

Wen-Tso Liu

List of Publications by Year in descending order

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Version: 2024-02-01

173
papers

14,905
citations

19657

61
h-index

21540

114
g-index

177
all docs

177
docs citations

177
times ranked

15372
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
2	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
3	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	9.8	360
4	Nanoparticles and their biological and environmental applications. <i>Journal of Bioscience and Bioengineering</i> , 2006, 102, 1-7.	2.2	351
5	Analysis of BIOLOG GN Substrate Utilization Patterns by Microbial Communities. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1220-1225.	3.1	342
6	Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. <i>ISME Journal</i> , 2014, 8, 541-551.	9.8	251
7	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. <i>ISME Journal</i> , 2016, 10, 2478-2487.	9.8	239
8	Analysis of 16S rRNA Amplicon Sequencing Options on the Roche/454 Next-Generation Titanium Sequencing Platform. <i>PLoS ONE</i> , 2011, 6, e25263.	2.5	221
9	Identification of a Novel Group of Bacteria in Sludge from a Deteriorated Biological Phosphorus Removal Reactor. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1251-1258.	3.1	220
10	Biofilm Formation Characteristics of Bacterial Isolates Retrieved from a Reverse Osmosis Membrane. <i>Environmental Science & Technology</i> , 2005, 39, 7541-7550.	10.0	219
11	Pyrosequencing Reveals Bacterial Communities in Unchlorinated Drinking Water Distribution System: An Integral Study of Bulk Water, Suspended Solids, Loose Deposits, and Pipe Wall Biofilm. <i>Environmental Science & Technology</i> , 2014, 48, 5467-5476.	10.0	204
12	In situ identification of polyphosphate- and polyhydroxyalkanoate-accumulating traits for microbial populations in a biological phosphorus removal process. <i>Environmental Microbiology</i> , 2001, 3, 110-122.	3.8	190
13	Response of gut microbiota to salinity change in two euryhaline aquatic animals with reverse salinity preference. <i>Aquaculture</i> , 2016, 454, 72-80.	3.5	188
14	Internal energy-based competition between polyphosphate- and glycogen-accumulating bacteria in biological phosphorus removal reactors—Effect of PC feeding ratio. <i>Water Research</i> , 1997, 31, 1430-1438.	11.3	185
15	Identification and occurrence of tetrad-forming Alphaproteobacteria in anaerobic-aerobic activated sludge processes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3741-3748.	1.8	179
16	Abundance and composition of indigenous bacterial communities in a multi-step biofiltration-based drinking water treatment plant. <i>Water Research</i> , 2014, 62, 40-52.	11.3	179
17	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
18	Drinking water microbiome assembly induced by water stagnation. <i>ISME Journal</i> , 2018, 12, 1520-1531.	9.8	172

