List of Publications by Year in descending order

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	23567	29157
12,171	58	104
citations	h-index	g-index
100	100	
132	132	10416
docs citations	times ranked	citing authors
	12,171 citations 132 docs citations	12,171 58 citations h-index 132 132 132 docs citations 132 times ranked

#	Article	IF	CITATIONS
1	Identification of Polyphosphate-Accumulating Organisms and Design of 16S rRNA-Directed Probes for Their Detection and Quantitation. Applied and Environmental Microbiology, 2000, 66, 1175-1182.	3.1	691
2	Metagenomic analysis reveals wastewater treatment plants as hotspots of antibiotic resistance genes and mobile genetic elements. Water Research, 2017, 123, 468-478.	11.3	604
3	Formation of Sphalerite (ZnS) Deposits in Natural Biofilms of Sulfate-Reducing Bacteria. , 2000, 290, 1744-1747.		554
4	An Archaeal Iron-Oxidizing Extreme Acidophile Important in Acid Mine Drainage. Science, 2000, 287, 1796-1799.	12.6	510
5	Glycogen-accumulating organisms in laboratory-scale and full-scale wastewater treatment processes b bThe GenBank accession numbers for the sequences reported in this paper are given in Methods Microbiology (United Kingdom), 2002, 148, 3353-3364.	1.8	377
6	The application of two-dimensional polyacrylamide gel electrophoresis and downstream analyses to a mixed community of prokaryotic microorganisms. Environmental Microbiology, 2004, 6, 911-920.	3.8	347
7	Metaproteomics: studying functional gene expression in microbial ecosystems. Trends in Microbiology, 2006, 14, 92-97.	7.7	326
8	Phylogeny of Microorganisms Populating a Thick, Subaerial, Predominantly Lithotrophic Biofilm at an Extreme Acid Mine Drainage Site. Applied and Environmental Microbiology, 2000, 66, 3842-3849.	3.1	325
9	Growth in sulfidic mineral environments: metal resistance mechanisms in acidophilic micro-organisms. Microbiology (United Kingdom), 2003, 149, 1959-1970.	1.8	286
10	Comparison of Acid Mine Drainage Microbial Communities in Physically and Geochemically Distinct Ecosystems. Applied and Environmental Microbiology, 2000, 66, 4962-4971.	3.1	282
11	Cathodic oxygen reduction catalyzed by bacteria in microbial fuel cells. ISME Journal, 2008, 2, 519-527.	9.8	268
12	Structural and Regulatory Genes Required to Make the Gas Dimethyl Sulfide in Bacteria. Science, 2007, 315, 666-669.	12.6	256
13	Antiepileptic drug carbamazepine promotes horizontal transfer of plasmid-borne multi-antibiotic resistance genes within and across bacterial genera. ISME Journal, 2019, 13, 509-522.	9.8	245
14	Identification of Some of the Major Groups of Bacteria in Efficient and Nonefficient Biological Phosphorus Removal Activated Sludge Systems. Applied and Environmental Microbiology, 1999, 65, 4077-4084.	3.1	202
15	Electron competition among nitrogen oxides reduction during methanol-utilizing denitrification in wastewater treatment. Water Research, 2013, 47, 3273-3281.	11.3	200
16	Characterization of Ferroplasma Isolates and Ferroplasma acidarmanus sp. nov., Extreme Acidophiles from Acid Mine Drainage and Industrial Bioleaching Environments. Applied and Environmental Microbiology, 2004, 70, 2079-2088.	3.1	186
17	Triclosan at environmentally relevant concentrations promotes horizontal transfer of multidrug resistance genes within and across bacterial genera. Environment International, 2018, 121, 1217-1226.	10.0	182
18	Initial development and structure of biofilms on microbial fuel cell anodes. BMC Microbiology, 2010, 10, 98.	3.3	180

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19	Both silver ions and silver nanoparticles facilitate the horizontal transfer of plasmid-mediated antibiotic resistance genes. Water Research, 2020, 169, 115229.	11.3	179
