

Tong Zhang

List of Publications by Year in descending order

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247
papers

29,005
citations

3334

91
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5988

160
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all docs

255
docs citations

255
times ranked

20392
citing authors

#	ARTICLE	IF	CITATIONS
1	454 Pyrosequencing reveals bacterial diversity of activated sludge from 14 sewage treatment plants. ISME Journal, 2012, 6, 1137-1147.	9.8	957
2	Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. ISME Journal, 2015, 9, 2490-2502.	9.8	928
3	Continental-scale pollution of estuaries with antibiotic resistance genes. Nature Microbiology, 2017, 2, 16270.	13.3	812
4	Antibiotic resistance genes in water environment. Applied Microbiology and Biotechnology, 2009, 82, 397-414.	3.6	801
5	Biodegradation and Adsorption of Antibiotics in the Activated Sludge Process. Environmental Science & Technology, 2010, 44, 3468-3473.	10.0	765
6	Management Options for Reducing the Release of Antibiotics and Antibiotic Resistance Genes to the Environment. Environmental Health Perspectives, 2013, 121, 878-885.	6.0	657
7	Sulfate Radical-Mediated Degradation of Sulfadiazine by CuFeO ₂ Rhombohedral Crystal-Catalyzed Peroxymonosulfate: Synergistic Effects and Mechanisms. Environmental Science & Technology, 2016, 50, 3119-3127.	10.0	563
8	Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195.	13.3	491
9	Metagenomic insights into chlorination effects on microbial antibiotic resistance in drinking water. Water Research, 2013, 47, 111-120.	11.3	423
10	Fate of antibiotic resistance genes in sewage treatment plant revealed by metagenomic approach. Water Research, 2014, 62, 97-106.	11.3	418
11	Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. ISME Journal, 2015, 9, 683-695.	9.8	393
12	Bacterial Community Shift Drives Antibiotic Resistance Promotion during Drinking Water Chlorination. Environmental Science & Technology, 2015, 49, 12271-12279.	10.0	384
13	ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. Bioinformatics, 2018, 34, 2263-2270.	4.1	375
14	Co-occurrence of antibiotic and metal resistance genes revealed in complete genome collection. ISME Journal, 2017, 11, 651-662.	9.8	351
15	Phthalates biodegradation in the environment. Applied Microbiology and Biotechnology, 2008, 80, 183-98.	3.6	336
16	Taxonomic relatedness shapes bacterial assembly in activated sludge of globally distributed wastewater treatment plants. Environmental Microbiology, 2014, 16, 2421-2432.	3.8	333
17	Metagenomic Profiles of Antibiotic Resistance Genes (ARGs) between Human Impacted Estuary and Deep Ocean Sediments. Environmental Science & Technology, 2013, 47, 12753-12760.	10.0	329
18	Antibiotics, Antibiotic Resistance Genes, and Bacterial Community Composition in Fresh Water Aquaculture Environment in China. Microbial Ecology, 2015, 70, 425-432.	2.8	322

