Tong Zhang

List of Publications by Year
in descending order

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247 papers	29,005 citations	3874 91 h-index	6872 160 g-index
255 all docs	255 docs citations	255 times ranked	22573 citing authors

#	Article	IF	Citations
1	Culturing the uncultured microbial majority in activated sludge: A critical review. Critical Reviews in Environmental Science and Technology, 2023, 53, 601-624.	6.6	13
2	Risks of antibiotic resistance genes and antimicrobial resistance under chlorination disinfection with public health concerns. Environment International, 2022, 158, 106978.	4.8	39
3	An assessment of resistome and mobilome in wastewater treatment plants through temporal and spatial metagenomic analysis. Water Research, 2022, 209, 117885.	5.3	31
4	Genome-centric metagenomics provides new insights into the microbial community and metabolic potential of landfill leachate microbiota. Science of the Total Environment, 2022, 816, 151635.	3.9	7
5	Rapid absolute quantification of pathogens and ARGs by nanopore sequencing. Science of the Total Environment, 2022, 809, 152190.	3.9	21
6	Siderophores provoke extracellular superoxide production by <i>Arthrobacter</i> strains during carbon sourcesâ€level fluctuation. Environmental Microbiology, 2022, 24, 894-904.	1.8	5
7	High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria. Microbiome, 2022, 10, 16.	4.9	18
8	Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge. Microbiome, 2022, 10, 20.	4.9	52
9	Response and resilience of anammox consortia to nutrient starvation. Microbiome, 2022, 10, 23.	4.9	16
10	Use of sewage surveillance for COVID-19 to guide public health response: A case study in Hong Kong. Science of the Total Environment, 2022, 821, 153250.	3.9	31
11	Comparison of virus concentration methods and RNA extraction methods for SARS-CoV-2 wastewater surveillance. Science of the Total Environment, 2022, 824, 153687.	3.9	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. Nature Communications, 2022, 13, 1908.	5.8	114
13	Wastewater as an information source of COVID-19. Science Bulletin, 2022, 67, 1090-1092.	4.3	10
14	Nationwide biogeography and health implications of bacterial communities in household drinking water. Water Research, 2022, 215, 118238.	5.3	7
15	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. Environmental Microbiomes, 2022, 17, 19.	2.2	6
16	Impacts of food waste to sludge ratios on microbial dynamics and functional traits in thermophilic digesters. Water Research, 2022, 219, 118590.	5.3	4
17	Use of Sewage Surveillance for COVID-19: A Large-Scale Evidence-Based Program in Hong Kong. Environmental Health Perspectives, 2022, 130, 57008.	2.8	20
18	Evaluation of RT-qPCR Primer-Probe Sets to Inform Public Health Interventions Based on COVID-19 Sewage Tests. Environmental Science & Technology, 2022, 56, 8875-8884.	4.6	11

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19	Real-time allelic assays of SARS-CoV-2 variants to enhance sewage surveillance. Water Research, 2022, 220, 118686.	5.3	17
20	Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. Environmental Science & Technology, 2022, 56, 14982-14993.	4.6	27
21	Quantification of SARS-CoV-2 RNA in wastewater treatment plants mirrors the pandemic trend in Hong Kong. Science of the Total Environment, 2022, 844, 157121.	3.9	22
22	Development of an efficient pathway construction strategy for rapid evolution of the biodegradation capacity of Pseudomonas putida KT2440 and its application in bioremediation. Science of the Total Environment, 2021, 761, 143239.	3.9	14
23	Role of wastewater treatment in COVID-19 control. Water Quality Research Journal of Canada, 2021, 56, 68-82.	1.2	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. Environmental Science & Technology, 2021, 55, 2662-2673.	4.6	11
25	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	161