20	A review and update of the microbiology of enhanced biological phosphorus removal in wastewater treatment plants. Antonie Van Leeuwenhoek, 2002, 81, 681-691.	1.7	161
21	A decade of metaproteomics: Where we stand and what the future holds. Proteomics, 2015, 15, 3409-3417.	2.2	161
22	Metabolically Active Eukaryotic Communities in Extremely Acidic Mine Drainage. Applied and Environmental Microbiology, 2004, 70, 6264-6271.	3.1	159
23	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. ISME Journal, 2008, 2, 853-864.	9.8	156
24	Metaproteomics Provides Functional Insight into Activated Sludge Wastewater Treatment. PLoS ONE, 2008, 3, e1778.	2.5	145
25	Surface neutralization and H2S oxidation at early stages of sewer corrosion: Influence of temperature, relative humidity and H2S concentration. Water Research, 2012, 46, 4235-4245.	11.3	141
26	Non-antibiotic pharmaceuticals enhance the transmission of exogenous antibiotic resistance genes through bacterial transformation. ISME Journal, 2020, 14, 2179-2196.	9.8	133
27	Nonnutritive sweeteners can promote the dissemination of antibiotic resistance through conjugative gene transfer. ISME Journal, 2021, 15, 2117-2130.	9.8	131
28	Geochemical and biological aspects of sulfide mineral dissolution: lessons from Iron Mountain, California. Chemical Geology, 2000, 169, 383-397.	3.3	129
29	How Does Poly(hydroxyalkanoate) Affect Methane Production from the Anaerobic Digestion of Waste-Activated Sludge?. Environmental Science & Technology, 2015, 49, 12253-12262.	10.0	125
30	Enhancing aerobic granulation for biological nutrient removal from domestic wastewater. Bioresource Technology, 2012, 103, 101-108.	9.6	124
31	Determining the long-term effects of H2S concentration, relative humidity and air temperature on concrete sewer corrosion. Water Research, 2014, 65, 157-169.	11.3	122
32	Efficient inactivation of antibiotic resistant bacteria and antibiotic resistance genes by photo-Fenton process under visible LED light and neutral pH. Water Research, 2020, 179, 115878.	11.3	112
33	Drivers of microbial community composition in mesophilic and thermophilic temperature-phased anaerobic digestion pre-treatment reactors. Water Research, 2013, 47, 7098-7108.	11.3	111
34	Improving wastewater management using free nitrous acid (FNA). Water Research, 2020, 171, 115382.	11.3	111
35	A wide hostâ€range metagenomic library from a waste water treatment plant yields a novel alcohol/aldehyde dehydrogenase. Environmental Microbiology, 2005, 7, 1917-1926.	3.8	107
36	Determining the mechanisms for aerobic granulation from mixed seed of floccular and crushed granules in activated sludge wastewater treatment. Water Research, 2012, 46, 761-771.	11.3	107

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37	Predicting concrete corrosion of sewers using artificial neural network. Water Research, 2016, 92, 52-60.	11.3	106
38	Achieving Stable Nitritation for Mainstream Deammonification by Combining Free Nitrous Acid-Based Sludge Treatment and Oxygen Limitation. Scientific Reports, 2016, 6, 25547.	3.3	104
39	Unraveling microbial structure and diversity of activated sludge in a full-scale simultaneous nitrogen and phosphorus removal plant using metagenomic sequencing. Enzyme and Microbial Technology, 2017, 102, 16-25.	3.2	100
40	Chlorine disinfection facilitates natural transformation through ROS-mediated oxidative stress. ISME Journal, 2021, 15, 2969-2985.	9.8	99
41	Expanding our view of genomic diversity in <scp><i>C</i></scp> <i>andidatus</i> â€ <scp>A</scp> ccumulibacter clades. Environmental Microbiology, 2015, 17, 1574-1585.	3.8	98
