

Wen-Tso Liu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

172
papers

10,650
citations

56
h-index

99
g-index

177
ext. papers

13,242
ext. citations

7.7
avg, IF

6.3
L-index

#	Paper	IF	Citations
172	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
171	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	44.5	648
170	Analysis of BIOLOG GN Substrate Utilization Patterns by Microbial Communities. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 1220-5	4.8	315
169	Nanoparticles and their biological and environmental applications. <i>Journal of Bioscience and Bioengineering</i> , 2006 , 102, 1-7	3.3	287
168	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015 , 9, 1710-22	11.9	232
167	Identification of a novel group of bacteria in sludge from a deteriorated biological phosphorus removal reactor. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 1251-8	4.8	201
166	Biofilm formation characteristics of bacterial isolates retrieved from a reverse osmosis membrane. <i>Environmental Science & Technology</i> , 2005 , 39, 7541-50	10.3	182
165	In situ identification of polyphosphate- and polyhydroxyalkanoate-accumulating traits for microbial populations in a biological phosphorus removal process. <i>Environmental Microbiology</i> , 2001 , 3, 110-22	5.2	167
164	Identification and occurrence of tetrad-forming Alphaproteobacteria in anaerobic-aerobic activated sludge processes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 3741-3748	2.9	163
163	Analysis of 16S rRNA amplicon sequencing options on the Roche/454 next-generation titanium sequencing platform. <i>PLoS ONE</i> , 2011 , 6, e25263	3.7	160
162	Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. <i>ISME Journal</i> , 2014 , 8, 541-551	11.9	159
161	Pyrosequencing analysis of bacterial biofilm communities in water meters of a drinking water distribution system. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5631-5	4.8	157
160	Internal energy-based competition between polyphosphate- and glycogen-accumulating bacteria in biological phosphorus removal reactorsEffect of PC feeding ratio. <i>Water Research</i> , 1997 , 31, 1430-1438	12.5	157
159	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, 5467-76	10.3	149
158	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. <i>ISME Journal</i> , 2016 , 10, 2478-87	11.9	146
157	Characterization of microbial consortia in a terephthalate-degrading anaerobic granular sludge system. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 373-382	2.9	136
156	Diversity and distribution of a deeply branched novel proteobacterial group found in anaerobic-aerobic activated sludge processes. <i>Environmental Microbiology</i> , 2002 , 4, 753-7	5.2	127

155	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	12.5	126
154	Optimization of an oligonucleotide microchip for microbial identification studies: a non-equilibrium dissociation approach. <i>Environmental Microbiology</i> , 2001 , 3, 619-29	5.2	125
153	Microbial community dynamics during start-up of acidogenic anaerobic reactors. <i>Water Research</i> , 2002 , 36, 3203-10	12.5	121
152	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, 597-8	4.8	119
151	Phylogeny and physiology of candidate phylum <i>Satribacteria</i> (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016 , 10, 273-86	11.9	118
150	Response of gut microbiota to salinity change in two euryhaline aquatic animals with reverse salinity preference. <i>Aquaculture</i> , 2016 , 454, 72-80	4.4	116
149	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
148	A microbiology-based multi-parametric approach towards assessing biological stability in drinking water distribution networks. <i>Water Research</i> , 2013 , 47, 3015-25	12.5	115
147	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, 2901-14	12.5	114
146	<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	2.2	114
145	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	12.5	113
144	The nexus of syntrophy-associated microbiota in anaerobic digestion revealed by long-term enrichment and community survey. <i>Environmental Microbiology</i> , 2015 , 17, 1707-20	5.2	111
143	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, 7856-65	4.8	105
142	Drinking water microbiome assembly induced by water stagnation. <i>ISME Journal</i> , 2018 , 12, 1520-1531	11.9	101
141	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		100
140	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011 , 5, 122-30	11.9	99
139	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, 466-73	5.7	98
138	Quantitative effects of position and type of single mismatch on single base primer extension. <i>Journal of Microbiological Methods</i> , 2009 , 77, 267-75	2.8	97