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19	Pyrosequencing Analysis of Bacterial Biofilm Communities in Water Meters of a Drinking Water Distribution System. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5631-5635.	3.1	166
20	Phylogeny and physiology of candidate phylum "Atribacteria"™ (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
21	A microbiology-based multi-parametric approach towards assessing biological stability in drinking water distribution networks. <i>Water Research</i> , 2013, 47, 3015-3025.	11.3	153
22	Characterization of microbial consortia in a terephthalate-degrading anaerobic granular sludge system The GenBank accession numbers for the sequences obtained in this work are AF229774"AF229793.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 373-382.	1.8	150
23	The nexus of syntrophy-associated microbiota in anaerobic digestion revealed by long-term enrichment and community survey. <i>Environmental Microbiology</i> , 2015, 17, 1707-1720.	3.8	149
24	Microbial Community Dynamics of an Urban Drinking Water Distribution System Subjected to Phases of Chloramination and Chlorination Treatments. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7856-7865.	3.1	147
25	Microbial community dynamics during start-up of acidogenic anaerobic reactors. <i>Water Research</i> , 2002, 36, 3203-3210.	11.3	142
26	Diversity and distribution of a deeply branched novel proteobacterial group found in anaerobic-aerobic activated sludge processes. <i>Environmental Microbiology</i> , 2002, 4, 753-757.	3.8	142
27	Glycogen accumulating population and its anaerobic substrate uptake in anaerobic-aerobic activated sludge without biological phosphorus removal. <i>Water Research</i> , 1996, 30, 75-82.	11.3	140
28	Optimization of an oligonucleotide microchip for microbial identification studies: a non-equilibrium dissociation approach. <i>Environmental Microbiology</i> , 2001, 3, 619-629.	3.8	138
29	Role of glycogen in acetate uptake and polyhydroxyalkanoate synthesis in anaerobic-aerobic activated sludge with a minimized polyphosphate content. <i>Journal of Bioscience and Bioengineering</i> , 1994, 77, 535-540.	0.9	131
30	Quantum Dots as a Novel Immunofluorescent Detection System for <i>Cryptosporidium parvum</i> and <i>Giardia lamblia</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 597-598.	3.1	131
31	In situ identification and characterization of the microbial community structure of full-scale enhanced biological phosphorous removal plants in Japan. <i>Water Research</i> , 2005, 39, 2901-2914.	11.3	130
32	Quantitative effects of position and type of single mismatch on single base primer extension. <i>Journal of Microbiological Methods</i> , 2009, 77, 267-275.	1.6	127
33	<i>Tetrasphaera elongata</i> sp. nov., a polyphosphate-accumulating bacterium isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 883-887.	1.7	125
34	Metagenomic characterization of biofilter microbial communities in a full-scale drinking water treatment plant. <i>Water Research</i> , 2018, 128, 278-285.	11.3	121
35	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	9.8	114
36	Characterization of microbial community in granular sludge treating brewery wastewater. <i>Water Research</i> , 2002, 36, 1767-1775.	11.3	111

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37	Responses of Bacterial Communities to Simulated Climate Changes in Alpine Meadow Soil of the Qinghai-Tibet Plateau. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6070-6077.	3.1	107
38	Community structure of microbial biofilms associated with membrane-based water purification processes as revealed using a polyphasic approach. <i>Applied Microbiology and Biotechnology</i> , 2004, 63, 466-473.	3.6	106
39	Impact of silver nanoparticles on natural marine biofilm bacteria. <i>Chemosphere</i> , 2011, 85, 961-966.	8.2	103
40	Community Structure Analysis of Reverse Osmosis Membrane Biofilms and the Significance of Rhizobiales Bacteria in Biofouling. <i>Environmental Science & Technology</i> , 2007, 41, 4728-4734.	10.0	100
41	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	12.8	99
42	Metagenomic analysis of DNA viruses in a wastewater treatment plant in tropical climate. <i>Environmental Microbiology</i> , 2012, 14, 441-452.	3.8	98
43	Role of Biofilm Roughness and Hydrodynamic Conditions in <i>Legionella pneumophila</i> Adhesion to and Detachment from Simulated Drinking Water Biofilms. <i>Environmental Science & Technology</i> , 2015, 49, 4274-4282.	10.0	91
44	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. <i>ISME Journal</i> , 2016, 10, 582-595.	9.8	91
45	Environmental microbiology-on-a-chip and its future impacts. <i>Trends in Biotechnology</i> , 2005, 23, 174-179.	9.3	87
46	Comparative Analysis of Fecal Microbiota in Infants with and without Eczema. <i>PLoS ONE</i> , 2010, 5, e9964.	2.5	87
47	Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. <i>Scientific Reports</i> , 2016, 6, 34090.	3.3	87
48	Roles of ionic strength and biofilm roughness on adhesion kinetics of <i>Escherichia coli</i> onto groundwater biofilm grown on PVC surfaces. <i>Water Research</i> , 2013, 47, 2531-2542.	11.3	86
49	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. <i>Water Research</i> , 2017, 124, 77-84.	11.3	82
50	Filter-based microfluidic device as a platform for immunofluorescent assay of microbial cells. <i>Lab on A Chip</i> , 2004, 4, 337.	6.0	79
51	Determination of virus abundance, diversity and distribution in a municipal wastewater treatment plant. <i>Water Research</i> , 2009, 43, 1101-1109.	11.3	78
52	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
53	Microbial community structure in a thermophilic anaerobic hybrid reactor degrading terephthalate. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3429-3440.	1.8	75
54	Identification of important microbial populations in the mesophilic and thermophilic phenol-degrading methanogenic consortia. <i>Water Research</i> , 2008, 42, 1963-1976.	11.3	72

