

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	Meta-Omics-Supervised Characterization of Respiration Activities Associated with Microbial Immigrants in Anaerobic Sludge Digesters. <i>Environmental Science & Technology</i> , 2022, 56, 6689-6698.	10.0	4
2	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
3	Disentangling the syntrophic electron transfer mechanisms of <i>Candidatus geobacter eutrophica</i> through electrochemical stimulation and machine learning. <i>Scientific Reports</i> , 2021, 11, 15140.	3.3	8
4	Relative Importance of Stochastic Assembly Process of Membrane Biofilm Increased as Biofilm Aged. <i>Frontiers in Microbiology</i> , 2021, 12, 708531.	3.5	10
5	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
6	Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. <i>Water Research</i> , 2020, 170, 115359.	11.3	5
7	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. <i>Microbiome</i> , 2020, 8, 111.	11.1	48
8	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degradors in Anaerobic Digesters. <i>Frontiers in Microbiology</i> , 2020, 11, 593006.	3.5	57
9	Ecogenomics-Based Mass Balance Model Reveals the Effects of Fermentation Conditions on Microbial Activity. <i>Frontiers in Microbiology</i> , 2020, 11, 595036.	3.5	8
10	Identifying anaerobic amino acids degraders through the comparison of short-term and long-term enrichments. <i>Environmental Microbiology Reports</i> , 2020, 12, 173-184.	2.4	8
11	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
12	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
13	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
14	Assessing the contribution of biofilm to bacterial growth during stagnation in shower hoses. <i>Water Science and Technology: Water Supply</i> , 2020, 20, 2564-2576.	2.1	5
15	Nexus of Stochastic and Deterministic Processes on Microbial Community Assembly in Biological Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 1536.	3.5	37
16	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
17	Quantifying the contribution of microbial immigration in engineered water systems. <i>Microbiome</i> , 2019, 7, 144.	11.1	41
18	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

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19	Drinking Water Microbiome Project: Is it Time?. Trends in Microbiology, 2019, 27, 670-677.	7.7	50
20	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. Water Research, 2019, 155, 275-287.	11.3	77
21	The application of molecular tools to study the drinking water microbiome – Current understanding and future needs. Critical Reviews in Environmental Science and Technology, 2019, 49, 1188-1235.	12.8	38
22	Warming counteracts grazing effects on the functional structure of the soil microbial community in a Tibetan grassland. Soil Biology and Biochemistry, 2019, 134, 113-121.	8.8	42
23	Drinking water microbiome assembly induced by water stagnation. ISME Journal, 2018, 12, 1520-1531.	9.8	172
24	Ugly ducklings—the dark side of plastic materials in contact with potable water. Npj Biofilms and Microbiomes, 2018, 4, 7.	6.4	28
25	Metagenomic characterization of biofilter microbial communities in a full-scale drinking water treatment plant. Water Research, 2018, 128, 278-285.	11.3	121
26	Distribution comparison and risk assessment of free-floating and particle-attached bacterial pathogens in urban recreational water: Implications for water quality management. Science of the Total Environment, 2018, 613-614, 428-438.	8.0	55
27	Novel Geobacter species and diverse methanogens contribute to enhanced methane production in media-added methanogenic reactors. Water Research, 2018, 147, 403-412.	11.3	69
28	Effect of divalent ions and a polyphosphate on composition, structure, and stiffness of simulated drinking water biofilms. Npj Biofilms and Microbiomes, 2018, 4, 15.	6.4	33
29	Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. Environmental Microbiology Reports, 2018, 10, 673-685.	2.4	22
30	Novel energy conservation strategies and behaviour of <i>Pelotomaculum schinkii</i> driving syntrophic propionate catabolism. Environmental Microbiology, 2018, 20, 4503-4511.	3.8	31
31	Effect of Disinfectant Exposure on <i>Legionella pneumophila</i> Associated with Simulated Drinking Water Biofilms: Release, Inactivation, and Infectivity. Environmental Science & Technology, 2017, 51, 2087-2095.	10.0	31
32	Complete Nutrient Removal Coupled to Nitrous Oxide Production as a Bioenergy Source by Denitrifying Polyphosphate-Accumulating Organisms. Environmental Science & Technology, 2017, 51, 4531-4540.	10.0	66
33	Impact of drinking water treatment and distribution on the microbiome continuum: an ecological disturbance's perspective. Environmental Microbiology, 2017, 19, 3163-3174.	3.8	56
34	Impacts of biostimulation and bioaugmentation on the performance and microbial ecology in methanogenic reactors treating purified terephthalic acid wastewater. Water Research, 2017, 122, 308-316.	11.3	22
35	Thermodynamically diverse syntrophic aromatic compound catabolism. Environmental Microbiology, 2017, 19, 4576-4586.	3.8	32
36	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. Water Research, 2017, 124, 77-84.	11.3	82

