

Satoshi Ishii

List of Publications by Year in descending order

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Version: 2024-02-01

115
papers

6,340
citations

70961

41
h-index

74018

75
g-index

118
all docs

118
docs citations

118
times ranked

6155
citing authors

#	ARTICLE	IF	CITATIONS
1	Erosion and deposition divergently affect the structure of soil bacterial communities and functionality. <i>Catena</i> , 2022, 209, 105805.	2.2	14
2	Unraveling encapsulated growth of <i>Nitrosomonas europaea</i> in alginate: An experimental and modeling study. <i>Water Research</i> , 2022, 208, 117857.	5.3	2
3	Bioaugmentation potential of a cold-adapted and nitrate-reducing fungus to enhance nitrate removal in woodchip bioreactors. <i>Bioresource Technology Reports</i> , 2022, 17, 100969.	1.5	1
4	Determination of ^{15}N / ^{14}N of Ammonium, Nitrite, Nitrate, Hydroxylamine, and Hydrazine Using Colorimetric Reagents and Matrix-Assisted Laser Desorption Ionization–Time-of-Flight Mass Spectrometry (MALDI-TOF MS). <i>Applied and Environmental Microbiology</i> , 2022, 88, e0241621.	1.4	1
5	Metagenomics reveals global-scale contrasts in nitrogen cycling and cyanobacterial light-harvesting mechanisms in glacier cryoconite. <i>Microbiome</i> , 2022, 10, 50.	4.9	10
6	Temporal dynamics of <i>Campylobacter</i> and <i>Arcobacter</i> in a freshwater lake that receives fecal inputs from migratory geese. <i>Water Research</i> , 2022, 217, 118397.	5.3	7
7	Halophytes increase rhizosphere microbial diversity, network complexity and function in inland saline ecosystem. <i>Science of the Total Environment</i> , 2022, 831, 154944.	3.9	28
8	Correction for Oshiki et al., “Determination of ^{15}N / ^{14}N of Ammonium, Nitrite, Nitrate, Hydroxylamine, and Hydrazine Using Colorimetric Reagents and Matrix-Assisted Laser Desorption Ionization–Time-of-Flight Mass Spectrometry (MALDI-TOF MS)”. <i>Applied and Environmental Microbiology</i> , 2022, , e0052522.	1.4	0
9	The Microbial Nitrogen Cycling, Bacterial Community Composition, and Functional Potential in a Natural Grassland Are Stable from Breaking Dormancy to Being Dormant Again. <i>Microorganisms</i> , 2022, 10, 923.	1.6	6
10	Invasive earthworms alter forest soil microbiomes and nitrogen cycling. <i>Soil Biology and Biochemistry</i> , 2022, 171, 108724.	4.2	11
11	Afforestation can lower microbial diversity and functionality in deep soil layers in a semiarid region. <i>Global Change Biology</i> , 2022, 28, 6086-6101.	4.2	40
12	Isolation of cold-adapted nitrate-reducing fungi that have potential to increase nitrate removal in woodchip bioreactors. <i>Journal of Applied Microbiology</i> , 2021, 131, 197-207.	1.4	16
13	Simultaneous removal of nitrate and heavy metals in a continuous flow nitrate-dependent ferrous iron oxidation (NDFO) bioreactor. <i>Chemosphere</i> , 2021, 262, 127838.	4.2	13
14	Erosion reduces soil microbial diversity, network complexity and multifunctionality. <i>ISME Journal</i> , 2021, 15, 2474-2489.	4.4	273
15	Fungal denitrification revisited – Recent advancements and future opportunities. <i>Soil Biology and Biochemistry</i> , 2021, 157, 108250.	4.2	49
16	Application of manure from cattle administered antibiotics has sustained multi-year impacts on soil resistome and microbial community structure. <i>Soil Biology and Biochemistry</i> , 2021, 157, 108252.	4.2	39
17	Genome Sequence of <i>Linnemannia hyalina</i> Strain SCG-10, a Cold-Adapted and Nitrate-Reducing Fungus Isolated from Cornfield Soil in Minnesota, USA. <i>Microbiology Resource Announcements</i> , 2021, 10, e0069221.	0.3	2
18	Encapsulating microorganisms to enhance biological nitrogen removal in wastewater: recent advancements and future opportunities. <i>Environmental Science: Water Research and Technology</i> , 2021, 7, 1402-1416.	1.2	10