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19	Exploring Variation of Antibiotic Resistance Genes in Activated Sludge over a Four-Year Period through a Metagenomic Approach. <i>Environmental Science & Technology</i> , 2013, 47, 10197-10205.	10.0	315
20	Sulfur-driven autotrophic denitrification: diversity, biochemistry, and engineering applications. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 1027-1042.	3.6	310
21	Antibiotic resistance genes and human bacterial pathogens: Co-occurrence, removal, and enrichment in municipal sewage sludge digesters. <i>Water Research</i> , 2016, 91, 1-10.	11.3	305
22	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes. <i>ISME Journal</i> , 2019, 13, 346-360.	9.8	289
23	Metagenomic Assembly Reveals Hosts of Antibiotic Resistance Genes and the Shared Resistome in Pig, Chicken, and Human Feces. <i>Environmental Science & Technology</i> , 2016, 50, 420-427.	10.0	287
24	Biohydrogen production from starch in wastewater under thermophilic condition. <i>Journal of Environmental Management</i> , 2003, 69, 149-156.	7.8	285
25	Plasmid Metagenome Reveals High Levels of Antibiotic Resistance Genes and Mobile Genetic Elements in Activated Sludge. <i>PLoS ONE</i> , 2011, 6, e26041.	2.5	272
26	Metagenomic and Metatranscriptomic Analysis of Microbial Community Structure and Gene Expression of Activated Sludge. <i>PLoS ONE</i> , 2012, 7, e38183.	2.5	267
27	The Prevalence of Integrons as the Carrier of Antibiotic Resistance Genes in Natural and Man-Made Environments. <i>Environmental Science & Technology</i> , 2017, 51, 5721-5728.	10.0	260
28	Fate of antibiotic resistance genes and their associations with bacterial community in livestock breeding wastewater and its receiving river water. <i>Water Research</i> , 2017, 124, 259-268.	11.3	255
29	ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. <i>Bioinformatics</i> , 2016, 32, 2346-2351.	4.1	254
30	Bacterial communities in different sections of a municipal wastewater treatment plant revealed by 16S rDNA 454 pyrosequencing. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 2681-2690.	3.6	253
31	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	12.8	248
32	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. <i>Microbiome</i> , 2017, 5, 84.	11.1	247
33	Occurrence, Abundance, and Diversity of Tetracycline Resistance Genes in 15 Sewage Treatment Plants across China and Other Global Locations. <i>Environmental Science & Technology</i> , 2011, 45, 2598-2604.	10.0	246
34	Widespread Production of Extracellular Superoxide by Heterotrophic Bacteria. <i>Science</i> , 2013, 340, 1223-1226.	12.6	236
35	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. <i>Environmental Science & Technology</i> , 2017, 51, 13061-13069.	10.0	236
36	Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing. <i>Microbiome</i> , 2019, 7, 44.	11.1	236

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37	Occurrence, Transformation, and Fate of Antibiotics in Municipal Wastewater Treatment Plants. <i>Critical Reviews in Environmental Science and Technology</i> , 2011, 41, 951-998.	12.8	229
38	Analysis of the bacterial community in a laboratory-scale nitrification reactor and a wastewater treatment plant by 454-pyrosequencing. <i>Water Research</i> , 2011, 45, 4390-4398.	11.3	217
39	Catalogue of antibiotic resistome and host-tracking in drinking water deciphered by a large scale survey. <i>Microbiome</i> , 2017, 5, 154.	11.1	215
40	Cellular adhesiveness and cellulolytic capacity in Anaerolineae revealed by omics-based genome interpretation. <i>Biotechnology for Biofuels</i> , 2016, 9, 111.	6.2	210
41	Applications of real-time polymerase chain reaction for quantification of microorganisms in environmental samples. <i>Applied Microbiology and Biotechnology</i> , 2006, 70, 281-289.	3.6	208
42	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	11.1	208
43	Effect of temperature on removal of antibiotic resistance genes by anaerobic digestion of activated sludge revealed by metagenomic approach. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7771-7779.	3.6	201
44	Rapid analysis of 21 antibiotics of multiple classes in municipal wastewater using ultra performance liquid chromatography-tandem mass spectrometry. <i>Analytica Chimica Acta</i> , 2009, 645, 64-72.	5.4	199
45	Detecting Human Bacterial Pathogens in Wastewater Treatment Plants by a High-Throughput Shotgun Sequencing Technique. <i>Environmental Science & Technology</i> , 2013, 47, 5433-5441.	10.0	199
46	Tetracycline Resistance Genes and Tetracycline Resistant Lactose-Fermenting <i>Enterobacteriaceae</i> in Activated Sludge of Sewage Treatment Plants. <i>Environmental Science & Technology</i> , 2009, 43, 3455-3460.	10.0	196
47	Pathogenic Bacteria in Sewage Treatment Plants as Revealed by 454 Pyrosequencing. <i>Environmental Science & Technology</i> , 2011, 45, 7173-7179.	10.0	186
48	Antibiotic-mediated changes in the fecal microbiome of broiler chickens define the incidence of antibiotic resistance genes. <i>Microbiome</i> , 2018, 6, 34.	11.1	185
49	Differentiating anthropogenic impacts on ARGs in the Pearl River Estuary by using suitable gene indicators. <i>Water Research</i> , 2013, 47, 2811-2820.	11.3	182
50	Metagenomic analysis of sludge from full-scale anaerobic digesters operated in municipal wastewater treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5709-5718.	3.6	179
51	Bacteria-mediated PAH degradation in soil and sediment. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1357-1371.	3.6	178
52	Characterization of tetracycline resistant bacterial community in saline activated sludge using batch stress incubation with high-throughput sequencing analysis. <i>Water Research</i> , 2013, 47, 4207-4216.	11.3	175
53	Profiling bulking and foaming bacteria in activated sludge by high throughput sequencing. <i>Water Research</i> , 2012, 46, 2772-2782.	11.3	172
54	Mass flows and removal of antibiotics in two municipal wastewater treatment plants. <i>Chemosphere</i> , 2011, 83, 1284-1289.	8.2	169