26	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. ISME Journal, 2021, 15, 2817-2829.	4.4	10
27	Reply to Shaw: Challenges for enrichment analysis of AMR gene-bearing plasmids. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2104557118.	3.3	0
28	Selective enrichment of comammox from activated sludge using antibiotics. Water Research, 2021, 197, 117087.	5.3	31
29	Reply to Partridge et al.: Complementary bioinformatics and experimental approaches to investigate the transfer of AMR genes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	2
30	An omics-based framework for assessing the health risk of antimicrobial resistance genes. Nature Communications, 2021, 12, 4765.	5.8	248
31	Underrepresented high diversity of class 1 integrons in the environment uncovered by PacBio sequencing using a new primer. Science of the Total Environment, 2021, 787, 147611.	3.9	11
32	Acesulfame aerobic biodegradation by enriched consortia and Chelatococcus spp.: Kinetics, transformation products, and genomic characterization. Water Research, 2021, 202, 117454.	5.3	21
33	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. Nature Communications, 2021, 12, 5398.	5.8	49
34	The first case study of wastewater-based epidemiology of COVID-19 in Hong Kong. Science of the Total Environment, 2021, 790, 148000.	3.9	50
35	Untangling Microbiota Diversity and Assembly Patterns in the World's Largest Water Diversion Canal. Water Research, 2021, 204, 117617.	5.3	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. Science of the Total Environment, 2021, 801, 149718.	3.9	13

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37	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9Âyears. Microbiome, 2021, 9, 199.	4.9	33
38	Charting the complexity of the activated sludge microbiome through a hybrid sequencing strategy. Microbiome, 2021, 9, 205.	4.9	29
39	Evidence for Long-Term Anthropogenic Pollution: The Hadal Trench as a Depository and Indicator for Dissemination of Antibiotic Resistance Genes. Environmental Science & Technology, 2021, 55, 15136-15148.	4.6	41
40	Identification and quantification of bacterial genomes carrying antibiotic resistance genes and virulence factor genes for aquatic microbiological risk assessment. Water Research, 2020, 168, 115160.	5.3	102
41	Challenges related to antimicrobial resistance in the framework of urban wastewater reuse. Water Research, 2020, 170, 115308.	5.3	9
42	Diversity of gut microbiomes in marine fishes is shaped by hostâ€related factors. Molecular Ecology, 2020, 29, 5019-5034.	2.0	57
43	Editorial: The Environmental Dimension of Antibiotic Resistance. FEMS Microbiology Ecology, 2020, 96, .	1.3	23
44	Source tracking of antibiotic resistance genes in the environment â€" Challenges, progress, and prospects. Water Research, 2020, 185, 116127.	5.3	82
45	Effects of Weathering on the Sorption Behavior and Toxicity of Polystyrene Microplastics in Multi-solute Systems. Water Research, 2020, 187, 116419.	5.3	61
46	High-quality bacterial genomes of a partial-nitritation/anammox system by an iterative hybrid assembly method. Microbiome, 2020, 8, 155.	4.9	29
47	Online searching platform for the antibiotic resistome in bacterial tree of life and global habitats. FEMS Microbiology Ecology, 2020, 96, .	1.3	19
48	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. Water Research, 2020, 181, 115858.	5.3	37
49	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. ISME Journal, 2020, 14, 2595-2609.	4.4	62
50	Selection for antimicrobial resistance is reduced when embedded in a natural microbial community. ISME Journal, 2019, 13, 2927-2937.	4.4	102
51	Genomic characterization, kinetics, and pathways of sulfamethazine biodegradation by Paenarthrobacter sp. A01. Environment International, 2019, 131, 104961.	4.8	56
52	Distribution of arsenic and its biotransformation genes in sediments from the East China Sea. Environmental Pollution, 2019, 253, 949-958.	3.7	35