42	The role of iron in sulfide induced corrosion ofÂsewer concrete. Water Research, 2014, 49, 166-174.	11.3	92
43	Characteristics of attachment and growth of Thiobacillus caldus on sulphide minerals: a chemotactic response to sulphur minerals?. Environmental Microbiology, 2000, 2, 324-332.	3.8	86
44	Extreme arsenic resistance by the acidophilic archaeon â€~Ferroplasma acidarmanus' Fer1. Extremophiles, 2007, 11, 425-434.	2.3	86
45	Wastewater-Enhanced Microbial Corrosion of Concrete Sewers. Environmental Science & Technology, 2016, 50, 8084-8092.	10.0	85
46	Analysis of differential protein expression during growth states of Ferroplasma strains and insights into electron transport for iron oxidation. Microbiology (United Kingdom), 2005, 151, 4127-4137.	1.8	80
47	Breakage and growth towards a stable aerobic granule size during the treatment of wastewater. Water Research, 2013, 47, 5338-5349.	11.3	80
48	Molecular insight into extreme copper resistance in the extremophilic archaeon â€~Ferroplasma acidarmanus' Fer1. Microbiology (United Kingdom), 2005, 151, 2637-2646.	1.8	79
49	Soil Bacterial Consortia and Previous Exposure Enhance the Biodegradation of Sulfonamides from Pig Manure. Microbial Ecology, 2012, 64, 140-151.	2.8	79
50	Identification of controlling factors for the initiation of corrosion of fresh concrete sewers. Water Research, 2015, 80, 30-40.	11.3	78
51	The Ecology of Acidophilic Microorganisms in the Corroding Concrete Sewer Environment. Frontiers in Microbiology, 2017, 8, 683.	3.5	78
52	Granule Formation Mechanisms within an Aerobic Wastewater System for Phosphorus Removal. Applied and Environmental Microbiology, 2010, 76, 7588-7597.	3.1	76
53	Non-antibiotic pharmaceuticals promote the transmission of multidrug resistance plasmids through intra- and intergenera conjugation. ISME Journal, 2021, 15, 2493-2508.	9.8	76
54	Triclosan at environmental concentrations can enhance the spread of extracellular antibiotic resistance genes through transformation. Science of the Total Environment, 2020, 713, 136621.	8.0	75

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55	Copper Oxide Nanoparticles Induce Lysogenic Bacteriophage and Metal-Resistance Genes in <i>Pseudomonas aeruginosa</i> PAO1. ACS Applied Materials & Interfaces, 2017, 9, 22298-22307.	8.0	72
56	Microbial community proteomics: elucidating the catalysts and metabolic mechanisms that drive the Earth's biogeochemical cycles. Current Opinion in Microbiology, 2009, 12, 310-317.	5.1	70
57	Screening a wide hostâ€range, wasteâ€water metagenomic library in tryptophan auxotrophs of <i>Rhizobium leguminosarum</i> and of <i>Escherichia coli</i> reveals different classes of cloned <i>trp</i> genes. Environmental Microbiology, 2005, 7, 1927-1936.	3.8	65
58	High-Throughput Amplicon Sequencing Reveals Distinct Communities within a Corroding Concrete Sewer System. Applied and Environmental Microbiology, 2012, 78, 7160-7162.	3.1	64
59	From lithotroph- to organotroph-dominant: directional shift of microbial community in sulphidic tailings during phytostabilization. Scientific Reports, 2015, 5, 12978.	3.3	64
60	Radiolabelled proteomics to determine differential functioning of <i>Accumulibacter</i> during the anaerobic and aerobic phases of a bioreactor operating for enhanced biological phosphorus removal. Environmental Microbiology, 2009, 11, 3029-3044.	3.8	60
61	Characterization of a nitrate-respiring bacterial community using the nitrate reductase gene (narG) as a functional marker. Microbiology (United Kingdom), 2003, 149, 229-237.	1.8	59
62	Evidence for bacteriophage activity causing community and performance changes in a phosphorus-removal activated sludge. FEMS Microbiology Ecology, 2010, 74, 631-642.	2.7	59