137	Characterization of microbial community in granular sludge treating brewery wastewater. <i>Water Research</i> , 2002 , 36, 1767-75	12.5	92
136	Impact of silver nanoparticles on natural marine biofilm bacteria. <i>Chemosphere</i> , 2011 , 85, 961-6	8.4	90
135	Community structure analysis of reverse osmosis membrane biofilms and the significance of Rhizobiales bacteria in biofouling. <i>Environmental Science & Technology</i> , 2007 , 41, 4728-34	10.3	85
134	Environmental microbiology-on-a-chip and its future impacts. <i>Trends in Biotechnology</i> , 2005 , 23, 174-9	15.1	77
133	Metagenomic analysis of DNA viruses in a wastewater treatment plant in tropical climate. <i>Environmental Microbiology</i> , 2012 , 14, 441-52	5.2	76
132	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. <i>ISME Journal</i> , 2016 , 10, 582-95	11.9	73
131	Microbial community structure in a thermophilic anaerobic hybrid reactor degrading terephthalate. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 3429-40	2.9	72
130	Metagenomic characterization of biofilter microbial communities in a full-scale drinking water treatment plant. <i>Water Research</i> , 2018 , 128, 278-285	12.5	71
129	Comparative analysis of fecal microbiota in infants with and without eczema. <i>PLoS ONE</i> , 2010 , 5, e9964	3.7	71
128	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, 2531-42	12.5	70
127	Filter-based microfluidic device as a platform for immunofluorescent assay of microbial cells. <i>Lab on A Chip</i> , 2004 , 4, 337-41	7.2	69
126	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, 4274-82	10.3	67
125	Identification of important microbial populations in the mesophilic and thermophilic phenol-degrading methanogenic consortia. <i>Water Research</i> , 2008 , 42, 1963-76	12.5	67
124	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, 6070-7	4.8	66
123	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	4.9	64
122	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. <i>Water Research</i> , 2017 , 124, 77-84	12.5	64
121	Determination of virus abundance, diversity and distribution in a municipal wastewater treatment plant. <i>Water Research</i> , 2009 , 43, 1101-9	12.5	63
120	Microfluidic device as a new platform for immunofluorescent detection of viruses. <i>Lab on A Chip</i> , 2005 , 5, 1327-30	7.2	62

119	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	7	59
118	Simultaneous nitrogen and phosphorus removal in the sulfur cycle-associated Enhanced Biological Phosphorus Removal (EBPR) process. <i>Water Research</i> , 2014 , 49, 251-64	12.5	56
117	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017 , 8, 1507	17.4	56
116	The genome of <i>Syntrophorhabdus aromaticivorans</i> strain UI provides new insights for syntrophic aromatic compound metabolism and electron flow. <i>Environmental Microbiology</i> , 2015 , 17, 4861-72	5.2	55
115	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	10.3	54
114	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	4.8	53
113	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	12.5	52
112	Microbial community changes in biological phosphate-removal systems on altering sludge phosphorus content. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 5), 1099-1107	2.9	51
111	<i>Halomonas sulfidaeris</i> -dominated microbial community inhabits a 1.8 km-deep subsurface Cambrian Sandstone reservoir. <i>Environmental Microbiology</i> , 2014 , 16, 1695-708	5.2	46
110	Microbial detection in microfluidic devices through dual staining of quantum dots-labeled immunoassay and RNA hybridization. <i>Analytica Chimica Acta</i> , 2006 , 556, 171-7	6.6	45
109	Response of Simulated Drinking Water Biofilm Mechanical and Structural Properties to Long-Term Disinfectant Exposure. <i>Environmental Science & Technology</i> , 2016 , 50, 1779-87	10.3	44
108	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	12.5	43
107	Membrane biofouling in a wastewater nitrification reactor: Microbial succession from autotrophic colonization to heterotrophic domination. <i>Water Research</i> , 2016 , 88, 337-345	12.5	41
106	Silicon nanopillar substrates for enhancing signal intensity in DNA microarrays. <i>Biosensors and Bioelectronics</i> , 2008 , 24, 723-8	11.8	41
105	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, 1082-90	10.2	40
104	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, 2882-93	4.8	40
103	Evaluation of methods for the extraction of DNA from drinking water distribution system biofilms. <i>Microbes and Environments</i> , 2012 , 27, 9-18	2.6	38
102	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, 6453-7	4.8	38