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55	Structure, Variation, and Co-occurrence of Soil Microbial Communities in Abandoned Sites of a Rare Earth Elements Mine. <i>Environmental Science & Technology</i> , 2016, 50, 11481-11490.	10.0	163
56	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	11.3	163
57	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	161
58	Metagenomic analysis on seasonal microbial variations of activated sludge from a full-scale wastewater treatment plant over 4 years. <i>Environmental Microbiology Reports</i> , 2014, 6, 80-89.	2.4	159
59	Optimization of fixation methods for observation of bacterial cell morphology and surface ultrastructures by atomic force microscopy. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 381-392.	3.6	157
60	Metagenomic Analysis Revealing Antibiotic Resistance Genes (ARGs) and Their Genetic Compartments in the Tibetan Environment. <i>Environmental Science & Technology</i> , 2016, 50, 6670-6679.	10.0	155
61	Antibiotic Resistance Genes and Correlations with Microbial Community and Metal Resistance Genes in Full-Scale Biogas Reactors As Revealed by Metagenomic Analysis. <i>Environmental Science & Technology</i> , 2017, 51, 4069-4080.	10.0	154
62	Microbial Structures, Functions, and Metabolic Pathways in Wastewater Treatment Bioreactors Revealed Using High-Throughput Sequencing. <i>Environmental Science & Technology</i> , 2012, 46, 13244-13252.	10.0	153
63	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. <i>Environment International</i> , 2018, 117, 146-153.	10.0	152
64	Impact of dairy manure pre-application treatment on manure composition, soil dynamics of antibiotic resistance genes, and abundance of antibiotic-resistance genes on vegetables at harvest. <i>Science of the Total Environment</i> , 2017, 581-582, 32-39.	8.0	148
65	Metagenomics Shows That Low-Energy Anaerobic Aerobic Treatment Reactors Reduce Antibiotic Resistance Gene Levels from Domestic Wastewater. <i>Environmental Science & Technology</i> , 2015, 49, 2577-2584.	10.0	147
66	Characterization of Thauera-dominated hydrogen-oxidizing autotrophic denitrifying microbial communities by using high-throughput sequencing. <i>Bioresource Technology</i> , 2013, 128, 703-710.	9.6	144
67	Antibiotic resistome in a large-scale healthy human gut microbiota deciphered by metagenomic and network analyses. <i>Environmental Microbiology</i> , 2018, 20, 355-368.	3.8	141
68	Biases during DNA extraction of activated sludge samples revealed by high throughput sequencing. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4607-4616.	3.6	139
69	Exploring antibiotic resistance genes and metal resistance genes in plasmid metagenomes from wastewater treatment plants. <i>Frontiers in Microbiology</i> , 2015, 6, 1025.	3.5	139
70	Antibiotic resistome in landfill leachate from different cities of China deciphered by metagenomic analysis. <i>Water Research</i> , 2018, 134, 126-139.	11.3	138
71	Profile and Fate of Bacterial Pathogens in Sewage Treatment Plants Revealed by High-Throughput Metagenomic Approach. <i>Environmental Science & Technology</i> , 2015, 49, 10492-10502.	10.0	137
72	Aerobic Degradation of Sulfadiazine by <i>Arthrobacter</i> spp.: Kinetics, Pathways, and Genomic Characterization. <i>Environmental Science & Technology</i> , 2016, 50, 9566-9575.	10.0	134