53	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. Pedosphere, 2019, 29, 273-282.	2.1	100
54	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. Nature Communications, 2019, 10, 4574.	5.8	90

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55	Exploration of the antibiotic resistome in a wastewater treatment plant by a nine-year longitudinal metagenomic study. Environment International, 2019, 133, 105270.	4.8	85
56	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitritation anammox reactor using integrated multi-omics. Microbiome, 2019, 7, 122.	4.9	65
57	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. Water Research, 2019, 166, 115073.	5.3	53
58	Phylogenetic characterization of bromate-reducing microbial community enriched anaerobically from activated sludge. Ecotoxicology and Environmental Safety, 2019, 184, 109630.	2.9	6
59	Mycobacterial species and their contribution to cholesterol degradation in wastewater treatment plants. Scientific Reports, 2019, 9, 836.	1.6	24
60	Uranium sequestration in sediment at an iron-rich contaminated site at Oak Ridge, Tennessee via. bioreduction followed by reoxidation. Journal of Environmental Sciences, 2019, 85, 156-167.	3.2	10
61	Mining traits for the enrichment and isolation of not-yet-cultured populations. Microbiome, 2019, 7, 96.	4.9	8
62	Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195.	5.9	491
63	Effluents of wastewater treatment plants promote the rapid stabilization of the antibiotic resistome in receiving freshwater bodies. Water Research, 2019, 158, 72-81.	5.3	82
64	Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing. Microbiome, 2019, 7, 44.	4.9	236
65	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. Water Research, 2019, 155, 275-287.	5.3	77
66	Metagenomic and Resistome Analysis of a Full-Scale Municipal Wastewater Treatment Plant in Singapore Containing Membrane Bioreactors. Frontiers in Microbiology, 2019, 10, 172.	1.5	58
67	An integrated meta-omics approach reveals substrates involved in synergistic interactions in a bisphenol A (BPA)-degrading microbial community. Microbiome, 2019, 7, 16.	4.9	89
68	Genomic resolution of bacterial populations in saccharin and cyclamate degradation. Science of the Total Environment, 2019, 658, 357-366.	3.9	10
69	New insights into antibiotic resistome in drinking water and management perspectives: A metagenomic based study of small-sized microbes. Water Research, 2019, 152, 191-201.	5.3	100
70	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. Science of the Total Environment, 2019, 651, 2148-2157.	3.9	25
71	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes. ISME Journal, 2019, 13, 346-360.	4.4	289
72	Bacteria That Make a Meal of Sulfonamide Antibiotics: Blind Spots and Emerging Opportunities. Environmental Science & Technology, 2018, 52, 3854-3868.	4.6	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. Applied and Environmental Microbiology, 2018, 84, .	1.4	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. Bioinformatics, 2018, 34, 2263-2270.	1.8	375
75	Antibiotic resistome in landfill leachate from different cities of China deciphered by metagenomic analysis. Water Research, 2018, 134, 126-139.	5.3	138
76	Partnership of <i>Arthrobacter</i> and <i>Pimelobacter</i> in Aerobic Degradation of Sulfadiazine Revealed by Metagenomics Analysis and Isolation. Environmental Science & Technology, 2018, 52, 2963-2972.	4.6	26
77	Effects of sample preservation and DNA extraction on enumeration of antibiotic resistance genes in wastewater. FEMS Microbiology Ecology, 2018, 94, .	1.3	33
78	Antibiotic-mediated changes in the fecal microbiome of broiler chickens define the incidence of antibiotic resistance genes. Microbiome, 2018, 6, 34.	4.9	185
79	Antibiotic resistome in a largeâ€scale healthy human gut microbiota deciphered by metagenomic and network analyses. Environmental Microbiology, 2018, 20, 355-368.	1.8	141