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55	The genome of <i>Syntrophorhabdus aromaticivorans</i> strain Ul provides new insights for syntrophic aromatic compound metabolism and electron flow. <i>Environmental Microbiology</i> , 2015, 17, 4861-4872.	3.8	72
56	Novel <i>Geobacter</i> species and diverse methanogens contribute to enhanced methane production in media-added methanogenic reactors. <i>Water Research</i> , 2018, 147, 403-412.	11.3	69
57	Structure of Microbial Communities in Activated Sludge: Potential Implications for Assessing the Biodegradability of Chemicals. <i>Ecotoxicology and Environmental Safety</i> , 2001, 49, 40-53.	6.0	67
58	Simultaneous nitrogen and phosphorus removal in the sulfur cycle-associated Enhanced Biological Phosphorus Removal (EBPR) process. <i>Water Research</i> , 2014, 49, 251-264.	11.3	67
59	Microfluidic device as a new platform for immunofluorescent detection of viruses. <i>Lab on A Chip</i> , 2005, 5, 1327.	6.0	66
60	Response of Simulated Drinking Water Biofilm Mechanical and Structural Properties to Long-Term Disinfectant Exposure. <i>Environmental Science & Technology</i> , 2016, 50, 1779-1787.	10.0	66
61	Complete Nutrient Removal Coupled to Nitrous Oxide Production as a Bioenergy Source by Denitrifying Polyphosphate-Accumulating Organisms. <i>Environmental Science & Technology</i> , 2017, 51, 4531-4540.	10.0	66
62	Microbial community changes in biological phosphate-removal systems on altering sludge phosphorus content The GenBank/EMBL/DDBJ accession numbers for the sequences obtained in this report are AF109792 (strain Lpha5), AF109793 (strain Lpha7) and AF124650 to AF124659.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1099-1107.	1.8	60
63	Effects of Target Length on the Hybridization Efficiency and Specificity of rRNA-Based Oligonucleotide Microarrays. <i>Applied and Environmental Microbiology</i> , 2007, 73, 73-82.	3.1	59
64	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degraders in Anaerobic Digesters. <i>Frontiers in Microbiology</i> , 2020, 11, 593006.	3.5	57
65	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. <i>Environmental Microbiology</i> , 2017, 19, 3163-3174.	3.8	56
66	Tracing fecal pollution sources in karst groundwater by Bacteroidales genetic biomarkers, bacterial indicators, and environmental variables. <i>Science of the Total Environment</i> , 2014, 490, 1082-1090.	8.0	55
67	Distribution comparison and risk assessment of free-floating and particle-attached bacterial pathogens in urban recreational water: Implications for water quality management. <i>Science of the Total Environment</i> , 2018, 613-614, 428-438.	8.0	55
68	<i>Halomonas sulfidaeris</i> -dominated microbial community inhabits a 1.8-km-deep subsurface Cambrian sandstone reservoir. <i>Environmental Microbiology</i> , 2014, 16, 1695-1708.	3.8	52
69	Silicon nanopillar substrates for enhancing signal intensity in DNA microarrays. <i>Biosensors and Bioelectronics</i> , 2008, 24, 723-728.	10.1	50
70	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	7.7	50
71	Microbial detection in microfluidic devices through dual staining of quantum dots-labeled immunoassay and RNA hybridization. <i>Analytica Chimica Acta</i> , 2006, 556, 171-177.	5.4	48
72	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. <i>Microbiome</i> , 2020, 8, 111.	11.1	48