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19	Role of wastewater treatment plants on environmental abundance of Antimicrobial Resistance Genes in Chilean rivers. <i>International Journal of Hygiene and Environmental Health</i> , 2020, 223, 56-64.	2.1	27
20	Redox stratification within cryoconite granules influences the nitrogen cycle on glaciers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
21	Fast, sensitive, and reliable detection of waterborne pathogens by digital PCR after coagulation and foam concentration. <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 76-81.	1.1	9
22	Quantification of antibiotic resistance genes for environmental monitoring: Current methods and future directions. <i>Current Opinion in Environmental Science and Health</i> , 2020, 16, 47-53.	2.1	19
23	Simple and reliable enumeration of <i>Escherichia coli</i> concentrations in wastewater samples by measuring β -d-glucuronidase (GUS) activities via a microplate reader. <i>Science of the Total Environment</i> , 2020, 715, 136928.	3.9	15
24	Isolation and characterization of denitrifiers from woodchip bioreactors for bioaugmentation application. <i>Journal of Applied Microbiology</i> , 2020, 129, 590-600.	1.4	22
25	Great Lakes <i>Cladophora</i> harbors phylogenetically diverse nitrogen-fixing microorganisms. <i>Environmental DNA</i> , 2019, 1, 186-195.	3.1	5
26	Growth and antibiotic resistance acquisition of <i>Escherichia coli</i> in a river that receives treated sewage effluent. <i>Science of the Total Environment</i> , 2019, 690, 696-704.	3.9	22
27	Antibiotic Resistance Genes in Freshwater Trout Farms in a Watershed in Chile. <i>Journal of Environmental Quality</i> , 2019, 48, 1462-1471.	1.0	16
28	Complete Genome Sequence of a Novel Myoviridae Phage, Sfl ₁ 01, Infecting <i>Shigella</i> spp. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
29	A microfluidic platform for the simultaneous quantification of methanogen populations in anaerobic digestion processes. <i>Environmental Microbiology</i> , 2019, 21, 1798-1808.	1.8	11
30	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 635.	1.5	33
31	Ecology of Pathogens and Antibiotic-resistant Bacteria in Environments: Challenges and Opportunities. <i>Microbes and Environments</i> , 2019, 34, 1-4.	0.7	12
32	Potentially Mobile Denitrification Genes Identified in <i>Azospirillum</i> sp. Strain TSH58. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	16
33	Impact of long-term grazing exclusion on soil microbial community composition and nutrient availability. <i>Biology and Fertility of Soils</i> , 2019, 55, 121-134.	2.3	66
34	Association between submerged aquatic vegetation and elevated levels of <i>Escherichia coli</i> and potential bacterial pathogens in freshwater lakes. <i>Science of the Total Environment</i> , 2019, 657, 319-324.	3.9	21
35	Experimental Evidence for in Situ Nitric Oxide Production in Anaerobic Ammonia-Oxidizing Bacterial Granules. <i>Environmental Science & Technology</i> , 2018, 52, 5744-5752.	4.6	19
36	Microfluidic quantification of multiple enteric and opportunistic bacterial pathogens in roof-harvested rainwater tank samples. <i>Environmental Monitoring and Assessment</i> , 2018, 190, 105.	1.3	11