80	Picoinjection-Enabled Multitarget Loop-Mediated Isothermal Amplification for Detection of Foodborne Pathogens. Analytical Chemistry, 2018, 90, 13173-13177.	3.2	62
81	Characterization of airborne antibiotic resistance genes from typical bioaerosol emission sources in the urban environment using metagenomic approach. Chemosphere, 2018, 213, 463-471.	4.2	71
82	Toward an Intensive Longitudinal Understanding of Activated Sludge Bacterial Assembly and Dynamics. Environmental Science & Technology, 2018, 52, 8224-8232.	4.6	32
83	Tracking antibiotic resistance gene pollution from different sources using machine-learning classification. Microbiome, 2018, 6, 93.	4.9	114
84	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. Microbiome, 2018, 6, 130.	4.9	83
85	Novel Insights into Selection for Antibiotic Resistance in Complex Microbial Communities. MBio, 2018, 9, .	1.8	110
86	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. Microbiome, 2018, 6, 16.	4.9	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. Biotechnology for Biofuels, 2018, 11, 47.	6.2	26
88	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. Environment International, 2018, 117, 146-153.	4.8	152
89	Bioreactor microbial ecosystems with differentiated methanogenic phenol biodegradation and competitive metabolic pathways unraveled with genome-resolved metagenomics. Biotechnology for Biofuels, 2018, 11, 135.	6.2	17
90	Temporal dynamics of activated sludge bacterial communities in two diversity variant full-scale sewage treatment plants. Applied Microbiology and Biotechnology, 2018, 102, 9379-9388.	1.7	26

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91	High-Resolution Temporal and Spatial Patterns of Virome in Wastewater Treatment Systems. Environmental Science & Technology, 2018, 52, 10337-10346.	4.6	25
92	Water and sanitation: an essential battlefront in the war on antimicrobial resistance. FEMS Microbiology Ecology, 2018, 94, .	1.3	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. Science of the Total Environment, 2017, 581-582, 32-39.	3.9	148
94	Continental-scale pollution of estuaries with antibiotic resistance genes. Nature Microbiology, 2017, 2, 16270.	5.9	812
95	Thermodynamic and physiological study of caproate and 1,3-propanediol co-production through glycerol fermentation and fatty acids chain elongation. Water Research, 2017, 114, 200-209.	5.3	62
96	Antibiotic Resistance Genes and Correlations with Microbial Community and Metal Resistance Genes in Full-Scale Biogas Reactors As Revealed by Metagenomic Analysis. Environmental Science & Technology, 2017, 51, 4069-4080.	4.6	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. Science of the Total Environment, 2017, 587-588, 214-222.	3.9	50
98	Linking Microbial Community, Environmental Variables, and Methanogenesis in Anaerobic Biogas Digesters of Chemically Enhanced Primary Treatment Sludge. Environmental Science & Technology, 2017, 51, 3982-3992.	4.6	107
99	The Prevalence of Integrons as the Carrier of Antibiotic Resistance Genes in Natural and Man-Made Environments. Environmental Science & Technology, 2017, 51, 5721-5728.	4.6	260
100	Macrobenthic communities in Hong Kong waters: Comparison between 2001 and 2012 and potential link to pollution control. Marine Pollution Bulletin, 2017, 124, 694-700.	2.3	16
101	A highly selective surface coating for enhanced membrane rejection of endocrine disrupting compounds: Mechanistic insights and implications. Water Research, 2017, 121, 197-203.	5.3	77
102	Comammox in drinking water systems. Water Research, 2017, 116, 332-341.	5.3	163
103	Co-occurrence of antibiotic and metal resistance genes revealed in complete genome collection. ISME Journal, 2017, 11, 651-662.	4.4	351
104	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. Environmental Science & Technology, 2017, 51, 13061-13069.	4.6	236