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73	Membrane biofouling in a wastewater nitrification reactor: Microbial succession from autotrophic colonization to heterotrophic domination. <i>Water Research</i> , 2016, 88, 337-345.	11.3	47
74	A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. <i>PLoS ONE</i> , 2016, 11, e0167788.	2.5	46
75	Relative Abundance of <i>Bacteroides</i> spp. in Stools and Wastewaters as Determined by Hierarchical Oligonucleotide Primer Extension. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2882-2893.	3.1	45
76	Community and Proteomic Analysis of Methanogenic Consortia Degrading Terephthalate. <i>Applied and Environmental Microbiology</i> , 2013, 79, 105-112.	3.1	44
77	Effects of hydraulic retention time on aerobic granulation and granule growth kinetics at steady state with a fast start-up strategy. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 469-477.	3.6	44
78	Evaluation of Methods for the Extraction of DNA from Drinking Water Distribution System Biofilms. <i>Microbes and Environments</i> , 2012, 27, 9-18.	1.6	43
79	A new biological phosphorus removal process in association with sulfur cycle. <i>Water Research</i> , 2013, 47, 3057-3069.	11.3	42
80	Warming counteracts grazing effects on the functional structure of the soil microbial community in a Tibetan grassland. <i>Soil Biology and Biochemistry</i> , 2019, 134, 113-121.	8.8	42
81	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. <i>Microbiome</i> , 2020, 8, 16.	11.1	42
82	Emission Characteristics of Fluorescent Labels with Respect to Temperature Changes and Subsequent Effects on DNA Microchip Studies. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6453-6457.	3.1	41
83	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , 2013, 86, 277-287.	2.7	41
84	Quantifying the contribution of microbial immigration in engineered water systems. <i>Microbiome</i> , 2019, 7, 144.	11.1	41
85	Effects of heat shocks on microbial community structure and microbial activity of a methanogenic enrichment degrading benzoate. <i>Letters in Applied Microbiology</i> , 2016, 63, 356-362.	2.2	40
86	Characterization of bacterial community dynamics in a full-scale drinking water treatment plant. <i>Journal of Environmental Sciences</i> , 2017, 51, 21-30.	6.1	40
87	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. <i>Water Research</i> , 2020, 178, 115815.	11.3	40
88	Characterization of Active Microbes in a Full-Scale Anaerobic Fluidized Bed Reactor Treating Phenolic Wastewater. <i>Microbes and Environments</i> , 2009, 24, 144-153.	1.6	39
89	The application of molecular tools to study the drinking water microbiome – Current understanding and future needs. <i>Critical Reviews in Environmental Science and Technology</i> , 2019, 49, 1188-1235.	12.8	38
90	Ecophysiology of <i>Defluviicoccus</i> -related tetrad-forming organisms in an anaerobic-aerobic activated sludge process. <i>Environmental Microbiology</i> , 2007, 9, 1485-1496.	3.8	37

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91	Nexus of Stochastic and Deterministic Processes on Microbial Community Assembly in Biological Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 1536.	3.5	37
92	Characterization of a 4-methylbenzoate-degrading methanogenic consortium as determined by small-subunit rDNA sequence analysis. <i>Journal of Bioscience and Bioengineering</i> , 2001, 91, 449-455.	2.2	36
93	Enrichment and characterization of microbial consortia degrading soluble microbial products discharged from anaerobic methanogenic bioreactors. <i>Water Research</i> , 2016, 90, 395-404.	11.3	36
94	Biological Filtration Limits Carbon Availability and Affects Downstream Biofilm Formation and Community Structure. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5702-5712.	3.1	35
95	Metagenomics Reveals a Novel Virophage Population in a Tibetan Mountain Lake. <i>Microbes and Environments</i> , 2016, 31, 173-177.	1.6	35
96	Assessing the transition effects in a drinking water distribution system caused by changing supply water quality: an indirect approach by characterizing suspended solids. <i>Water Research</i> , 2020, 168, 115159.	11.3	35
97	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
98	Microbial succession of glycogen accumulating organisms in an anaerobic-aerobic membrane bioreactor with no phosphorus removal. <i>Water Science and Technology</i> , 2006, 54, 29-37.	2.5	34
99	A spatially addressable bead-based biosensor for simple and rapid DNA detection. <i>Biosensors and Bioelectronics</i> , 2008, 23, 803-810.	10.1	34
100	Metagenomic characterization of <i>Candidatus</i> <i>Delfluviicoccus tetraformis</i> strain TFO71 TM , a tetrad-forming organism, predominant in an anaerobic-aerobic membrane bioreactor with deteriorated biological phosphorus removal. <i>Environmental Microbiology</i> , 2014, 16, 2739-2751.	3.8	34
101	Miniaturized platforms for the detection of single-nucleotide polymorphisms. <i>Analytical and Bioanalytical Chemistry</i> , 2006, 386, 427-434.	3.7	33
102	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010, 12, 1803-1805.	3.8	33
103	Effect of divalent ions and a polyphosphate on composition, structure, and stiffness of simulated drinking water biofilms. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 15.	6.4	33
104	360-Degree Distribution of Biofilm Quantity and Community in an Operational Unchlorinated Drinking Water Distribution Pipe. <i>Environmental Science & Technology</i> , 2020, 54, 5619-5628.	10.0	33
105	Thermodynamically diverse syntrophic aromatic compound catabolism. <i>Environmental Microbiology</i> , 2017, 19, 4576-4586.	3.8	32
106	Quantitative detection of culturable methanogenic archaea abundance in anaerobic treatment systems using the sequence-specific rRNA cleavage method. <i>ISME Journal</i> , 2009, 3, 522-535.	9.8	31
107	Effect of Disinfectant Exposure on <i>Legionella pneumophila</i> Associated with Simulated Drinking Water Biofilms: Release, Inactivation, and Infectivity. <i>Environmental Science & Technology</i> , 2017, 51, 2087-2095.	10.0	31
108	Novel energy conservation strategies and behaviour of <i>Pelotomaculum schinkii</i> driving syntrophic propionate catabolism. <i>Environmental Microbiology</i> , 2018, 20, 4503-4511.	3.8	31