101	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	10.2	36
100	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	3.3	36
99	A new biological phosphorus removal process in association with sulfur cycle. <i>Water Research</i> , 2013 , 47, 3057-69	12.5	35
98	Characterization of active microbes in a full-scale anaerobic fluidized bed reactor treating phenolic wastewater. <i>Microbes and Environments</i> , 2009 , 24, 144-53	2.6	35
97	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , 2013 , 86, 277-87	4.3	33
96	A spatially addressable bead-based biosensor for simple and rapid DNA detection. <i>Biosensors and Bioelectronics</i> , 2008 , 23, 803-10	11.8	33
95	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, 469-77	5.7	31
94	Enrichment and characterization of microbial consortia degrading soluble microbial products discharged from anaerobic methanogenic bioreactors. <i>Water Research</i> , 2016 , 90, 395-404	12.5	31
93	Quantitative detection of culturable methanogenic archaea abundance in anaerobic treatment systems using the sequence-specific rRNA cleavage method. <i>ISME Journal</i> , 2009 , 3, 522-35	11.9	31
92	Miniaturized platforms for the detection of single-nucleotide polymorphisms. <i>Analytical and Bioanalytical Chemistry</i> , 2006 , 386, 427-34	4.4	31
91	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	2.2	31
90	Ecophysiology of <i>Defluviiicoccus</i> -related tetrad-forming organisms in an anaerobic-aerobic activated sludge process. <i>Environmental Microbiology</i> , 2007 , 9, 1485-96	5.2	30
89	Biological filtration limits carbon availability and affects downstream biofilm formation and community structure. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 5702-12	4.8	30
88	A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. <i>PLoS ONE</i> , 2016 , 11, e0167788	3.7	30
87	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. <i>Environmental Microbiology</i> , 2017 , 19, 3163-3174	5.2	29
86	Community and proteomic analysis of methanogenic consortia degrading terephthalate. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 105-12	4.8	28
85	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019 , 27, 670-677	12.4	27
84	Characterization of bacterial community dynamics in a full-scale drinking water treatment plant. <i>Journal of Environmental Sciences</i> , 2017 , 51, 21-30	6.4	27

83	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	2.9	26
82	Metagenomic characterization of <i>Candidatus Defluviicoccus tetraformis</i> strain TFO715 a tetrad-forming organism, predominant in an anaerobic-aerobic membrane bioreactor with deteriorated biological phosphorus removal. <i>Environmental Microbiology</i> , 2014 , 16, 2739-51	5.2	26
81	Quantitative multiplexing analysis of PCR-amplified ribosomal RNA genes by hierarchical oligonucleotide primer extension reaction. <i>Nucleic Acids Research</i> , 2007 , 35, e82	20.1	26
80	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, 830-3	7.2	24
79	Rapid discrimination of single-nucleotide mismatches using a microfluidic device with monolayered beads. <i>Analytica Chimica Acta</i> , 2007 , 582, 295-303	6.6	24
78	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	4.9	24
77	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	10.3	23
76	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010 , 12, 1803-5	5.2	23
75	Evaluating single-base-pair discriminating capability of planar oligonucleotide microchips using a non-equilibrium dissociation approach. <i>Environmental Microbiology</i> , 2004 , 6, 1197-202	5.2	23
74	Metagenomics Reveals a Novel Virophage Population in a Tibetan Mountain Lake. <i>Microbes and Environments</i> , 2016 , 31, 173-7	2.6	21
73	MS2 bacteriophage reduction and microbial communities in biosand filters. <i>Environmental Science & Technology</i> , 2014 , 48, 6702-9	10.3	21
72	Thermodynamically diverse syntrophic aromatic compound catabolism. <i>Environmental Microbiology</i> , 2017 , 19, 4576-4586	5.2	21
71	Impact of chloramination on the development of laboratory-grown biofilms fed with filter-pretreated groundwater. <i>Microbes and Environments</i> , 2013 , 28, 50-7	2.6	21
70	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, 1672-81	5.2	21
69	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	3.3	21
68	<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	2.2	21
67	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	11.1	20
66	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	8.2	20

65	Microbial community analysis of anaerobic reactors treating soft drink wastewater. <i>PLoS ONE</i> , 2015 , 10, e0119131	3.7	20
64	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	12.5	20
63	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <i>Microbes and Environments</i> , 2016 , 31, 288-92	2.6	19
62	Quantifying the contribution of microbial immigration in engineered water systems. <i>Microbiome</i> , 2019 , 7, 144	16.6	19
61	Genomic composition and dynamics among Methanomicrobiales predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017 , 11, 87-99	11.9	19
60	Isolation, characterization and identification of polyhydroxyalkanoate-accumulating bacteria from activated sludge. <i>Journal of Bioscience and Bioengineering</i> , 2000 , 90, 494-500	3.3	19
59	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	12.5	18
58	Ugly ducklings-the dark side of plastic materials in contact with potable water. <i>Npj Biofilms and Microbiomes</i> , 2018 , 4, 7	8.2	18
57	Microbial population dynamics of granular aerobic sequencing batch reactors during start-up and steady state periods. <i>Water Science and Technology</i> , 2010 , 62, 1281-7	2.2	18
56	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, 614-22	4.4	18
55	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. <i>Microbiome</i> , 2020 , 8, 16	16.6	17
54	Nexus of Stochastic and Deterministic Processes on Microbial Community Assembly in Biological Systems. <i>Frontiers in Microbiology</i> , 2019 , 10, 1536	5.7	17
53	Draft Genome Sequence of Syntrophorhabdus aromaticivorans Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. <i>Genome Announcements</i> , 2014 , 2,		17
52	DNA Microarray Technology in Microbial Ecology Studies-Principle, Applications and Current Limitations.. <i>Microbes and Environments</i> , 2003 , 18, 175-187	2.6	17
51	Tetrasphaera elongata sp. nov., a polyphosphate-accumulating bacterium isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002 , 52, 883-887	2.2	17
50	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. <i>Water Research</i> , 2020 , 178, 115815	12.5	17
49	Novel energy conservation strategies and behaviour of Pelotomaculum schinkii driving syntrophic propionate catabolism. <i>Environmental Microbiology</i> , 2018 , 20, 4503-4511	5.2	16
48	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , 2008 , 72, 82-90	2.8	16