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37	Nitrogen Cycle Evaluation (NiCE) Chip for Simultaneous Analysis of Multiple N Cycle-Associated Genes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
38	A Microfluidic Quantitative Polymerase Chain Reaction Method for the Simultaneous Analysis of Dozens of Antibiotic Resistance and Heavy Metal Resistance Genes. <i>Environmental Science and Technology Letters</i> , 2018, 5, 20-25.	3.9	38
39	Improved simultaneous quantification of multiple waterborne pathogens and fecal indicator bacteria with the use of a sample process control. <i>Water Research</i> , 2018, 137, 193-200.	5.3	25
40	Presence of Cu-Type (NirK) and <i>cd</i> -Type (NirS) Nitrite Reductase Genes in the Denitrifying Bacterium <i>Bradyrhizobium nitroreducens</i> sp. nov.. <i>Microbes and Environments</i> , 2018, 33, 326-331.	0.7	37
41	High-Throughput <i>flaA</i> Short Variable Region Sequencing to Assess <i>Campylobacter</i> Diversity in Fecal Samples From Birds. <i>Frontiers in Microbiology</i> , 2018, 9, 2201.	1.5	8
42	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.	4.8	92
43	Microfluidic PCR Amplification and MiSeq Amplicon Sequencing Techniques for High-Throughput Detection and Genotyping of Human Pathogenic RNA Viruses in Human Feces, Sewage, and Oysters. <i>Frontiers in Microbiology</i> , 2018, 9, 830.	1.5	29
44	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> Strain S05, a Fouling-Causing Bacterium Isolated from a Membrane Bioreactor. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
45	Investigation of <i>Escherichia coli</i> in Urban Steam with Inflow of Treated Wastewater. <i>Journal of Japan Society on Water Environment</i> , 2018, 41, 19-26.	0.1	2
46	Environmental <i>Escherichia coli</i> : ecology and public health implications-a review. <i>Journal of Applied Microbiology</i> , 2017, 123, 570-581.	1.4	477
47	Microbial competition among anammox bacteria in nitrite-limited bioreactors. <i>Water Research</i> , 2017, 125, 249-258.	5.3	101
48	Target virus log ₁₀ reduction values determined for two reclaimed wastewater irrigation scenarios in Japan based on tolerable annual disease burden. <i>Water Research</i> , 2017, 125, 438-448.	5.3	20
49	Virulence and biodegradation potential of dynamic microbial communities associated with decaying <i>Cladophora</i> in Great Lakes. <i>Science of the Total Environment</i> , 2017, 574, 872-880.	3.9	22
50	<i>Noviherbaspirillum denitrificans</i> sp. nov., a denitrifying bacterium isolated from rice paddy soil and <i>Noviherbaspirillum autotrophicum</i> sp. nov., a denitrifying, facultatively autotrophic bacterium isolated from rice paddy soil and proposal to reclassify <i>Herbaspirillum massiliense</i> as <i>Noviherbaspirillum massiliense</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1841-1848.	0.8	43
51	Genome Sequence of <i>Enterobacter cloacae</i> Strain SENG-6, a Bacterium Producing Histo-Blood Group Antigen-Like Substances That Can Bind with Human Noroviruses. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
52	EVIDENCE-BASED DETERMINATION OF THE HYGIENE STANDARD VALUE IN ENVIRONMENTAL WATER. <i>Journal of Japan Society of Civil Engineers Ser G (Environmental Research)</i> , 2016, 72, 40-49.	0.1	1
53	Denitrification and Nitrate-Dependent Fe(II) Oxidation in Various <i>Pseudogulbenkiania</i> Strains. <i>Microbes and Environments</i> , 2016, 31, 293-298.	0.7	38
54	Evaluation of virus reduction efficiency in wastewater treatment unit processes as a credit value in the multiple-barrier system for wastewater reclamation and reuse. <i>Journal of Water and Health</i> , 2016, 14, 879-889.	1.1	10

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55	Estimation of concentration ratio of indicator to pathogen-related gene in environmental water based on left-censored data. <i>Journal of Water and Health</i> , 2016, 14, 14-25.	1.1	7
56	Specific Single-Cell Isolation of <i>Escherichia coli</i> O157 from Environmental Water Samples by Using Flow Cytometry and Fluorescence-Activated Cell Sorting. <i>Foodborne Pathogens and Disease</i> , 2016, 13, 456-461.	0.8	7
57	Membrane fouling potentials and cellular properties of bacteria isolated from fouled membranes in a MBR treating municipal wastewater. <i>Water Research</i> , 2016, 100, 448-457.	5.3	69
58	Correlations between pathogen concentration and fecal indicator marker genes in beach environments. <i>Science of the Total Environment</i> , 2016, 573, 826-830.	3.9	41
59	Bacterial histo-blood group antigens contributing to genotype-dependent removal of human noroviruses with a microfiltration membrane. <i>Water Research</i> , 2016, 95, 383-391.	5.3	23
60	Source identification of nitrous oxide emission pathways from a single-stage nitrification-anammox granular reactor. <i>Water Research</i> , 2016, 102, 147-157.	5.3	106
61	Rapid and successful start-up of anammox process by immobilizing the minimal quantity of biomass in PVA-SA gel beads. <i>Water Research</i> , 2015, 79, 147-157.	5.3	152
62	Application of a Microfluidic Quantitative Polymerase Chain Reaction Technique To Monitor Bacterial Pathogens in Beach Water and Complex Environmental Matrices. <i>Environmental Science and Technology Letters</i> , 2015, 2, 347-351.	3.9	28
63	Effects of dissolved oxygen and pH on nitrous oxide production rates in autotrophic partial nitrification granules. <i>Bioresource Technology</i> , 2015, 197, 15-22.	4.8	72
64	Identification of key nitrous oxide production pathways in aerobic partial nitrifying granules. <i>Environmental Microbiology</i> , 2014, 16, 3168-3180.	1.8	49
65	Microfluidic Quantitative PCR for Simultaneous Quantification of Multiple Viruses in Environmental Water Samples. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7505-7511.	1.4	90
66	Inoculation with N ₂ -generating denitrifier strains mitigates N ₂ O emission from agricultural soil fertilized with poultry manure. <i>Biology and Fertility of Soils</i> , 2014, 50, 1001-1007.	2.3	46
67	The nitrogen cycle in cryoconites: naturally occurring nitrification-denitrification granules on a glacier. <i>Environmental Microbiology</i> , 2014, 16, 3250-3262.	1.8	72
68	Water Quality Monitoring and Risk Assessment by Simultaneous Multipathogen Quantification. <i>Environmental Science & Technology</i> , 2014, 48, 4744-4749.	4.6	57
69	Chicken- and duck-associated <i>Bacteroides</i> and <i>Prevotella</i> genetic markers for detecting fecal contamination in environmental water. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 7427-7437.	1.7	40
70	Use of a genetically-engineered <i>Escherichia coli</i> strain as a sample process control for quantification of the host-specific bacterial genetic markers. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9165-9173.	1.7	13
71	Source identification of nitrous oxide on autotrophic partial nitrification in a granular sludge reactor. <i>Water Research</i> , 2013, 47, 7078-7086.	5.3	62
72	Development and characterization of the partial nitrification aerobic granules in a sequencing batch airlift reactor. <i>Bioresource Technology</i> , 2013, 139, 285-291.	4.8	39