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109	Comparison of Particle-Associated Bacteria from a Drinking Water Treatment Plant and Distribution Reservoirs with Different Water Sources. <i>Scientific Reports</i> , 2016, 6, 20367.	3.3	30
110	Genomic composition and dynamics among <i>Methanomicrobiales</i> predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017, 11, 87-99.	9.8	29
111	Ugly ducklings—the dark side of plastic materials in contact with potable water. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 7.	6.4	28
112	Quantitative multiplexing analysis of PCR-amplified ribosomal RNA genes by hierarchical oligonucleotide primer extension reaction. <i>Nucleic Acids Research</i> , 2007, 35, e82.	14.5	27
113	Enhanced microfiltration devices configured with hydrodynamic trapping and a rain drop bypass filtering architecture for microbial cells detection. <i>Lab on A Chip</i> , 2008, 8, 830.	6.0	27
114	MS2 Bacteriophage Reduction and Microbial Communities in Biosand Filters. <i>Environmental Science & Technology</i> , 2014, 48, 6702-6709.	10.0	27
115	Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. <i>PLoS ONE</i> , 2015, 10, e0119131.	2.5	27
116	Coupling growth kinetics modeling with machine learning reveals microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. <i>Microbiome</i> , 2019, 7, 65.	11.1	27
117	East Tibetan Lakes Harbour Novel Clusters of Picocyanobacteria as Inferred from the 16S–23S rRNA Internal Transcribed Spacer Sequences. <i>Microbial Ecology</i> , 2010, 59, 614-622.	2.8	26
118	Denaturing gradient gel electrophoresis polymorphism for rapid 16S rDNA clone screening and microbial diversity study. <i>Journal of Bioscience and Bioengineering</i> , 2002, 93, 101-103.	2.2	25
119	Rapid discrimination of single-nucleotide mismatches using a microfluidic device with monolayered beads. <i>Analytica Chimica Acta</i> , 2007, 582, 295-303.	5.4	25
120	<i>Tetrasphaera elongata</i> sp. nov., a polyphosphate-accumulating bacterium isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 883-887.	1.7	24
121	Evaluating single-base-pair discriminating capability of planar oligonucleotide microchips using a non-equilibrium dissociation approach. <i>Environmental Microbiology</i> , 2004, 6, 1197-1202.	3.8	23
122	Impact of Chloramination on the Development of Laboratory-Grown Biofilms Fed with Filter-Pre-treated Groundwater. <i>Microbes and Environments</i> , 2013, 28, 50-57.	1.6	23
123	Draft Genome Sequence of <i>Syntrophorhabdus aromaticivorans</i> Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. <i>Genome Announcements</i> , 2014, 2, .	0.8	23
124	A high-throughput and quantitative hierarchical oligonucleotide primer extension (HOPE)-based approach to identify sources of faecal contamination in water bodies. <i>Environmental Microbiology</i> , 2009, 11, 1672-1681.	3.8	22
125	Global metabolomic responses of <i>Nitrosomonas europaea</i> 19718 to cold stress and altered ammonia feeding patterns. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1843-1852.	3.6	22
126	Impacts of biostimulation and bioaugmentation on the performance and microbial ecology in methanogenic reactors treating purified terephthalic acid wastewater. <i>Water Research</i> , 2017, 122, 308-316.	11.3	22

