

Tomo Aoyagi

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

730
citations

566801

15
h-index

552369

26
g-index

42
all docs

42
docs citations

42
times ranked

911
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimal start-up conditions for the efficient treatment of acid mine drainage using sulfate-reducing bioreactors based on physicochemical and microbiome analyses. <i>Journal of Hazardous Materials</i> , 2022, 423, 127089.	6.5	15
2	Draft Genome Sequences of <i>Sulfurovum</i> spp. TSL1 and TSL6, Two Sulfur-Oxidizing Bacteria Isolated from Marine Sediment. <i>Microbiology Resource Announcements</i> , 2022, 11, e0092221.	0.3	3
3	Low nitrous oxide concentration and spatial microbial community transition across an urban river affected by treated sewage. <i>Water Research</i> , 2022, 216, 118276.	5.3	12
4	Evaluation of dye decolorization using anaerobic granular sludge from an expanded granular sludge bed based on spectrometric and microbiome analyses. <i>Journal of General and Applied Microbiology</i> , 2022, , .	0.4	0
5	Direct comparison of bacterial communities in soils contaminated with different levels of radioactive cesium from the first Fukushima nuclear power plant accident. <i>Science of the Total Environment</i> , 2021, 756, 143844.	3.9	12
6	Effective Se reduction by lactate-stimulated indigenous microbial communities in excavated waste rocks. <i>Journal of Hazardous Materials</i> , 2021, 403, 123908.	6.5	4
7	Comparative insights into genome signatures of ferric iron oxide- and anode-stimulated <i>Desulfuromonas</i> spp. strains. <i>BMC Genomics</i> , 2021, 22, 475.	1.2	9
8	Nitrate-Driven Trophic Association of Sulfur-Cycling Microorganisms in Tsunami-Deposited Marine Sediment Revealed by High-Sensitivity ¹³ C-Bicarbonate Probing. <i>Environmental Science & Technology</i> , 2021, 55, 8410-8421.	4.6	4
9	Efficient conversion of organic nitrogenous wastewater to nitrate solution driven by comammox <i>Nitrospira</i> . <i>Water Research</i> , 2021, 197, 117088.	5.3	19
10	Increase in sedimentary organic carbon with a change from hypoxic to oxic conditions. <i>Marine Pollution Bulletin</i> , 2021, 168, 112397.	2.3	2
11	Draft Genome Sequences of the Ferric Iron-Reducing <i>Geobacter</i> sp. Strains AOG1 and AOG2, Isolated from Enrichment Cultures on Crystalline Iron(III) Oxides. <i>Microbiology Resource Announcements</i> , 2021, 10, e0091321.	0.3	0
12	Long-term acclimatization of sludge microbiome for treatment of high-strength organic solid waste in anaerobic membrane bioreactor. <i>Biochemical Engineering Journal</i> , 2020, 154, 107461.	1.8	14
13	Transition of microbial community structures after development of membrane fouling in membrane bioreactors (MBRs). <i>AMB Express</i> , 2020, 10, 18.	1.4	5
14	Complete Genome Sequence of <i>Desulfuromonas</i> sp. Strain AOP6, an Iron(III) Reducer Isolated from Subseafloor Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
15	Design, application, and microbiome of sulfate-reducing bioreactors for treatment of mining-influenced water. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6893-6903.	1.7	20
16	Unexpected diversity of acetate degraders in anaerobic membrane bioreactor treating organic solid waste revealed by high-sensitivity stable isotope probing. <i>Water Research</i> , 2020, 176, 115750.	5.3	21
17	Clarifying prokaryotic and eukaryotic biofilm microbiomes in anaerobic membrane bioreactor by non-destructive microscopy and high-throughput sequencing. <i>Chemosphere</i> , 2020, 254, 126810.	4.2	8
18	Microbial community in an anaerobic membrane bioreactor and its performance in treating organic solid waste under controlled and deteriorated conditions. <i>Journal of Environmental Management</i> , 2020, 269, 110786.	3.8	18