105	Cultivation-dependent and high-throughput sequencing approaches studying the co-occurrence of antibiotic resistance genes in municipal sewage system. Applied Microbiology and Biotechnology, 2017, 101, 8197-8207.	1.7	11
106	Investigation on the anaerobic co-digestion of food waste with sewage sludge. Applied Microbiology and Biotechnology, 2017, 101, 7755-7766.	1.7	20
107	Sorption Behavior of Bisphenol A and Triclosan by Graphene: Comparison with Activated Carbon. ACS Omega, 2017, 2, 5378-5384.	1.6	53
108	Fate of antibiotic resistance genes and their associations with bacterial community in livestock breeding wastewater and its receiving river water. Water Research, 2017, 124, 259-268.	5.3	255

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109	Editorial: Antibiotic Resistance in Aquatic Systems. Frontiers in Microbiology, 2017, 8, 14.	1.5	88
110	MinION Nanopore Sequencing Enables Correlation between Resistome Phenotype and Genotype of Coliform Bacteria in Municipal Sewage. Frontiers in Microbiology, 2017, 8, 2105.	1.5	39
111	Catalogue of antibiotic resistome and host-tracking in drinking water deciphered by a large scale survey. Microbiome, 2017, 5, 154.	4.9	215
112	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. Microbiome, 2017, 5, 84.	4.9	247
113	Bioprospecting for Î²-lactam resistance genes using a metagenomics-guided strategy. Applied Microbiology and Biotechnology, 2017, 101, 6253-6260.	1.7	2
114	Exploring the Shift in Structure and Function of Microbial Communities Performing Biological Phosphorus Removal. PLoS ONE, 2016, 11, e0161506.	1.1	9
115	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	1.5	120
116	Discovery of new cellulases from the metagenome by a metagenomics-guided strategy. Biotechnology for Biofuels, 2016, 9, 138.	6.2	74
117	Comparative genomics analyses on EPS biosynthesis genes required for floc formation of Zoogloea resiniphila and other activated sludge bacteria. Water Research, 2016, 102, 494-504.	5.3	117
118	Development of Quantitative Real-time PCR Assays for Different Clades of â€œCandidatus Accumulibacterâ€. Scientific Reports, 2016, 6, 23993.	1.6	32
119	Cellular adhesiveness and cellulolytic capacity in Anaerolineae revealed by omics-based genome interpretation. Biotechnology for Biofuels, 2016, 9, 111.	6.2	210
120	Population Dynamics of Bulking and Foaming Bacteria in a Full-scale Wastewater Treatment Plant over Five Years. Scientific Reports, 2016, 6, 24180.	1.6	30
121	Metagenomic Analysis Revealing Antibiotic Resistance Genes (ARGs) and Their Genetic Compartments in the Tibetan Environment. Environmental Science & Technology, 2016, 50, 6670-6679.	4.6	155
122	Structure, Variation, and Co-occurrence of Soil Microbial Communities in Abandoned Sites of a Rare Earth Elements Mine. Environmental Science & Technology, 2016, 50, 11481-11490.	4.6	163
123	Anaerobic digestion of chemically enhanced primary treatment (CEPT) sludge and the microbial community structure. Applied Microbiology and Biotechnology, 2016, 100, 8975-8982.	1.7	46
124	Aerobic Degradation of Sulfadiazine by <i>Arthrobacter</i> spp.: Kinetics, Pathways, and Genomic Characterization. Environmental Science & Technology, 2016, 50, 9566-9575.	4.6	134
125	Does Hydrophilic Polydopamine Coating Enhance Membrane Rejection of Hydrophobic Endocrine-Disrupting Compounds?. Environmental Science and Technology Letters, 2016, 3, 332-338.	3.9	117
126	Impacts of human activities on distribution of sulfate-reducing prokaryotes and antibiotic resistance genes in marine coastal sediments of Hong Kong. FEMS Microbiology Ecology, 2016, 92, fiw128.	1.3	37

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127	Novel nitrifiers and comammox in a full-scale hybrid biofilm and activated sludge reactor revealed by metagenomic approach. Applied Microbiology and Biotechnology, 2016, 100, 8225-8237.	1.7	90