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127	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. <i>Environmental Microbiology Reports</i> , 2018, 10, 673-685.	2.4	22
128	Characterization of a 4-Methylbenzoate-Degrading Methanogenic Consortium as Determined by Small-Subunit rDNA Sequence Analysis. <i>Journal of Bioscience and Bioengineering</i> , 2001, 91, 449-455.	2.2	22
129	Isolation, characterization and identification of polyhydroxyalkanoate-accumulating bacteria from activated sludge. <i>Journal of Bioscience and Bioengineering</i> , 2000, 90, 494-500.	2.2	21
130	<i>Kineosphaera limosa</i> gen. nov., sp. nov., a novel Gram-positive polyhydroxyalkanoate-accumulating coccus isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1845-1849.	1.7	21
131	Phenotypic and Phylogenetic Identification of Coliform Bacteria Obtained Using 12 Coliform Methods Approved by the U.S. Environmental Protection Agency. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6012-6023.	3.1	21
132	Microbial population dynamics of granular aerobic sequencing batch reactors during start-up and steady state periods. <i>Water Science and Technology</i> , 2010, 62, 1281-1287.	2.5	20
133	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	2.7	19
134	Immobilization of Selenite via Two Parallel Pathways during In Situ Bioremediation. <i>Environmental Science & Technology</i> , 2015, 49, 4543-4550.	10.0	19
135	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <i>Microbes and Environments</i> , 2016, 31, 288-292.	1.6	19
136	DNA Microarray Technology in Microbial Ecology Studies-Principle, Applications and Current Limitations. <i>Microbes and Environments</i> , 2003, 18, 175-187.	1.6	18
137	Cell loss in integrated microfluidic device. <i>Biomedical Microdevices</i> , 2007, 9, 745-750.	2.8	18
138	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , 2008, 72, 82-90.	1.6	16
139	Benefits of Genomic Insights and CRISPR-Cas Signatures to Monitor Potential Pathogens across Drinking Water Production and Distribution Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 2036.	3.5	15
140	Recent advances in molecular techniques for the detection of phylogenetic markers and functional genes in microbial communities. <i>FEMS Microbiology Letters</i> , 2007, 275, 183-190.	1.8	14
141	Diversity and geochemical community assembly processes of the living rare biosphere in a sand-and-gravel aquifer ecosystem in the Midwestern United States. <i>Scientific Reports</i> , 2019, 9, 13484.	3.3	14
142	Saliva-Based Diagnostics Using 16S rRNA Microarrays and Microfluidics. <i>Annals of the New York Academy of Sciences</i> , 2007, 1098, 345-361.	3.8	13
143	Membrane biofouling characterization: effects of sample preparation procedures on biofilm structure and the microbial community. <i>Biofouling</i> , 2014, 30, 813-821.	2.2	13
144	Immune-modulatory genomic properties differentiate gut microbiota of infants with and without eczema. <i>PLoS ONE</i> , 2017, 12, e0184955.	2.5	12

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145	LabArray: real-time imaging and analytical tool for microarrays. <i>Bioinformatics</i> , 2005, 21, 689-690.	4.1	11
146	Draft Genome Sequence of a Novel SAR11 Clade Species Abundant in a Tibetan Lake. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
147	Direct treatment of high-strength soft drink wastewater using a down-flow hanging sponge reactor: performance and microbial community dynamics. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5925-5936.	3.6	10
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