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19	Activated sludge microbiome in a membrane bioreactor for treating Ramen noodle-soup wastewater. <i>Journal of General and Applied Microbiology</i> , 2020, 66, 339-343.	0.4	6
20	Activated sludge microbial communities of a chemical plant wastewater treatment facility with high-strength bromide ions and aromatic substances. <i>Journal of General and Applied Microbiology</i> , 2019, 65, 106-110.	0.4	7
21	<i>Desulfosporosinus</i> spp. were the most predominant sulfate-reducing bacteria in pilot- and laboratory-scale passive bioreactors for acid mine drainage treatment. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7783-7793.	1.7	29
22	Dead bacterial biomass-assimilating bacterial populations in compost revealed by high-sensitivity stable isotope probing. <i>Environment International</i> , 2019, 133, 105235.	4.8	8
23	Soil Microbial Communities Involved in Reductive Dissolution of Arsenic from Arsenate-Laden Minerals with Different Carbon Sources. <i>Environmental Science & Technology</i> , 2019, 53, 12398-12406.	4.6	21
24	Stratification of Sulfur Species and Microbial Community in Launched Marine Sediment by an Improved Sulfur-Fractionation Method and 16S rRNA Gene Sequencing. <i>Microbes and Environments</i> , 2019, 34, 199-205.	0.7	11
25	Draft Genome Sequence of a Novel Lactate-Fermenting Bacterial Strain of the Family <i>Sporomusaceae</i> within the Class <i>Negativicutes</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
26	Effects of the Wastewater Flow Rate on Interactions between the Genus <i>Nitrosomonas</i> and Diverse Populations in an Activated Sludge Microbiome. <i>Microbes and Environments</i> , 2019, 34, 89-94.	0.7	6
27	Nitrifiers activity and community characteristics under stress conditions in partial nitrification systems treating ammonium-rich wastewater. <i>Journal of Environmental Sciences</i> , 2018, 73, 1-8.	3.2	19
28	Eukaryotic Microbiomes of Membrane-Attached Biofilms in Membrane Bioreactors Analyzed by High-Throughput Sequencing and Microscopic Observations. <i>Microbes and Environments</i> , 2018, 33, 98-101.	0.7	14
29	Draft Genome Sequence of <i>Azospira</i> sp. Strain I13, a Nitrous Oxide-Reducing Bacterium Harboring Clade II Type <i>nosZ</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	6
30	Microbial community analysis of sulfate-reducing passive bioreactor for treating acid mine drainage under failure conditions after long-term continuous operation. <i>Journal of Environmental Chemical Engineering</i> , 2018, 6, 5795-5800.	3.3	15
31	Identification of active and taxonomically diverse 1,4-dioxane degraders in a full-scale activated sludge system by high-sensitivity stable isotope probing. <i>ISME Journal</i> , 2018, 12, 2376-2388.	4.4	42
32	Draft Genome Sequence of <i>Geobacter pelophilus</i> Strain Dfr2, a Ferric Iron-Reducing Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
33	Hydraulic retention time and pH affect the performance and microbial communities of passive bioreactors for treatment of acid mine drainage. <i>AMB Express</i> , 2017, 7, 142.	1.4	41
34	Sulfur-Oxidizing Bacteria Mediate Microbial Community Succession and Element Cycling in Launched Marine Sediment. <i>Frontiers in Microbiology</i> , 2017, 8, 152.	1.5	32
35	High and Rapid L-lactic Acid Production by Alkaliphilic <i>Enterococcus</i> sp. by Adding Wheat Bran Hydrolysate. <i>Fermentation Technology</i> , 2016, 06, .	0.1	2
36	Dynamic transition of chemolithotrophic sulfur-oxidizing bacteria in response to amendment with nitrate in deposited marine sediments. <i>Frontiers in Microbiology</i> , 2015, 6, 426.	1.5	32

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37	Survival of free-living <i>Acholeplasma</i> in aerated pig manure slurry revealed by ¹³ C-labeled bacterial biomass probing. <i>Frontiers in Microbiology</i> , 2015, 6, 1206.	1.5	15
38	Isolation of microorganisms involved in reduction of crystalline iron(III) oxides in natural environments. <i>Frontiers in Microbiology</i> , 2015, 6, 386.	1.5	104
39	High-Resolution Dynamics of Microbial Communities during Dissimilatory Selenate Reduction in Anoxic Soil. <i>Environmental Science & Technology</i> , 2015, 49, 7684-7691.	4.6	37
40	Ultra-high sensitivity stable isotope probing of <i>rRNA</i> by high-throughput sequencing of isopycnic centrifugation gradients. <i>Environmental Microbiology Reports</i> , 2015, 7, 282-287.	1.0	63
41	Biodegradation Potential of Organically Enriched Sediments under Sulfate- and Iron-Reducing Conditions as Revealed by the 16S <i>rRNA</i> Deep Sequencing. <i>Journal of Water and Environment Technology</i> , 2014, 12, 357-366.	0.3	19
42	A Fine-Scale Phylogenetic Analysis of Free-Living <i>Burkholderia</i> Species in Sugarcane Field Soil. <i>Microbes and Environments</i> , 2014, 29, 434-437.	0.7	24