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37	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
38	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	12.8	99
39	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
40	Genomic composition and dynamics among <i>Methanomicrobiales</i> predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017, 11, 87-99.	9.8	29
41	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
42	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
43	Immune-modulatory genomic properties differentiate gut microbiota of infants with and without eczema. <i>PLoS ONE</i> , 2017, 12, e0184955.	2.5	12
44	Draft Genome Sequence of <i>Syntrophomonas wolfei</i> subsp. <i>methylbutyratica</i> Strain 4J5 ^T (JCM 14075), a Mesophilic Butyrate- and 2-Methylbutyrate-Degrading Syntroph. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
45	Evolution and adaptation of SAR11 and <i>Cyanobium</i> in a saline Tibetan lake. <i>Environmental Microbiology Reports</i> , 2016, 8, 595-604.	2.4	7
46	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
47	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
48	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <i>Microbes and Environments</i> , 2016, 31, 288-292.	1.6	19
49	Metagenomics Reveals a Novel Virophage Population in a Tibetan Mountain Lake. <i>Microbes and Environments</i> , 2016, 31, 173-177.	1.6	35
50	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
51	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
52	Complete Genome Sequence of the Intracellular Bacterial Symbiont TC1 in the Anaerobic Ciliate <i>Trimyema compressum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	6
53	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
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	Phylogeny and physiology of candidate phylum "Atribacteria"™ (OP9/S1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
62	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
63	Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. <i>PLoS ONE</i> , 2015, 10, e0119131.	2.5	27
64	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
65	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	9.8	360
66	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
67	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
68	Immobilization of Selenite via Two Parallel Pathways during In Situ Bioremediation. <i>Environmental Science & Technology</i> , 2015, 49, 4543-4550.	10.0	19
69	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
70	Microbial Community Involved in Anaerobic Purified Terephthalic Acid Treatment Process. , 2015, , 31-48.		4
71	Development and Application of Anaerobic Technology for the Treatment of Chemical Effluents in Taiwan. , 2015, , 243-262.		0
72	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, 4861-4872.	3.8	72

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73	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
74	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
75	Complete Genome Sequence of <i>Methanoregula formicica</i> SMSP ^T , a Mesophilic Hydrogenotrophic Methanogen Isolated from a Methanogenic Upflow Anaerobic Sludge Blanket Reactor. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
76	<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
77	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
78	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
79	Metagenomic characterization of <i>Candidatus</i> <i>Dechlorococcus</i> <i>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
80	MS2 Bacteriophage Reduction and Microbial Communities in Biosand Filters. <i>Environmental Science & Technology</i> , 2014, 48, 6702-6709.	10.0	27
81	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
82	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
83	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
84	Complete Genome Sequence of <i>Methanolinea tarda</i> NOBI-1 ^T , a Hydrogenotrophic Methanogen Isolated from Methanogenic Digester Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
85	Draft Genome Sequence of a Novel SAR11 Clade Species Abundant in a Tibetan Lake. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
86	The Family Dermatophilaceae. , 2014, , 317-325.		0
87	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
88	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
89	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
90	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

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91	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	2.7	19
92	A new biological phosphorus removal process in association with sulfur cycle. <i>Water Research</i> , 2013, 47, 3057-3069.	11.3	42
93	Community and Proteomic Analysis of Methanogenic Consortia Degrading Terephthalate. <i>Applied and Environmental Microbiology</i> , 2013, 79, 105-112.	3.1	44
94	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
95	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
96	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
97	Metagenomic analysis of DNA viruses in a wastewater treatment plant in tropical climate. <i>Environmental Microbiology</i> , 2012, 14, 441-452.	3.8	98
98	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	9.8	114
99	Impact of silver nanoparticles on natural marine biofilm bacteria. <i>Chemosphere</i> , 2011, 85, 961-966.	8.2	103
100	Full-scale Use of Glycogen-accumulating Organisms for Excess Biological Carbon Removal. <i>Water Environment Research</i> , 2011, 83, 855-864.	2.7	6
101	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
102	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
103	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
104	Spatially addressable bead-based biosensor for rapid detection of beta-thalassemia mutations. <i>Analytica Chimica Acta</i> , 2010, 658, 193-196.	5.4	6
105	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010, 12, 1803-1805.	3.8	33
106	Comparative Analysis of Fecal Microbiota in Infants with and without Eczema. <i>PLoS ONE</i> , 2010, 5, e9964.	2.5	87
107	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
108	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, 2573-2576.	3.1	4