63	Arsenic resistance in the archaeon "Ferroplasma acidarmanus": new insights into the structure and evolution of the ars genes. Extremophiles, 2003, 7, 123-130.	2.3	56
64	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. Environmental Science & Technology, 2018, 52, 5386-5397.	10.0	52
65	Monitoring associations between clade-level variation, overall community structure and ecosystem function in enhanced biological phosphorus removal (EBPR) systems using terminal-restriction fragment length polymorphism (T-RFLP). Water Research, 2010, 44, 4908-4923.	11.3	51
66	A novel and simple treatment for control of sulfide induced sewer concrete corrosion using free nitrous acid. Water Research, 2015, 70, 279-287.	11.3	51
67	Metagenomic and metaproteomic analyses of Accumulibacter phosphatisâ€enriched floccular and granular biofilm. Environmental Microbiology, 2016, 18, 273-287.	3.8	51
68	Biofilm development in the extremely acidophilic archaeon â€~Ferroplasma acidarmanus' Fer1. Extremophiles, 2010, 14, 485-491.	2.3	49
69	Determining Multiple Responses of <i>Pseudomonas aeruginosa</i> PAO1 to an Antimicrobial Agent, Free Nitrous Acid. Environmental Science & Technology, 2016, 50, 5305-5312.	10.0	48
70	Bacterial diversity in response to direct revegetation in the Pb–Zn–Cu tailings under subtropical and semi-arid conditions. Ecological Engineering, 2014, 68, 233-240.	3.6	47
71	Evaluation of data-driven models for predicting the service life of concrete sewer pipes subjected to corrosion. Journal of Environmental Management, 2019, 234, 431-439.	7.8	47
72	Physiological and transcriptomic analyses reveal CuO nanoparticle inhibition of anabolic and catabolic activities of sulfate-reducing bacterium. Environment International, 2019, 125, 65-74.	10.0	46

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73	Bioenergetic models for acetate and phosphate transport in bacteria important in enhanced biological phosphorus removal. Environmental Microbiology, 2008, 10, 87-98.	3.8	45
74	Anaerobic phosphate release from activated sludge with enhanced biological phosphorus removal. A possible mechanism of intracellular pH control. Biotechnology and Bioengineering, 1999, 63, 507-515.	3.3	44
75	Towards exposure of elusive metabolic mixed-culture processes: the application of metaproteomic analyses to activated sludge. Water Science and Technology, 2006, 54, 217-226.	2.5	44
76	Distinct microbially induced concrete corrosion at the tidal region of reinforced concrete sewers. Water Research, 2019, 150, 392-402.	11.3	43
77	Establishing microbial diversity and functions in weathered and neutral Cu–Pb–Zn tailings with native soil addition. Geoderma, 2015, 247-248, 108-116.	5.1	41
78	Evidence of differential adaptation to decreased temperature by anammox bacteria. Environmental Microbiology, 2018, 20, 3514-3528.	3.8	39
79	Pandemic pharmaceutical dosing effects on wastewater treatment: no adaptation of activated sludge bacteria to degrade the antiviral drug Oseltamivir (Tamiflu®) and loss of nutrient removal performance. FEMS Microbiology Letters, 2011, 315, 17-22.	1.8	38
80	Use of SWATH mass spectrometry for quantitative proteomic investigation of Shewanella oneidensis MR-1 biofilms grown on graphite cloth electrodes. Systematic and Applied Microbiology, 2015, 38, 135-139.	2.8	36
81	Corrosion of reinforcing steel in concrete sewers. Science of the Total Environment, 2019, 649, 739-748.	8.0	35
82	Prediction of concrete corrosion in sewers with hybrid Gaussian processes regression model. RSC Advances, 2017, 7, 30894-30903.	3.6	34
83	Increased Resistance of Nitrite-Admixed Concrete to Microbially Induced Corrosion in Real Sewers. Environmental Science & Technology, 2020, 54, 2323-2333.	10.0	33
