ASCE</i> , 2014 , 140,	2	54
343	Influence of soil aging on sorption and bioavailability of simazine. <i>Journal of Agricultural and Food Chemistry</i> , 2006 , 54, 1373-9	5.7	54
342	Comparison of genotypic-based microbial source tracking methods requiring a host origin database. <i>Journal of Water and Health</i> , 2003 , 1, 167-180	2.2	54
341	Allophanate hydrolase, not urease, functions in bacterial cyanuric acid metabolism. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 4437-45	4.8	54
340	Identification of a <i>Brevibacterium</i> marker gene specific to poultry litter and development of a quantitative PCR assay. <i>Journal of Applied Microbiology</i> , 2010 , 109, 334-47	4.7	53

339	Beach sand and the potential for infectious disease transmission: observations and recommendations. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016 , 96, 101-120 ^{1.1}	53
338	Enteric pathogen-plant interactions: molecular connections leading to colonization and growth and implications for food safety. <i>Microbes and Environments</i> , 2014 , 29, 123-35	2.6 52
337	Nitrification gene ratio and free ammonia explain nitrite and nitrous oxide production in urea-amended soils. <i>Soil Biology and Biochemistry</i> , 2017 , 111, 143-153	7.5 51
336	Atrazine chlorohydrolase from <i>Pseudomonas</i> sp. strain ADP is a metalloenzyme. <i>Biochemistry</i> , 2002 , 41, 14430-7	3.2 51
335	Antimicrobial peptides targeting Gram-negative pathogens, produced and delivered by lactic acid bacteria. <i>ACS Synthetic Biology</i> , 2013 , 2, 643-50	5.7 50
334	Structure of bacterial communities in soil following cover crop and organic fertilizer incorporation. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 9331-9341	5.7 50
333	A Selective Medium for the Isolation and Quantification of <i>Bradyrhizobium japonicum</i> and <i>Bradyrhizobium elkanii</i> Strains from Soils and Inoculants. <i>Applied and Environmental Microbiology</i> , 1994 , 60, 581-6	4.8 49
332	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018 , 6, 166	16.6 49
331	Evaluation of molecular community analysis methods for discerning fecal sources and human waste. <i>Water Research</i> , 2013 , 47, 6862-72	12.5 48
330	Evaluation of the repeatability and reproducibility of a suite of qPCR-based microbial source tracking methods. <i>Water Research</i> , 2013 , 47, 6839-48	12.5 48
329	Large scale analysis of virulence genes in <i>Escherichia coli</i> strains isolated from Avalon Bay, CA. <i>Water Research</i> , 2010 , 44, 5463-73	12.5 48
328	Substrate specificity and colorimetric assay for recombinant TrzN derived from <i>Arthrobacter aureus</i> TC1. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 2214-20	4.8 48
327	Population structure of <i>Cladophora</i> -borne <i>Escherichia coli</i> in nearshore water of Lake Michigan. <i>Water Research</i> , 2007 , 41, 3649-54	12.5 47
326	Competition of <i>Rhizobium japonicum</i> Strains in Early Stages of Soybean Nodulation. <i>Applied and Environmental Microbiology</i> , 1983 , 46, 870-3	4.8 47
325	Multi-laboratory evaluations of the performance of <i>Catellibacillus marimammalius</i> PCR assays developed to target gull fecal sources. <i>Water Research</i> , 2013 , 47, 6883-96	12.5 46
324	Biogenic formation of As-S nanotubes by diverse <i>Shewanella</i> strains. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6896-9	4.8 46
323	Select and resequence reveals relative fitness of bacteria in symbiotic and free-living environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2425-2430	11.5 45
322	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. <i>Environmental Science & Technology</i> , 2017 , 51, 14225-14232	10.3 45

321	Purification, substrate range, and metal center of AtzC: the N-isopropylammelide aminohydrolase involved in bacterial atrazine metabolism. <i>Journal of Bacteriology</i> , 2002 , 184, 5376-84	3.5	45
320	Plasmids pJP4 and r68.45 Can Be Transferred between Populations of Bradyrhizobia in Nonsterile Soil. <i>Applied and Environmental Microbiology</i> , 1993 , 59, 1762-6	4.8	45
319	Endophytic Bacterial Communities Associated with Roots and Leaves of Plants Growing in Chilean Extreme Environments. <i>Scientific Reports</i> , 2019 , 9, 4950	4.9	44
318	Development of goose- and duck-specific DNA markers to determine sources of Escherichia coli in waterways. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 4012-9	4.8	44
317	Soybean Genotype Restricting Nodulation of a Previously Unrestricted Serocluster 123 Bradyrhizobia. <i>Crop Science</i> , 1989 , 29, 307	2.4	44
316	Factors controlling long-term survival and growth of naturalized Escherichia coli populations in temperate field soils. <i>Microbes and Environments</i> , 2010 , 25, 8-14	2.6	43
315	Effects of incorporated corn residues on glyphosate mineralization and sorption in soil. <i>Journal of Agricultural and Food Chemistry</i> , 2005 , 53, 4110-7	5.7	43
314	Purification and characterization of allophanate hydrolase (AtzF) from Pseudomonas sp. strain ADP. <i>Journal of Bacteriology</i> , 2005 , 187, 3731-8	3.5	43
313	Tellurium and Selenium Resistance in Rhizobia and Its Potential Use for Direct Isolation of Rhizobium meliloti from Soil. <i>Applied and Environmental Microbiology</i> , 1994 , 60, 1674-7	4.8	43
312	Application of SourceTracker for Accurate Identification of Fecal Pollution in Recreational Freshwater: A Double-Blinded Study. <i>Environmental Science & Technology</i> , 2018 , 52, 4207-4217	10.3	42
311	Recent changes to the classification of symbiotic, nitrogen-fixing, legume-associating bacteria: a review. <i>Symbiosis</i> , 2017 , 71, 91-109	3	42
310	TrzN from Arthrobacter aureus TC1 Is a zinc amidohydrolase. <i>Journal of Bacteriology</i> , 2006 , 188, 5859-5864	3.54	42
309	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. <i>Journal of Dairy Science</i> , 2015 , 98, 3568-76	4	41
308	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, Medicago truncatula. <i>BMC Genomics</i> , 2017 , 18, 578	4.5	41
307	Diversity among Field Populations of Bradyrhizobium japonicum in Poland. <i>Applied and Environmental Microbiology</i> , 1995 , 61, 1194-200	4.8	41
306	The population structure of Escherichia coli isolated from subtropical and temperate soils. <i>Science of the Total Environment</i> , 2012 , 417-418, 273-9	10.2	40
305	A High-Throughput DNA-Sequencing Approach for Determining Sources of Fecal Bacteria in a Lake Superior Estuary. <i>Environmental Science & Technology</i> , 2017 , 51, 8263-8271	10.3	40
304	The occurrence of virulence traits among high-level aminoglycosides resistant Enterococcus isolates obtained from feces of humans, animals, and birds in South Korea. <i>International Journal of Food Microbiology</i> , 2011 , 144, 387-92	5.8	40

303	Biodegradation and mineralization of metolachlor and alachlor by <i>Candida xestobii</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2011 , 59, 619-27	5.7	39
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