128	Metagenomic profiles of antibiotic resistance genes in paddy soils from South China. FEMS Microbiology Ecology, 2016, 92, fiw023.	1.3	87
129	Shift in antibiotic resistance gene profiles associated with nanosilver during wastewater treatment. FEMS Microbiology Ecology, 2016, 92, fiw022.	1.3	35
130	ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. Bioinformatics, 2016, 32, 2346-2351.	1.8	254
131	Sulfate Radical-Mediated Degradation of Sulfadiazine by CuFeO₂ Rhombohedral Crystal-Catalyzed Peroxymonosulfate: Synergistic Effects and Mechanisms. Environmental Science & Technology, 2016, 50, 3119-3127.	4.6	563
132	Antibiotic resistance genes and human bacterial pathogens: Co-occurrence, removal, and enrichment in municipal sewage sludge digesters. Water Research, 2016, 91, 1-10.	5.3	305
133	Metagenomic analysis revealed highly diverse microbial arsenic metabolism genes in paddy soils with low-arsenic contents. Environmental Pollution, 2016, 211, 1-8.	3.7	125
134	Metagenomic Assembly Reveals Hosts of Antibiotic Resistance Genes and the Shared Resistome in Pig, Chicken, and Human Feces. Environmental Science & Technology, 2016, 50, 420-427.	4.6	287
135	Biotransformation and adsorption of pharmaceutical and personal care products by activated sludge after correcting matrix effects. Science of the Total Environment, 2016, 544, 980-986.	3.9	37
136	Dominant and novel clades of Candidatus Accumulibacter phosphatis in 18 globally distributed full-scale wastewater treatment plants. Scientific Reports, 2015, 5, 11857.	1.6	64
137	Phylogeny-structured carbohydrate metabolism across microbiomes collected from different units in wastewater treatment process. Biotechnology for Biofuels, 2015, 8, 172.	6.2	17
138	Exploring antibiotic resistance genes and metal resistance genes in plasmid metagenomes from wastewater treatment plants. Frontiers in Microbiology, 2015, 6, 1025.	1.5	139
139	Performance of nanofiltration membrane in rejecting trace organic compounds: Experiment and model prediction. Desalination, 2015, 370, 7-16.	4.0	85
140	Evidence of compositional and ultrastructural shifts during the development of calcareous tubes in the biofouling tubeworm, Hydroides elegans. Journal of Structural Biology, 2015, 189, 230-237.	1.3	10
141	Metagenomics Shows That Low-Energy Anaerobicâˆ’Aerobic Treatment Reactors Reduce Antibiotic Resistance Gene Levels from Domestic Wastewater. Environmental Science & Technology, 2015, 49, 2577-2584.	4.6	147
142	Antibiotics, Antibiotic Resistance Genes, and Bacterial Community Composition in Fresh Water Aquaculture Environment in China. Microbial Ecology, 2015, 70, 425-432.	1.4	322
143	Diversity and functions of bacterial community in drinking water biofilms revealed by high-throughput sequencing. Scientific Reports, 2015, 5, 10044.	1.6	71
144	Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. ISME Journal, 2015, 9, 2490-2502.	4.4	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. Microbial Ecology, 2015, 70, 701-709.	1.4	12
146	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. Applied Microbiology and Biotechnology, 2015, 99, 4119-4129.	1.7	79
147	Bacterial Community Shift Drives Antibiotic Resistance Promotion during Drinking Water Chlorination. Environmental Science & Technology, 2015, 49, 12271-12279.	4.6	384
148	Profile and Fate of Bacterial Pathogens in Sewage Treatment Plants Revealed by High-Throughput Metagenomic Approach. Environmental Science & Technology, 2015, 49, 10492-10502.	4.6	137
149	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640.	4.6	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. Applied Microbiology and Biotechnology, 2015, 99, 7771-7779.	1.7	201
152	Metagenome approaches revealed a biological prospect for improvement on mesophilic cellulose degradation. Applied Microbiology and Biotechnology, 2015, 99, 10871-10879.	1.7	6
