

# 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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255  
all docs

255  
docs citations

255  
times ranked

20392  
citing authors

#	ARTICLE	IF	CITATIONS
1	Culturing the uncultured microbial majority in activated sludge: A critical review. <i>Critical Reviews in Environmental Science and Technology</i> , 2023, 53, 601-624.	12.8	13
2	Risks of antibiotic resistance genes and antimicrobial resistance under chlorination disinfection with public health concerns. <i>Environment International</i> , 2022, 158, 106978.	10.0	39
3	An assessment of resistome and mobilome in wastewater treatment plants through temporal and spatial metagenomic analysis. <i>Water Research</i> , 2022, 209, 117885.	11.3	31
4	Genome-centric metagenomics provides new insights into the microbial community and metabolic potential of landfill leachate microbiota. <i>Science of the Total Environment</i> , 2022, 816, 151635.	8.0	7
5	Rapid absolute quantification of pathogens and ARGs by nanopore sequencing. <i>Science of the Total Environment</i> , 2022, 809, 152190.	8.0	21
6	Siderophores provoke extracellular superoxide production by <i>Arthrobacter</i> strains during carbon sources level fluctuation. <i>Environmental Microbiology</i> , 2022, 24, 894-904.	3.8	5
7	High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria. <i>Microbiome</i> , 2022, 10, 16.	11.1	18
8	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
9	Response and resilience of anammox consortia to nutrient starvation. <i>Microbiome</i> , 2022, 10, 23.	11.1	16
10	Use of sewage surveillance for COVID-19 to guide public health response: A case study in Hong Kong. <i>Science of the Total Environment</i> , 2022, 821, 153250.	8.0	31
11	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
12	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
13	Wastewater as an information source of COVID-19. <i>Science Bulletin</i> , 2022, 67, 1090-1092.	9.0	10
14	Nationwide biogeography and health implications of bacterial communities in household drinking water. <i>Water Research</i> , 2022, 215, 118238.	11.3	7
15	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. <i>Environmental Microbiomes</i> , 2022, 17, 19.	5.0	6
16	Impacts of food waste to sludge ratios on microbial dynamics and functional traits in thermophilic digesters. <i>Water Research</i> , 2022, 219, 118590.	11.3	4
17	Use of Sewage Surveillance for COVID-19: A Large-Scale Evidence-Based Program in Hong Kong. <i>Environmental Health Perspectives</i> , 2022, 130, 57008.	6.0	20
18	Evaluation of RT-qPCR Primer-Probe Sets to Inform Public Health Interventions Based on COVID-19 Sewage Tests. <i>Environmental Science &amp; Technology</i> , 2022, 56, 8875-8884.	10.0	11

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19	Real-time allelic assays of SARS-CoV-2 variants to enhance sewage surveillance. <i>Water Research</i> , 2022, 220, 118686.	11.3	17
20	Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. <i>Environmental Science &amp; Technology</i> , 2022, 56, 14982-14993.	10.0	27
21	Quantification of SARS-CoV-2 RNA in wastewater treatment plants mirrors the pandemic trend in Hong Kong. <i>Science of the Total Environment</i> , 2022, 844, 157121.	8.0	22
22	Development of an efficient pathway construction strategy for rapid evolution of the biodegradation capacity of <i>Pseudomonas putida</i> KT2440 and its application in bioremediation. <i>Science of the Total Environment</i> , 2021, 761, 143239.	8.0	14
23	Role of wastewater treatment in COVID-19 control. <i>Water Quality Research Journal of Canada</i> , 2021, 56, 68-82.	2.7	16
24	Seasonal Prevalence of Ammonia-Oxidizing Archaea in a Full-Scale Municipal Wastewater Treatment Plant Treating Saline Wastewater Revealed by a 6-Year Time-Series Analysis. <i>Environmental Science &amp; Technology</i> , 2021, 55, 2662-2673.	10.0	11
25	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
26	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. <i>ISME Journal</i> , 2021, 15, 2817-2829.	9.8	10
27	Reply to Shaw: Challenges for enrichment analysis of AMR gene-bearing plasmids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2104557118.	7.1	0
28	Selective enrichment of comamox from activated sludge using antibiotics. <i>Water Research</i> , 2021, 197, 117087.	11.3	31
29	Reply to Partridge et al.: Complementary bioinformatics and experimental approaches to investigate the transfer of AMR genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	2
30	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	12.8	248
31	Underrepresented high diversity of class 1 integrons in the environment uncovered by PacBio sequencing using a new primer. <i>Science of the Total Environment</i> , 2021, 787, 147611.	8.0	11
32	Acesulfame aerobic biodegradation by enriched consortia and <i>Chelatococcus</i> spp.: Kinetics, transformation products, and genomic characterization. <i>Water Research</i> , 2021, 202, 117454.	11.3	21
33	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
34	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
35	Untangling Microbiota Diversity and Assembly Patterns in the World's Largest Water Diversion Canal. <i>Water Research</i> , 2021, 204, 117617.	11.3	57
36	Impact of chicken litter pre-application treatment on the abundance, field persistence, and transfer of antibiotic resistant bacteria and antibiotic resistance genes to vegetables. <i>Science of the Total Environment</i> , 2021, 801, 149718.	8.0	13