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109	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, 1901-1909.	2.5	6
110	Fabrication of three-dimensional hemispherical structures using photolithography. <i>Microfluidics and Nanofluidics</i> , 2009, 7, 721-726.	2.2	6
111	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
112	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
113	Determination of virus abundance, diversity and distribution in a municipal wastewater treatment plant. <i>Water Research</i> , 2009, 43, 1101-1109.	11.3	78
114	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
115	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
116	A spatially addressable bead-based biosensor for simple and rapid DNA detection. <i>Biosensors and Bioelectronics</i> , 2008, 23, 803-810.	10.1	34
117	Silicon nanopillar substrates for enhancing signal intensity in DNA microarrays. <i>Biosensors and Bioelectronics</i> , 2008, 24, 723-728.	10.1	50
118	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , 2008, 72, 82-90.	1.6	16
119	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
120	Microbial diversity and metagenomics insights of terephthalate-degrading methanogenic processes. <i>Journal of Biotechnology</i> , 2008, 136, S603-S604.	3.8	0
121	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
122	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
123	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
124	Fabrication technology of Si microfluidic devices for microbial cell trapping. , 2007, , .		0
125	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
126	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

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127	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
128	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
129	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
130	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
131	Cell loss in integrated microfluidic device. <i>Biomedical Microdevices</i> , 2007, 9, 745-750.	2.8	18
132	Nanoparticles and their biological and environmental applications. <i>Journal of Bioscience and Bioengineering</i> , 2006, 102, 1-7.	2.2	351
133	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
134	Technology Development to Explore the Relationship Between Oral Health and the Oral Microbial Community. <i>BMC Oral Health</i> , 2006, 6, S10.	2.3	5
135	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
136	Miniaturized platforms for the detection of single-nucleotide polymorphisms. <i>Analytical and Bioanalytical Chemistry</i> , 2006, 386, 427-434.	3.7	33
137	Proliferation of glycogen accumulating organisms induced by Fe(III) dosing in a domestic wastewater treatment plant. <i>Water Science and Technology</i> , 2006, 54, 101-109.	2.5	9
138	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
139	Environmental microbiology-on-a-chip and its future impacts. <i>Trends in Biotechnology</i> , 2005, 23, 174-179.	9.3	87
140	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
141	LabArray: real-time imaging and analytical tool for microarrays. <i>Bioinformatics</i> , 2005, 21, 689-690.	4.1	11
142	Microfluidic device as a new platform for immunofluorescent detection of viruses. <i>Lab on A Chip</i> , 2005, 5, 1327.	6.0	66
143	Biofilm Formation Characteristics of Bacterial Isolates Retrieved from a Reverse Osmosis Membrane. <i>Environmental Science & Technology</i> , 2005, 39, 7541-7550.	10.0	219
144	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

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145	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
146	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
147	Microbial community structure in a thermophilic anaerobic hybrid reactor degrading terephthalate. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3429-3440.	1.8	75
148	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
149	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
150	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
151	DNA Microarray Technology in Microbial Ecology Studies-Principle, Applications and Current Limitations.. <i>Microbes and Environments</i> , 2003, 18, 175-187.	1.6	18
152	<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
153	<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
154	Characterization of microbial community in granular sludge treating brewery wastewater. <i>Water Research</i> , 2002, 36, 1767-1775.	11.3	111
155	Microbial community dynamics during start-up of acidogenic anaerobic reactors. <i>Water Research</i> , 2002, 36, 3203-3210.	11.3	142
156	<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
157	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
158	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
159	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	5
160	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
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	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
164	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-â€AF229793.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 373-382.	1.8	150
165	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
166	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
167	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
168	Isolation, Characterization and Identification of Polyhydroxyalkanoate-Accumulating Bacteria from Activated Sludge.. <i>Journal of Bioscience and Bioengineering</i> , 2000, 90, 494-500.	2.2	4
169	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
170	Analysis of BIOLOG GN Substrate Utilization Patterns by Microbial Communities. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1220-1225.	3.1	342
171	Internal energy-based competition between polyphosphate- and glycogen-accumulating bacteria in biological phosphorus removal reactorsâ€™Effect of PC feeding ratio. <i>Water Research</i> , 1997, 31, 1430-1438.	11.3	185
172	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
173	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