47	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, 6012-23	4.8	15
46	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	10.3	15
45	Cell loss in integrated microfluidic device. <i>Biomedical Microdevices</i> , 2007 , 9, 745-50	3.7	15
44	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, 449-55	3.3	15
43	Immobilization of selenite via two parallel pathways during in situ bioremediation. <i>Environmental Science & Technology</i> , 2015 , 49, 4543-50	10.3	14
42	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	7.5	14
41	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	16.6	13
40	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. <i>Environmental Microbiology Reports</i> , 2018 , 10, 673-685	3.7	12
39	Recent advances in molecular techniques for the detection of phylogenetic markers and functional genes in microbial communities. <i>FEMS Microbiology Letters</i> , 2007 , 275, 183-90	2.9	12
38	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	5.7	11
37	Membrane biofouling characterization: effects of sample preparation procedures on biofilm structure and the microbial community. <i>Biofouling</i> , 2014 , 30, 813-21	3.3	11
36	Immune-modulatory genomic properties differentiate gut microbiota of infants with and without eczema. <i>PLoS ONE</i> , 2017 , 12, e0184955	3.7	11
35	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. <i>Microbiome</i> , 2020 , 8, 111	16.6	11
34	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	5.7	10
33	Saliva-based diagnostics using 16S rRNA microarrays and microfluidics. <i>Annals of the New York Academy of Sciences</i> , 2007 , 1098, 345-61	6.5	10
32	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013 , 84, 259-69	4.3	9
31	LabArray: real-time imaging and analytical tool for microarrays. <i>Bioinformatics</i> , 2005 , 21, 689-90	7.2	9
30	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021 , 12, 3076	17.4	9

29	Draft Genome Sequence of a Novel SAR11 Clade Species Abundant in a Tibetan Lake. <i>Genome Announcements</i> , 2014 , 2,		8
28	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	5-7	8
27	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	4-9	7
26	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	5-7	7
25	Complete Genome Sequence of the Intracellular Bacterial Symbiont TC1 in the Anaerobic Ciliate <i>Trimyema compressum</i> . <i>Genome Announcements</i> , 2016 , 4,		6
24	Quantitative fluorescent in-situ hybridization: a hypothesized competition mode between two dominant bacteria groups in hydrogen-producing anaerobic sludge processes. <i>Water Science and Technology</i> , 2009 , 59, 1901-9	2.2	6
23	Spatially addressable bead-based biosensor for rapid detection of beta-thalassemia mutations. <i>Analytica Chimica Acta</i> , 2010 , 658, 193-6	6.6	6
22	Ecology and molecular targets of hypermutation in the global microbiome		6
21	Fabrication of three-dimensional hemispherical structures using photolithography. <i>Microfluidics and Nanofluidics</i> , 2009 , 7, 721-726	2.8	5
20	Technology development to explore the relationship between oral health and the oral microbial community. <i>BMC Oral Health</i> , 2006 , 6 Suppl 1, S10	3-7	5
19	Microbial Community Involved in Anaerobic Purified Terephthalic Acid Treatment Process 2015 , 31-48		4
18	Identifying anaerobic amino acids degraders through the comparison of short-term and long-term enrichments. <i>Environmental Microbiology Reports</i> , 2020 , 12, 173-184	3-7	4
17	Hierarchical oligonucleotide primer extension as a time- and cost-effective approach for quantitative determination of <i>Bifidobacterium</i> spp. in infant feces. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2573-6	4.8	4
16	Proliferation of glycogen accumulating organisms induced by Fe(III) dosing in a domestic wastewater treatment plant. <i>Water Science and Technology</i> , 2006 , 54, 101-9	2.2	4
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