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37	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	11.1	33
38	Charting the complexity of the activated sludge microbiome through a hybrid sequencing strategy. <i>Microbiome</i> , 2021, 9, 205.	11.1	29
39	Evidence for Long-Term Anthropogenic Pollution: The Hadal Trench as a Depository and Indicator for Dissemination of Antibiotic Resistance Genes. <i>Environmental Science &amp; Technology</i> , 2021, 55, 15136-15148.	10.0	41
40	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
41	Challenges related to antimicrobial resistance in the framework of urban wastewater reuse. <i>Water Research</i> , 2020, 170, 115308.	11.3	9
42	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. <i>Molecular Ecology</i> , 2020, 29, 5019-5034.	3.9	57
43	Editorial: The Environmental Dimension of Antibiotic Resistance. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	23
44	Source tracking of antibiotic resistance genes in the environment – Challenges, progress, and prospects. <i>Water Research</i> , 2020, 185, 116127.	11.3	82
45	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
46	High-quality bacterial genomes of a partial-nitrification/anammox system by an iterative hybrid assembly method. <i>Microbiome</i> , 2020, 8, 155.	11.1	29
47	Online searching platform for the antibiotic resistome in bacterial tree of life and global habitats. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
48	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. <i>Water Research</i> , 2020, 181, 115858.	11.3	37
49	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
50	Selection for antimicrobial resistance is reduced when embedded in a natural microbial community. <i>ISME Journal</i> , 2019, 13, 2927-2937.	9.8	102
51	Genomic characterization, kinetics, and pathways of sulfamethazine biodegradation by <i>Paenarthrobacter</i> sp. A01. <i>Environment International</i> , 2019, 131, 104961.	10.0	56
52	Distribution of arsenic and its biotransformation genes in sediments from the East China Sea. <i>Environmental Pollution</i> , 2019, 253, 949-958.	7.5	35
53	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	4.0	100
54	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

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55	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
56	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
57	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. <i>Water Research</i> , 2019, 166, 115073.	11.3	53
58	Phylogenetic characterization of bromate-reducing microbial community enriched anaerobically from activated sludge. <i>Ecotoxicology and Environmental Safety</i> , 2019, 184, 109630.	6.0	6
59	Mycobacterial species and their contribution to cholesterol degradation in wastewater treatment plants. <i>Scientific Reports</i> , 2019, 9, 836.	3.3	24
60	Uranium sequestration in sediment at an iron-rich contaminated site at Oak Ridge, Tennessee via. bioreduction followed by reoxidation. <i>Journal of Environmental Sciences</i> , 2019, 85, 156-167.	6.1	10
61	Mining traits for the enrichment and isolation of not-yet-cultured populations. <i>Microbiome</i> , 2019, 7, 96.	11.1	8
62	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	13.3	491
63	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
64	Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing. <i>Microbiome</i> , 2019, 7, 44.	11.1	236
65	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
66	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
67	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
68	Genomic resolution of bacterial populations in saccharin and cyclamate degradation. <i>Science of the Total Environment</i> , 2019, 658, 357-366.	8.0	10
69	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
70	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. <i>Science of the Total Environment</i> , 2019, 651, 2148-2157.	8.0	25
71	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
72	Bacteria That Make a Meal of Sulfonamide Antibiotics: Blind Spots and Emerging Opportunities. <i>Environmental Science &amp; Technology</i> , 2018, 52, 3854-3868.	10.0	97