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73	Ammonia-oxidizing archaea and ammonia-oxidizing bacteria in six full-scale wastewater treatment bioreactors. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1215-1225.	3.6	133
74	Tracking human sewage microbiome in a municipal wastewater treatment plant. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3317-3326.	3.6	126
75	Metagenomic analysis revealed highly diverse microbial arsenic metabolism genes in paddy soils with low-arsenic contents. <i>Environmental Pollution</i> , 2016, 211, 1-8.	7.5	125
76	Surface-enhanced Raman scattering (SERS) revealing chemical variation during biofilm formation: from initial attachment to mature biofilm. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1465-1475.	3.7	124
77	Characterization and quantification of class 1 integrons and associated gene cassettes in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1169-1177.	3.6	120
78	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	3.5	120
79	Comparative genomics analyses on EPS biosynthesis genes required for floc formation of <i>Zoogloea resiniphila</i> and other activated sludge bacteria. <i>Water Research</i> , 2016, 102, 494-504.	11.3	117
80	Does Hydrophilic Polydopamine Coating Enhance Membrane Rejection of Hydrophobic Endocrine-Disrupting Compounds?. <i>Environmental Science and Technology Letters</i> , 2016, 3, 332-338.	8.7	117
81	Metagenomic analysis reveals significant changes of microbial compositions and protective functions during drinking water treatment. <i>Scientific Reports</i> , 2013, 3, 3550.	3.3	116
82	Tracking antibiotic resistance gene pollution from different sources using machine-learning classification. <i>Microbiome</i> , 2018, 6, 93.	11.1	114
83	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. <i>Nature Communications</i> , 2022, 13, 1908.	12.8	114
84	Metagenomic Analysis of Antibiotic Resistance Genes in Dairy Cow Feces following Therapeutic Administration of Third Generation Cephalosporin. <i>PLoS ONE</i> , 2015, 10, e0133764.	2.5	113
85	Novel Insights into Selection for Antibiotic Resistance in Complex Microbial Communities. <i>MBio</i> , 2018, 9, .	4.1	110
86	Linking Microbial Community, Environmental Variables, and Methanogenesis in Anaerobic Biogas Digesters of Chemically Enhanced Primary Treatment Sludge. <i>Environmental Science & Technology</i> , 2017, 51, 3982-3992.	10.0	107
87	Water and sanitation: an essential battlefront in the war on antimicrobial resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	104
88	Selection for antimicrobial resistance is reduced when embedded in a natural microbial community. <i>ISME Journal</i> , 2019, 13, 2927-2937.	9.8	102
89	Identification and quantification of bacterial genomes carrying antibiotic resistance genes and virulence factor genes for aquatic microbiological risk assessment. <i>Water Research</i> , 2020, 168, 115160.	11.3	102
90	Characterization and quantification of ammonia-oxidizing archaea (AOA) and bacteria (AOB) in a nitrogen-removing reactor using T-RFLP and qPCR. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 1167-1176.	3.6	101

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91	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	4.0	100
92	New insights into antibiotic resistome in drinking water and management perspectives: A metagenomic based study of small-sized microbes. <i>Water Research</i> , 2019, 152, 191-201.	11.3	100
93	Shifts in the Microbial Community, Nitrifiers and Denitrifiers in the Biofilm in a Full-scale Rotating Biological Contactor. <i>Environmental Science & Technology</i> , 2014, 48, 8044-8052.	10.0	99
94	Bacteria That Make a Meal of Sulfonamide Antibiotics: Blind Spots and Emerging Opportunities. <i>Environmental Science & Technology</i> , 2018, 52, 3854-3868.	10.0	97
95	Metagenomic analysis reveals potential biodegradation pathways of persistent pesticides in freshwater and marine sediments. <i>Science of the Total Environment</i> , 2014, 470-471, 983-992.	8.0	92
96	Novel nitrifiers and comammox in a full-scale hybrid biofilm and activated sludge reactor revealed by metagenomic approach. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8225-8237.	3.6	90
97	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	12.8	90
98	An integrated meta-omics approach reveals substrates involved in synergistic interactions in a bisphenol A (BPA)-degrading microbial community. <i>Microbiome</i> , 2019, 7, 16.	11.1	89
99	Editorial: Antibiotic Resistance in Aquatic Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 14.	3.5	88
100	Abundant rifampin resistance genes and significant correlations of antibiotic resistance genes and plasmids in various environments revealed by metagenomic analysis. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5195-5204.	3.6	87
101	Metagenomic profiles of antibiotic resistance genes in paddy soils from South China. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw023.	2.7	87
102	Performance of nanofiltration membrane in rejecting trace organic compounds: Experiment and model prediction. <i>Desalination</i> , 2015, 370, 7-16.	8.2	85
103	Exploration of the antibiotic resistome in a wastewater treatment plant by a nine-year longitudinal metagenomic study. <i>Environment International</i> , 2019, 133, 105270.	10.0	85
104	Microbial community and biochemistry process in autosulfurotrophic denitrifying biofilm. <i>Chemosphere</i> , 2005, 58, 1041-1047.	8.2	84
105	Taxonomic Precision of Different Hypervariable Regions of 16S rRNA Gene and Annotation Methods for Functional Bacterial Groups in Biological Wastewater Treatment. <i>PLoS ONE</i> , 2013, 8, e76185.	2.5	84
106	Class 1 integronase gene and tetracycline resistance genes tetA and tetC in different water environments of Jiangsu Province, China. <i>Ecotoxicology</i> , 2009, 18, 652-660.	2.4	83
107	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. <i>Microbiome</i> , 2018, 6, 130.	11.1	83
108	Effluents of wastewater treatment plants promote the rapid stabilization of the antibiotic resistome in receiving freshwater bodies. <i>Water Research</i> , 2019, 158, 72-81.	11.3	82