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73	Seasonal Transition of Active Bacterial and Archaeal Communities in Relation to Water Management in Paddy Soils. <i>Microbes and Environments</i> , 2013, 28, 370-380.	0.7	44
74	Nitrate-Dependent Ferrous Iron Oxidation by Anaerobic Ammonium Oxidation (Anammox) Bacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4087-4093.	1.4	160
75	Simultaneous Quantification of Multiple Food- and Waterborne Pathogens by Use of Microfluidic Quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2891-2898.	1.4	131
76	Identification and Phylogenetic Characterization of Cobalamin Biosynthetic Genes of <i>Ensifer adhaerens</i> . <i>Microbes and Environments</i> , 2013, 28, 153-155.	0.7	10
77	Complete Genome Sequence of the Denitrifying and N ₂ O-Reducing Bacterium <i>Azoarcus</i> sp. Strain KH32C. <i>Journal of Bacteriology</i> , 2012, 194, 1255-1255.	1.0	29
78	Identification of Active Denitrifiers in Rice Paddy Soil by DNA- and RNA-Based Analyses. <i>Microbes and Environments</i> , 2012, 27, 456-461.	0.7	77
79	Advantages of functional single-cell isolation method over standard agar plate dilution method as a tool for studying denitrifying bacteria in rice paddy soil. <i>AMB Express</i> , 2012, 2, 50.	1.4	19
80	The population structure of <i>Escherichia coli</i> isolated from subtropical and temperate soils. <i>Science of the Total Environment</i> , 2012, 417-418, 273-279.	3.9	46
81	Identification and isolation of active N ₂ O reducers in rice paddy soil. <i>ISME Journal</i> , 2011, 5, 1936-1945.	4.4	78
82	Identifying the functional diversity of denitrifying bacteria in rice paddy soil. <i>Kagaku To Seibutsu</i> , 2011, 49, 666-668.		
83	Phylogenetic and Functional Diversity of Denitrifying Bacteria Isolated from Various Rice Paddy and Rice-Soybean Rotation Fields. <i>Microbes and Environments</i> , 2011, 26, 30-35.	0.7	69
84	Waterfowl Abundance Does Not Predict the Dominant Avian Source of Beach <i>Escherichia coli</i> . <i>Journal of Environmental Quality</i> , 2011, 40, 1924-1931.	1.0	10
85	Nitrogen Cycling in Rice Paddy Environments: Past Achievements and Future Challenges. <i>Microbes and Environments</i> , 2011, 26, 282-292.	0.7	180
86	Isolation of Oligotrophic Denitrifiers Carrying Previously Uncharacterized Functional Gene Sequences. <i>Applied and Environmental Microbiology</i> , 2011, 77, 338-342.	1.4	54
87	Complete Genome Sequence of the Denitrifying and N ₂ O-Reducing Bacterium <i>Pseudogulbenkiania</i> sp. Strain NH8B. <i>Journal of Bacteriology</i> , 2011, 193, 6395-6396.	1.0	15
88	Factors Controlling Long-Term Survival and Growth of Naturalized <i>Escherichia coli</i> Populations in Temperate Field Soils. <i>Microbes and Environments</i> , 2010, 25, 8-14.	0.7	58
89	Title is missing!. <i>Kagaku To Seibutsu</i> , 2010, 48, 666-668.	0.0	0
90	Isolation of functional single cells from environments using a micromanipulator: application to study denitrifying bacteria. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 1211-1217.	1.7	71