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73	Bacterial Community Shift and Coexisting/Coexcluding Patterns Revealed by Network Analysis in a Uranium-Contaminated Site after Bioreduction Followed by Reoxidation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	37
74	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. <i>Bioinformatics</i> , 2018, 34, 2263-2270.	4.1	375
75	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
76	Partnership of <i>Arthrobacter</i> and <i>Pimelobacter</i> in Aerobic Degradation of Sulfadiazine Revealed by Metagenomics Analysis and Isolation. <i>Environmental Science &amp; Technology</i> , 2018, 52, 2963-2972.	10.0	26
77	Effects of sample preservation and DNA extraction on enumeration of antibiotic resistance genes in wastewater. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	33
78	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
79	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
80	Picoinjection-Enabled Multitarget Loop-Mediated Isothermal Amplification for Detection of Foodborne Pathogens. <i>Analytical Chemistry</i> , 2018, 90, 13173-13177.	6.5	62
81	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
82	Toward an Intensive Longitudinal Understanding of Activated Sludge Bacterial Assembly and Dynamics. <i>Environmental Science &amp; Technology</i> , 2018, 52, 8224-8232.	10.0	32
83	Tracking antibiotic resistance gene pollution from different sources using machine-learning classification. <i>Microbiome</i> , 2018, 6, 93.	11.1	114
84	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
85	Novel Insights into Selection for Antibiotic Resistance in Complex Microbial Communities. <i>MBio</i> , 2018, 9, .	4.1	110
86	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	11.1	208
87	Microbial effects of part-stream low-frequency ultrasonic pretreatment on sludge anaerobic digestion as revealed by high-throughput sequencing-based metagenomics and metatranscriptomics. <i>Biotechnology for Biofuels</i> , 2018, 11, 47.	6.2	26
88	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. <i>Environment International</i> , 2018, 117, 146-153.	10.0	152
89	Bioreactor microbial ecosystems with differentiated methanogenic phenol biodegradation and competitive metabolic pathways unraveled with genome-resolved metagenomics. <i>Biotechnology for Biofuels</i> , 2018, 11, 135.	6.2	17
90	Temporal dynamics of activated sludge bacterial communities in two diversity variant full-scale sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9379-9388.	3.6	26

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91	High-Resolution Temporal and Spatial Patterns of Virome in Wastewater Treatment Systems. <i>Environmental Science &amp; Technology</i> , 2018, 52, 10337-10346.	10.0	25
92	Water and sanitation: an essential battlefield in the war on antimicrobial resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	104
93	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
94	Continental-scale pollution of estuaries with antibiotic resistance genes. <i>Nature Microbiology</i> , 2017, 2, 16270.	13.3	812
95	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
96	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 &amp; Technology</i> , 2017, 51, 4069-4080.	10.0	154
97	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
98	Linking Microbial Community, Environmental Variables, and Methanogenesis in Anaerobic Biogas Digesters of Chemically Enhanced Primary Treatment Sludge. <i>Environmental Science &amp; Technology</i> , 2017, 51, 3982-3992.	10.0	107
99	The Prevalence of Integrons as the Carrier of Antibiotic Resistance Genes in Natural and Man-Made Environments. <i>Environmental Science &amp; Technology</i> , 2017, 51, 5721-5728.	10.0	260
100	Macrobenthic communities in Hong Kong waters: Comparison between 2001 and 2012 and potential link to pollution control. <i>Marine Pollution Bulletin</i> , 2017, 124, 694-700.	5.0	16
101	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
102	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	11.3	163
103	Co-occurrence of antibiotic and metal resistance genes revealed in complete genome collection. <i>ISME Journal</i> , 2017, 11, 651-662.	9.8	351
104	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. <i>Environmental Science &amp; Technology</i> , 2017, 51, 13061-13069.	10.0	236
105	Cultivation-dependent and high-throughput sequencing approaches studying the co-occurrence of antibiotic resistance genes in municipal sewage system. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8197-8207.	3.6	11
106	Investigation on the anaerobic co-digestion of food waste with sewage sludge. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7755-7766.	3.6	20
107	Sorption Behavior of Bisphenol A and Triclosan by Graphene: Comparison with Activated Carbon. <i>ACS Omega</i> , 2017, 2, 5378-5384.	3.5	53
108	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