84	A rapid, non-destructive methodology to monitor activity of sulfide-induced corrosion of concrete based on H2S uptake rate. Water Research, 2014, 59, 229-238.	11.3	32
85	Antimicrobial Effects of Free Nitrous Acid on Desulfovibrio vulgaris: Implications for Sulfide-Induced Corrosion of Concrete. Applied and Environmental Microbiology, 2016, 82, 5563-5575.	3.1	30
86	Effects of surface washing on the mitigation of concrete corrosion under sewer conditions. Cement and Concrete Composites, 2016, 68, 88-95.	10.7	30
87	The concentration-determined and population-specific antimicrobial effects of free nitrous acid on Pseudomonas aeruginosa PAO1. Applied Microbiology and Biotechnology, 2015, 99, 2305-2312.	3.6	29
88	Silver nanoparticles stimulate the proliferation of sulfate reducing bacterium Desulfovibrio vulgaris. Water Research, 2018, 129, 163-171.	11.3	29
89	New insights of the bacterial response to exposure of differently sized silver nanomaterials. Water Research, 2020, 169, 115205.	11.3	29
90	Impact of fluctuations in gaseous H 2 S concentrations on sulfide uptake by sewer concrete: The effect of high H 2 S loads. Water Research, 2015, 81, 84-91.	11.3	28

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91	The use of 16S rDNA clone libraries to describe the microbial diversity of activated sludge communities. Water Science and Technology, 1998, 37, 451.	2.5	27
92	Assessing the genetic diversity of Cu resistance in mine tailings through high-throughput recovery of full-length copA genes. Scientific Reports, 2015, 5, 13258.	3.3	27
93	Nitrite admixed concrete for wastewater structures: Mechanical properties, leaching behavior and biofilm development. Construction and Building Materials, 2020, 233, 117341.	7.2	27
94	Comparison of microbial communities across sections of a corroding sewer pipe and the effects of wastewater flooding. Biofouling, 2017, 33, 780-792.	2.2	24
95	Deciphering the electric code of Geobacter sulfurreducens in cocultures with Pseudomonas aeruginosa via SWATH-MS proteomics. Bioelectrochemistry, 2018, 119, 150-160.	4.6	24
96	Previously unclassified bacteria dominate during thermophilic and mesophilic anaerobic pre-treatment of primary sludge. Systematic and Applied Microbiology, 2013, 36, 281-290.	2.8	22
97	Effect of the anode potential on the physiology and proteome of Shewanella oneidensis MR-1. Bioelectrochemistry, 2018, 119, 172-179.	4.6	22
98	Structural Changes in Cell-Wall and Cell-Membrane Organic Materials Following Exposure to Free Nitrous Acid. Environmental Science & Technology, 2020, 54, 10301-10312.	10.0	21
99	First use of two-dimensional polyacrylamide gel electrophoresis to determine phylogenetic relationships. Journal of Microbiological Methods, 2004, 58, 297-302.	1.6	19
100	Towards determining details of anaerobic growth coupled to ferric iron reduction by the acidophilic archaeon â€~Ferroplasma acidarmanus' Fer1. Extremophiles, 2007, 11, 159-168.	2.3	19
101	Bioelectrochemical reduction of an azo dye by a Shewanella oneidensis MR-1 formed biocathode. International Biodeterioration and Biodegradation, 2016, 115, 250-256.	3.9	19
102	Structural changes in model compounds of sludge extracellular polymeric substances caused by exposure to free nitrous acid. Water Research, 2021, 188, 116553.	11.3	19
103	Characterisation of enhanced biological phosphorus removal activated sludges with dissimilar phosphorus removal performances. Water Science and Technology, 1998, 37, 567-571.	2.5	19
104	Bio-P and non-bio-P bacteria identification by a novel microbial approach. Water Science and Technology, 1999, 39, 13.	2.5	16