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109	Source tracking of antibiotic resistance genes in the environment – Challenges, progress, and prospects. <i>Water Research</i> , 2020, 185, 116127.	11.3	82
110	Aerobic degradation of diethyl phthalate by <i>Sphingomonas</i> sp.. <i>Bioresource Technology</i> , 2007, 98, 717-720.	9.6	79
111	Different removal behaviours of multiple trace antibiotics in municipal wastewater chlorination. <i>Water Research</i> , 2013, 47, 2970-2982.	11.3	79
112	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4119-4129.	3.6	79
113	A highly selective surface coating for enhanced membrane rejection of endocrine disrupting compounds: Mechanistic insights and implications. <i>Water Research</i> , 2017, 121, 197-203.	11.3	77
114	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. <i>Water Research</i> , 2019, 155, 275-287.	11.3	77
115	Title is missing!. <i>Biotechnology Letters</i> , 2000, 22, 399-405.	2.2	75
116	Discovery of new cellulases from the metagenome by a metagenomics-guided strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 138.	6.2	74
117	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science & Technology</i> , 2015, 49, 12628-12640.	10.0	72
118	Diversity and functions of bacterial community in drinking water biofilms revealed by high-throughput sequencing. <i>Scientific Reports</i> , 2015, 5, 10044.	3.3	71
119	Characterization of airborne antibiotic resistance genes from typical bioaerosol emission sources in the urban environment using metagenomic approach. <i>Chemosphere</i> , 2018, 213, 463-471.	8.2	71
120	Anaerobic degradation of dimethyl phthalate in wastewater in a UASB reactor. <i>Water Research</i> , 2007, 41, 2879-2884.	11.3	70
121	Enhanced anoxic bioremediation of PAHs-contaminated sediment. <i>Bioresource Technology</i> , 2012, 104, 51-58.	9.6	69
122	pH significantly affects removal of trace antibiotics in chlorination of municipal wastewater. <i>Water Research</i> , 2012, 46, 3703-3713.	11.3	65
123	Metagenomic exploration reveals high levels of microbial arsenic metabolism genes in activated sludge and coastal sediments. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9579-9588.	3.6	65
124	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	11.1	65
125	Direct rapid analysis of multiple PPCPs in municipal wastewater using ultrahigh performance liquid chromatography–tandem mass spectrometry without SPE pre-concentration. <i>Analytica Chimica Acta</i> , 2012, 738, 59-68.	5.4	64
126	Genome Reconstruction and Gene Expression of <i>Candidatus</i> <i>Accumulibacter phosphatis</i> Clade IB Performing Biological Phosphorus Removal. <i>Environmental Science & Technology</i> , 2014, 48, 10363-10371.	10.0	64

