## Jingrang Lu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12037666/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	The Bacterial Community Diversity of Bathroom Hot Tap Water Was Significantly Lower Than That of Cold Tap and Shower Water. Frontiers in Microbiology, 2021, 12, 625324.	3.5	8
2	Legionella and other opportunistic pathogens in full-scale chloraminated municipal drinking water distribution systems. Water Research, 2021, 205, 117571.	11.3	32
3	Comparative Study on the Performance of Anaerobic and Aerobic Biotrickling Filter for Removal of Chloroform. Environmental Engineering Science, 2018, 35, 462-471.	1.6	3
4	Annual variations and effects of temperature on Legionella spp. and other potential opportunistic pathogens in a bathroom. Environmental Science and Pollution Research, 2017, 24, 2326-2336.	5.3	32
5	Exposure to Synthetic Gray Water Inhibits Amoeba Encystation and Alters Expression of Legionella pneumophila Virulence Genes. Applied and Environmental Microbiology, 2015, 81, 630-639.	3.1	12
6	Preferential colonization and release of Legionella pneumophila from mature drinking water biofilms grown on copper versus unplasticized polyvinylchloride coupons. International Journal of Hygiene and Environmental Health, 2014, 217, 219-225.	4.3	40
7	Microbial diversities (16S and 18S rRNA gene pyrosequencing) and environmental pathogens within drinking water biofilms grown on the common premise plumbing materials unplasticized polyvinylchloride and copper. FEMS Microbiology Ecology, 2014, 88, 280-295.	2.7	67
8	Impacts of Migratory Sandhill Cranes (Grus canadensis) on Microbial Water Quality in the Central Platte River, Nebraska, USA. Water, Air, and Soil Pollution, 2013, 224, 1.	2.4	19
9	Eukaryotic diversity in premise drinking water using 18S rDNA sequencing: implications for health risks. Environmental Science and Pollution Research, 2013, 20, 6351-6366.	5.3	43
10	Development and Evaluation of a Quantitative PCR Assay Targeting Sandhill Crane (Grus canadensis) Fecal Pollution. Applied and Environmental Microbiology, 2012, 78, 4338-4345.	3.1	27
11	Distribution and potential significance of a gull fecal marker in urban coastal and riverine areas of southern Ontario, Canada. Water Research, 2011, 45, 3960-3968.	11.3	42
12	Molecular Detection of Campylobacter spp. in California Gull (Larus californicus) Excreta. Applied and Environmental Microbiology, 2011, 77, 5034-5039.	3.1	34
13	Microbial Diversity and Host-Specific Sequences of Canada Goose Feces. Applied and Environmental Microbiology, 2009, 75, 5919-5926.	3.1	68
14	Turkey fecal microbial community structure and functional gene diversity revealed by 16S rRNA gene and metagenomic sequences. Journal of Microbiology, 2008, 46, 469-477.	2.8	44
15	Quantitative PCR for Detection and Enumeration of Genetic Markers of Bovine Fecal Pollution. Applied and Environmental Microbiology, 2008, 74, 745-752.	3.1	183
16	Phylogenetic Diversity and Molecular Detection of Bacteria in Gull Feces. Applied and Environmental Microbiology, 2008, 74, 3969-3976.	3.1	163
17	Identification of Bacterial DNA Markers for the Detection of Human Fecal Pollution in Water. Applied and Environmental Microbiology, 2007, 73, 2416-2422.	3.1	61
18	Identification of chicken-specific fecal microbial sequences using a metagenomic approach. Water Research, 2007, 41, 3561-3574.	11.3	73

JINGRANG LU

#	Article	IF	CITATIONS
19	Evaluation of Broiler Litter with Reference to the Microbial Composition as Assessed by Using 16S rRNA and Functional Gene Markers. Applied and Environmental Microbiology, 2003, 69, 901-908.	3.1	176
20	Genomic Sequence and Evolution of Marine Cyanophage P60: a New Insight on Lytic and Lysogenic Phages. Applied and Environmental Microbiology, 2002, 68, 2589-2594.	3.1	158
21	Distribution, Isolation, Host Specificity, and Diversity of Cyanophages Infecting Marine Synechococcus spp. in River Estuaries. Applied and Environmental Microbiology, 2001, 67, 3285-3290.	3.1	109