105	Characterisation of enhanced biological phosphorus removal activated sludges with dissimilar phosphorus removal performances. Water Science and Technology, 1998, 37, 567.	2.5	15
106	Characterizing the premise plumbing microbiome in both water and biofilms of a 50-year-old building. Science of the Total Environment, 2021, 798, 149225.	8.0	15
107	Characterization of an ATP-dependent DNA ligase from the acidophilic archaeon "Ferroplasma acidarmanus―Fer1. Extremophiles, 2007, 11, 315-327.	2.3	13
108	Data on metagenomic profiles of activated sludge from a full-scale wastewater treatment plant. Data in Brief, 2017, 15, 833-839.	1.0	13

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109	A comparative proteomic analysis of Desulfovibrio vulgaris Hildenborough in response to the antimicrobial agent free nitrous acid. Science of the Total Environment, 2019, 672, 625-633.	8.0	13
110	Reactive nitrogen species from free nitrous acid (FNA) cause cell lysis. Water Research, 2022, 217, 118401.	11.3	13
111	Further limitations of phylogenetic group-specific probes used for detection of bacteria in environmental samples. ISME Journal, 2010, 4, 959-961.	9.8	12
112	Periodic deprivation of gaseous hydrogen sulfide affects the activity of the concrete corrosion layer in sewers. Water Research, 2019, 157, 463-471.	11.3	12
113	Diversity of As Metabolism Functional Genes in Pb-Zn Mine Tailings. Pedosphere, 2017, 27, 630-637.	4.0	11
114	Synergistic effect on concrete corrosion control in sewer environment achieved by applying surface washing on calcium nitrite admixed concrete. Construction and Building Materials, 2021, 302, 124184.	7.2	11
115	Evidence of compositional differences between the extracellular and intracellular DNA of a granular sludge biofilm. Letters in Applied Microbiology, 2011, 53, 1-7.	2.2	10
116	Free sulfurous acid (FSA) inhibition of biological thiosulfate reduction (BTR) in the sulfur cycle-driven wastewater treatment process. Chemosphere, 2017, 176, 212-220.	8.2	10
117	Corrosion mitigation by nitrite spray on corroded concrete in a real sewer system. Science of the Total Environment, 2022, 806, 151328.	8.0	10
118	Evaluation of continuous and intermittent trickling strategies for the removal of hydrogen sulfide in a biotrickling filter. Chemosphere, 2022, 291, 132723.	8.2	10
119	Microbial community analysis during continuous fermentation of thermally hydrolysed waste activated sludge. Water Science and Technology, 2012, 65, 7-14.	2.5	9
120	Sequence-specific and DNA structure-dependent interactions of Escherichia coli MutS and human p53 with DNA. Analytical Biochemistry, 2013, 442, 51-61.	2.4	9
121	Improved degradation of anaerobically digested sludge during post aerobic digestion using ultrasonic pretreatment. Environmental Science: Water Research and Technology, 2017, 3, 857-864.	2.4	8
122	Bio-P and non-bio-P bacteria identification by a novel microbial approach. Water Science and Technology, 1999, 39, 13-20.	2.5	8
123	Molecular diversity of arbuscular mycorrhizal fungal communities across the gradient of alkaline Fe ore tailings, revegetated waste rock to natural soil sites. Environmental Science and Pollution Research, 2020, 27, 11968-11979.	5.3	7
124	Adaptive Evolution of Geobacter sulfurreducens in Coculture with Pseudomonas aeruginosa. MBio, 2020, 11, .	4.1	5
125	Enhanced Growth of Pilin-Deficient Geobacter sulfurreducens Mutants in Carbon Poor and Electron Donor Limiting Conditions. Microbial Ecology, 2019, 78, 618-630.	2.8	1
126	Engineering biological nitrogen removal in wastewater treatment via the control of nitrite oxidising bacteria using free nitrous acid. Microbiology Australia, 2018, 39, 47.	0.4	0