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109	Editorial: Antibiotic Resistance in Aquatic Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 14.	3.5	88
110	MinION Nanopore Sequencing Enables Correlation between Resistome Phenotype and Genotype of Coliform Bacteria in Municipal Sewage. <i>Frontiers in Microbiology</i> , 2017, 8, 2105.	3.5	39
111	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
112	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. <i>Microbiome</i> , 2017, 5, 84.	11.1	247
113	Bioprospecting for $\beta$ -lactam resistance genes using a metagenomics-guided strategy. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6253-6260.	3.6	2
114	Exploring the Shift in Structure and Function of Microbial Communities Performing Biological Phosphorus Removal. <i>PLoS ONE</i> , 2016, 11, e0161506.	2.5	9
115	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	3.5	120
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	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
118	Development of Quantitative Real-time PCR Assays for Different Clades of <i>Candidatus Accumulibacter</i> . <i>Scientific Reports</i> , 2016, 6, 23993.	3.3	32
119	Cellular adhesiveness and cellulolytic capacity in <i>Anaerolineae</i> revealed by omics-based genome interpretation. <i>Biotechnology for Biofuels</i> , 2016, 9, 111.	6.2	210
120	Population Dynamics of Bulking and Foaming Bacteria in a Full-scale Wastewater Treatment Plant over Five Years. <i>Scientific Reports</i> , 2016, 6, 24180.	3.3	30
121	Metagenomic Analysis Revealing Antibiotic Resistance Genes (ARGs) and Their Genetic Compartments in the Tibetan Environment. <i>Environmental Science &amp; Technology</i> , 2016, 50, 6670-6679.	10.0	155
122	Structure, Variation, and Co-occurrence of Soil Microbial Communities in Abandoned Sites of a Rare Earth Elements Mine. <i>Environmental Science &amp; Technology</i> , 2016, 50, 11481-11490.	10.0	163
123	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
124	Aerobic Degradation of Sulfadiazine by <i>Arthrobacter</i> spp.: Kinetics, Pathways, and Genomic Characterization. <i>Environmental Science &amp; Technology</i> , 2016, 50, 9566-9575.	10.0	134
125	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
126	Impacts of human activities on distribution of sulfate-reducing prokaryotes and antibiotic resistance genes in marine coastal sediments of Hong Kong. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw128.	2.7	37



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127	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
128	Metagenomic profiles of antibiotic resistance genes in paddy soils from South China. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw023.	2.7	87
129	Shift in antibiotic resistance gene profiles associated with nanosilver during wastewater treatment. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw022.	2.7	35
130	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
131	Sulfate Radical-Mediated Degradation of Sulfadiazine by CuFeO <sub>2</sub> Rhombohedral Crystal-Catalyzed Peroxymonosulfate: Synergistic Effects and Mechanisms. <i>Environmental Science &amp; Technology</i> , 2016, 50, 3119-3127.	10.0	563
132	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
133	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
134	Metagenomic Assembly Reveals Hosts of Antibiotic Resistance Genes and the Shared Resistome in Pig, Chicken, and Human Feces. <i>Environmental Science &amp; Technology</i> , 2016, 50, 420-427.	10.0	287
135	Biotransformation and adsorption of pharmaceutical and personal care products by activated sludge after correcting matrix effects. <i>Science of the Total Environment</i> , 2016, 544, 980-986.	8.0	37
136	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
137	Phylogeny-structured carbohydrate metabolism across microbiomes collected from different units in wastewater treatment process. <i>Biotechnology for Biofuels</i> , 2015, 8, 172.	6.2	17
138	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
139	Performance of nanofiltration membrane in rejecting trace organic compounds: Experiment and model prediction. <i>Desalination</i> , 2015, 370, 7-16.	8.2	85
140	Evidence of compositional and ultrastructural shifts during the development of calcareous tubes in the biofouling tubeworm, <i>Hydroides elegans</i> . <i>Journal of Structural Biology</i> , 2015, 189, 230-237.	2.8	10
141	Metagenomics Shows That Low-Energy Anaerobic <sup>+</sup> Aerobic Treatment Reactors Reduce Antibiotic Resistance Gene Levels from Domestic Wastewater. <i>Environmental Science &amp; Technology</i> , 2015, 49, 2577-2584.	10.0	147
142	Antibiotics, Antibiotic Resistance Genes, and Bacterial Community Composition in Fresh Water Aquaculture Environment in China. <i>Microbial Ecology</i> , 2015, 70, 425-432.	2.8	322
143	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
144	Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. <i>ISME Journal</i> , 2015, 9, 2490-2502.	9.8	928

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145	Deciphering Cyanide-Degrading Potential of Bacterial Community Associated with the Coking Wastewater Treatment Plant with a Novel Draft Genome. <i>Microbial Ecology</i> , 2015, 70, 701-709.	2.8	12
146	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
147	Bacterial Community Shift Drives Antibiotic Resistance Promotion during Drinking Water Chlorination. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12271-12279.	10.0	384
148	Profile and Fate of Bacterial Pathogens in Sewage Treatment Plants Revealed by High-Throughput Metagenomic Approach. <i>Environmental Science &amp; Technology</i> , 2015, 49, 10492-10502.	10.0	137
149	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12628-12640.	10.0	72
150	Application of Metagenomics in Environmental Anaerobic Technology. , 2015, , 73-108.		1
151	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
152	Metagenome approaches revealed a biological prospect for improvement on mesophilic cellulose degradation. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10871-10879.	3.6	6
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