153	Co-occurrence correlations of heavy metals in sediments revealed using network analysis. Chemosphere, 2015, 119, 1305-1313.	4.2	43
154	Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. ISME Journal, 2015, 9, 683-695.	4.4	393
155	Metagenomic Analysis of Antibiotic Resistance Genes in Dairy Cow Feces following Therapeutic Administration of Third Generation Cephalosporin. PLoS ONE, 2015, 10, e0133764.	1.1	113
156	Bacterial Communities in Different Sections of a Municipal Wastewater Treatment Plant Revealed by 16S rDNA 454 Pyrosequencing. , 2015, , 3-23.		0
157	Taxonomic Precision of Different Hypervariable Regions of 16S rRNA Gene and Annotation Methods for Functional Bacterial Groups in Biological Wastewater Treatment. , 2015, , 25-53.		0
158	Evaluation of a Hybrid Approach Using UBLAST and BLASTX for Metagenomic Sequences Annotation of Specific Functional Genes. PLoS ONE, 2014, 9, e110947.	1.1	36
159	Abundance and distribution of Macrolide-Lincosamide-Streptogramin resistance genes in an anaerobic-aerobic system treating spiramycin production wastewater. Water Research, 2014, 63, 33-41.	5.3	63
160	Potentially novel copper resistance genes in copper-enriched activated sludge revealed by metagenomic analysis. Applied Microbiology and Biotechnology, 2014, 98, 10255-10266.	1.7	30
161	Metagenomic analysis on seasonal microbial variations of activated sludge from a fullâ€scale wastewater treatment plant over 4 years. Environmental Microbiology Reports, 2014, 6, 80-89.	1.0	159
162	Nitric oxide removal by wastewater bacteria in a biotrickling filter. Journal of Environmental Sciences, 2014, 26, 555-565.	3.2	17

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163	Metagenomic analysis of sludge from full-scale anaerobic digesters operated in municipal wastewater treatment plants. Applied Microbiology and Biotechnology, 2014, 98, 5709-5718.	1.7	179
164	Detecting the Nonviable and Heat-Tolerant Bacteria in Activated Sludge by Minimizing DNA from Dead Cells. Microbial Ecology, 2014, 67, 829-836.	1.4	22
165	Abundant rifampin resistance genes and significant correlations of antibiotic resistance genes and plasmids in various environments revealed by metagenomic analysis. Applied Microbiology and Biotechnology, 2014, 98, 5195-5204.	1.7	87
166	Taxonomic relatedness shapes bacterial assembly in activated sludge of globally distributed wastewater treatment plants. Environmental Microbiology, 2014, 16, 2421-2432.	1.8	333
167	Reconstructing a Thauera genome from a hydrogenotrophic-denitrifying consortium using metagenomic sequence data. Applied Microbiology and Biotechnology, 2014, 98, 6885-6895.	1.7	38
168	Hydrophobicity of diverse bacterial populations in activated sludge and biofilm revealed by microbial adhesion to hydrocarbons assay and high-throughput sequencing. Colloids and Surfaces B: Biointerfaces, 2014, 114, 379-385.	2.5	36
169	Metagenomic analysis reveals potential biodegradation pathways of persistent pesticides in freshwater and marine sediments. Science of the Total Environment, 2014, 470-471, 983-992.	3.9	92
170	Genome Reconstruction and Gene Expression of â€œ<i>Candidatus</i> Accumulibacter phosphatisâ€•Clade IB Performing Biological Phosphorus Removal. Environmental Science & Technology, 2014, 48, 10363-10371.	4.6	64
171	Shifts in the Microbial Community, Nitrifiers and Denitrifiers in the Biofilm in a Full-scale Rotating Biological Contactor. Environmental Science & Technology, 2014, 48, 8044-8052.	4.6	99
172	Novel Microbial Populations in Ambient and Mesophilic Biogas-Producing and Phenol-Degrading Consortia Unraveled by High-Throughput Sequencing. Microbial Ecology, 2014, 68, 235-246.	1.4	54
173	Metabolic Characteristics of a Glycogen-Accumulating Organism in Defluviicoccus Cluster II Revealed by Comparative Genomics. Microbial Ecology, 2014, 68, 716-728.	1.4	22
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