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91	Single-cell analysis and isolation for microbiology and biotechnology: methods and applications. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 1281-1292.	1.7	97
92	Microbial populations in various paddy soils respond differently to denitrification-inducing conditions, albeit background bacterial populations are similar. <i>Soil Science and Plant Nutrition</i> , 2010, 56, 220-224.	0.8	14
93	nirK-Harboring Denitrifiers Are More Responsive to Denitrification-Inducing Conditions in Rice Paddy Soil Than nirS-Harboring Bacteria. <i>Microbes and Environments</i> , 2010, 25, 45-48.	0.7	85
94	Large scale analysis of virulence genes in <i>Escherichia coli</i> strains isolated from Avalon Bay, CA. <i>Water Research</i> , 2010, 44, 5463-5473.	5.3	55
95	Stable Isotope Probing as a Tool to Identify Active Microbial Populations in Soil. <i>Radioisotopes</i> , 2010, 59, 703-705.	0.1	0
96	<i>Escherichia coli</i> Populations in Great Lakes Waterfowl Exhibit Spatial Stability and Temporal Shifting. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1546-1551.	1.4	16
97	Microbial Populations Responsive to Denitrification-Inducing Conditions in Rice Paddy Soil, as Revealed by Comparative 16S rRNA Gene Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7070-7078.	1.4	94
98	Temporal shifts in diversity and quantity of nirS and nirK in a rice paddy field soil. <i>Soil Biology and Biochemistry</i> , 2009, 41, 2044-2051.	4.2	168
99	Applications of the rep-PCR DNA fingerprinting technique to study microbial diversity, ecology and evolution. <i>Environmental Microbiology</i> , 2009, 11, 733-740.	1.8	116
100	Seasonal stability of <i>Cladophora</i> -associated <i>Salmonella</i> in Lake Michigan watersheds. <i>Water Research</i> , 2009, 43, 806-814.	5.3	80
101	Application of a clustering-based peak alignment algorithm to analyze various DNA fingerprinting data. <i>Journal of Microbiological Methods</i> , 2009, 78, 344-350.	0.7	18
102	Sources and Sinks of <i>Escherichia coli</i> in Benthic and Pelagic Fish. <i>Journal of Great Lakes Research</i> , 2008, 34, 228-234.	0.8	21
103	<i>Escherichia coli</i> in the Environment: Implications for Water Quality and Human Health. <i>Microbes and Environments</i> , 2008, 23, 101-108.	0.7	393
104	Identification of Novel Betaproteobacteria in a Succinate-Assimilating Population in Denitrifying Rice Paddy Soil by Using Stable Isotope Probing. <i>Microbes and Environments</i> , 2008, 23, 192-200.	0.7	72
105	Presence and Sources of Fecal Coliform Bacteria in Epilithic Periphyton Communities of Lake Superior. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3771-3778.	1.4	99
106	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, 5703-5710.	1.4	104
107	Population structure of <i>Cladophora</i> -borne <i>Escherichia coli</i> in nearshore water of Lake Michigan. <i>Water Research</i> , 2007, 41, 3649-3654.	5.3	50
108	Beach Sand and Sediments are Temporal Sinks and Sources of <i>Escherichia coli</i> in Lake Superior. <i>Environmental Science & Technology</i> , 2007, 41, 2203-2209.	4.6	185

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109	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, 504-513.	1.8	181
110	<i>Cladophora</i> (Chlorophyta) spp. Harbor Human Bacterial Pathogens in Nearshore Water of Lake Michigan. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4545-4553.	1.4	150
111	Presence and Growth of Naturalized <i>Escherichia coli</i> in Temperate Soils from Lake Superior Watersheds. <i>Applied and Environmental Microbiology</i> , 2006, 72, 612-621.	1.4	440
112	Rapid and reliable DNA extraction techniques from trypan-blue-stained mycorrhizal roots: comparison of two methods. <i>Mycorrhiza</i> , 2004, 14, 271-275.	1.3	17
113	Gonadal development and expression profiles of gonadotropin genes in wild sea conger, <i>Ariosoma meeki</i> . <i>Fish Physiology and Biochemistry</i> , 2003, 28, 95-96.	0.9	5
114	Involvement of a sperm aminopeptidase in fertilization of the sea urchin. <i>Experientia</i> , 1991, 47, 100-103.	1.2	6
115	Environmental Sources of Fecal Bacteria. , 0, , 93-110.		13