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127	Dominant and novel clades of <i>Candidatus Accumulibacter phosphatis</i> in 18 globally distributed full-scale wastewater treatment plants. <i>Scientific Reports</i> , 2015, 5, 11857.	3.3	64
128	Ammonia-oxidizing bacteria dominates over ammonia-oxidizing archaea in a saline nitrification reactor under low DO and high nitrogen loading. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2544-2552.	3.3	63
129	Abundance and distribution of Macrolide-Lincosamide-Streptogramin resistance genes in an anaerobic-aerobic system treating spiramycin production wastewater. <i>Water Research</i> , 2014, 63, 33-41.	11.3	63
130	Thermophilic microbial cellulose decomposition and methanogenesis pathways recharacterized by metatranscriptomic and metagenomic analysis. <i>Scientific Reports</i> , 2014, 4, 6708.	3.3	62
131	Thermodynamic and physiological study of caproate and 1,3-propanediol co-production through glycerol fermentation and fatty acids chain elongation. <i>Water Research</i> , 2017, 114, 200-209.	11.3	62
132	Picoinjection-Enabled Multitarget Loop-Mediated Isothermal Amplification for Detection of Foodborne Pathogens. <i>Analytical Chemistry</i> , 2018, 90, 13173-13177.	6.5	62
133	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. <i>ISME Journal</i> , 2020, 14, 2595-2609.	9.8	62
134	Effects of Weathering on the Sorption Behavior and Toxicity of Polystyrene Microplastics in Multi-solute Systems. <i>Water Research</i> , 2020, 187, 116419.	11.3	61
135	Metagenomic and Resistome Analysis of a Full-Scale Municipal Wastewater Treatment Plant in Singapore Containing Membrane Bioreactors. <i>Frontiers in Microbiology</i> , 2019, 10, 172.	3.5	58
136	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. <i>Molecular Ecology</i> , 2020, 29, 5019-5034.	3.9	57
137	Untangling Microbiota Diversity and Assembly Patterns in the World's Largest Water Diversion Canal. <i>Water Research</i> , 2021, 204, 117617.	11.3	57
138	Genomic characterization, kinetics, and pathways of sulfamethazine biodegradation by <i>Paenarthrobacter</i> sp. A01. <i>Environment International</i> , 2019, 131, 104961.	10.0	56
139	Biodegradation of naphthalene by enriched marine denitrifying bacteria. <i>International Biodeterioration and Biodegradation</i> , 2011, 65, 204-211.	3.9	55
140	Novel Microbial Populations in Ambient and Mesophilic Biogas-Producing and Phenol-Degrading Consortia Unraveled by High-Throughput Sequencing. <i>Microbial Ecology</i> , 2014, 68, 235-246.	2.8	54
141	Autotrophic denitrification and its effect on metal speciation during marine sediment remediation. <i>Water Research</i> , 2009, 43, 2961-2968.	11.3	53
142	Sorption Behavior of Bisphenol A and Triclosan by Graphene: Comparison with Activated Carbon. <i>ACS Omega</i> , 2017, 2, 5378-5384.	3.5	53
143	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. <i>Water Research</i> , 2019, 166, 115073.	11.3	53
144	Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge. <i>Microbiome</i> , 2022, 10, 20.	11.1	52

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145	Title is missing!. <i>Biotechnology Letters</i> , 2001, 23, 405-409.	2.2	51
146	Impact of pre-application treatment on municipal sludge composition, soil dynamics of antibiotic resistance genes, and abundance of antibiotic-resistance genes on vegetables at harvest. <i>Science of the Total Environment</i> , 2017, 587-588, 214-222.	8.0	50
147	The first case study of wastewater-based epidemiology of COVID-19 in Hong Kong. <i>Science of the Total Environment</i> , 2021, 790, 148000.	8.0	50
148	Construction of Customized Sub-Databases from NCBI-nr Database for Rapid Annotation of Huge Metagenomic Datasets Using a Combined BLAST and MEGAN Approach. <i>PLoS ONE</i> , 2013, 8, e59831.	2.5	49
149	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. <i>Nature Communications</i> , 2021, 12, 5398.	12.8	49
150	Comparison of virus concentration methods and RNA extraction methods for SARS-CoV-2 wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 824, 153687.	8.0	49
151	Quantification and characterization of β -lactam resistance genes in 15 sewage treatment plants from East Asia and North America. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 1351-1358.	3.6	48
152	Anaerobic digestion of chemically enhanced primary treatment (CEPT) sludge and the microbial community structure. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8975-8982.	3.6	46
153	Effect of pH change on the performance and microbial community of enhanced biological phosphate removal process. <i>Biotechnology and Bioengineering</i> , 2005, 92, 173-182.	3.3	45
154	Mining of Novel Thermo-Stable Cellulolytic Genes from a Thermophilic Cellulose-Degrading Consortium by Metagenomics. <i>PLoS ONE</i> , 2013, 8, e53779.	2.5	44
155	Co-occurrence correlations of heavy metals in sediments revealed using network analysis. <i>Chemosphere</i> , 2015, 119, 1305-1313.	8.2	43
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