

Helmut BÃ¼rgmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5101312/publications.pdf>

Version: 2024-02-01

77
papers

8,531
citations

101384

36
h-index

74018

75
g-index

83
all docs

83
docs citations

83
times ranked

11290
citing authors

#	ARTICLE	IF	CITATIONS
1	Wastewater bypass is a major temporary point-source of antibiotic resistance genes and multi-resistance risk factors in a Swiss river. <i>Water Research</i> , 2022, 208, 117827.	5.3	12
2	Successful mainstream nitritation through NOB inactivation. <i>Science of the Total Environment</i> , 2022, 822, 153546.	3.9	14
3	Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge. <i>Microbiome</i> , 2022, 10, 20.	4.9	52
4	Microbial Nitrogen Transformation Potential in Sediments of Two Contrasting Lakes Is Spatially Structured but Seasonally Stable. <i>MSphere</i> , 2022, 7, e0101321.	1.3	10
5	When rain overwhelms the sewers, antibiotic-resistant bacteria flood the river. , 2022, 3, .		0
6	Microeukaryotic gut parasites in wastewater treatment plants: diversity, activity, and removal. <i>Microbiome</i> , 2022, 10, 27.	4.9	15
7	Successful year-round mainstream partial nitritation anammox: Assessment of effluent quality, performance and N ₂ O emissions. <i>Water Research X</i> , 2022, 16, 100145.	2.8	28
8	Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. <i>Environmental Science & Technology</i> , 2022, 56, 14982-14993.	4.6	27
9	Temperature modulates stress response in mainstream anammox reactors. <i>Communications Biology</i> , 2021, 4, 23.	2.0	15
10	Nitrogen isotope effects can be used to diagnose N transformations in wastewater anammox systems. <i>Scientific Reports</i> , 2021, 11, 7850.	1.6	4
11	Linking seasonal N ₂ O emissions and nitrification failures to microbial dynamics in a SBR wastewater treatment plant. <i>Water Research X</i> , 2021, 11, 100098.	2.8	26
12	Unraveling the riverine antibiotic resistome: The downstream fate of anthropogenic inputs. <i>Water Research</i> , 2021, 197, 117050.	5.3	50
13	Distinct growth stages controlled by the interplay of deterministic and stochastic processes in functional anammox biofilms. <i>Water Research</i> , 2021, 200, 117225.	5.3	39
14	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 10862-10874.	4.6	60
15	Microbial methane oxidation efficiency and robustness during lake overturn. <i>Limnology and Oceanography Letters</i> , 2021, 6, 320-328.	1.6	11
16	Niche partitioning of methane-oxidizing bacteria along the oxygen-methane counter gradient of stratified lakes. <i>ISME Journal</i> , 2020, 14, 274-287.	4.4	63
17	A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. <i>Environment International</i> , 2020, 144, 106035.	4.8	55
18	Environmental and Microbial Interactions Shape Methane-Oxidizing Bacterial Communities in a Stratified Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 579427.	1.5	18

#	ARTICLE	IF	CITATIONS
19	Growth and rapid succession of methanotrophs effectively limit methane release during lake overturn. <i>Communications Biology</i> , 2020, 3, 108.	2.0	40
20	Every fifth published metagenome is not available to science. <i>PLoS Biology</i> , 2020, 18, e3000698.	2.6	18
21	Lake mixing regime selects apparent methane oxidation kinetics of the methanotroph assemblage. <i>Biogeosciences</i> , 2020, 17, 4247-4259.	1.3	12
22	Aerobic methane oxidation under copper scarcity in a stratified lake. <i>Scientific Reports</i> , 2019, 9, 4817.	1.6	20
23	Predator-induced changes in dissolved organic carbon dynamics. <i>Oikos</i> , 2019, 128, 430-440.	1.2	13
24	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes. <i>ISME Journal</i> , 2019, 13, 346-360.	4.4	289
25	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. <i>ISME Journal</i> , 2018, 12, 1344-1359.	4.4	84
26	Water and sanitation: an essential battlefront in the war on antimicrobial resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	104
27	A historical legacy of antibiotic utilization on bacterial seed banks in sediments. <i>PeerJ</i> , 2018, 6, e4197.	0.9	8
28	Dissemination of antibiotic resistance genes associated with the sporobiota in sediments impacted by wastewater. <i>PeerJ</i> , 2018, 6, e4989.	0.9	12
29	Growth of <i>Nitrosococcus</i> -Related Ammonia Oxidizing Bacteria Coincides with Extremely Low pH Values in Wastewater with High Ammonia Content. <i>Environmental Science & Technology</i> , 2017, 51, 6857-6866.	4.6	64
30	The effect of top-down predator presence and phenotype on aquatic microbial communities. <i>Ecology and Evolution</i> , 2017, 7, 1572-1582.	0.8	9
31	Strong impact of anthropogenic contamination on the occurrence patterns of a riverine microbial community. <i>Environmental Microbiology</i> , 2017, 19, 4993-5009.	1.8	213
32	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. <i>Environmental Science & Technology</i> , 2017, 51, 13061-13069.	4.6	236
33	Bacteria-induced mixing in natural waters. <i>Geophysical Research Letters</i> , 2017, 44, 9424-9432.	1.5	38
34	Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. <i>Frontiers in Microbiology</i> , 2016, 7, 214.	1.5	479
35	Inactivation of Antibiotic Resistant Bacteria and Resistance Genes by Ozone: From Laboratory Experiments to Full-Scale Wastewater Treatment. <i>Environmental Science & Technology</i> , 2016, 50, 11862-11871.	4.6	175
36	Hydrologic linkages drive spatial structuring of bacterial assemblages and functioning in alpine floodplains. <i>Frontiers in Microbiology</i> , 2015, 6, 1221.	1.5	21

#	ARTICLE	IF	CITATIONS
37	Does human activity impact the natural antibiotic resistance background? Abundance of antibiotic resistance genes in 21 Swiss lakes. <i>Environment International</i> , 2015, 81, 45-55.	4.8	209
38	Tackling antibiotic resistance: the environmental framework. <i>Nature Reviews Microbiology</i> , 2015, 13, 310-317.	13.6	1,612
39	Estimating Bacterial Diversity for Ecological Studies: Methods, Metrics, and Assumptions. <i>PLoS ONE</i> , 2015, 10, e0125356.	1.1	89
40	Spatio-Temporal Patterns of Major Bacterial Groups in Alpine Waters. <i>PLoS ONE</i> , 2014, 9, e113524.	1.1	17
41	Physical Extraction of Microorganisms From Water-Saturated, Packed Sediment. <i>Water Environment Research</i> , 2014, 86, 407-416.	1.3	1
42	In-situ Sonication for Enhanced Recovery of Aquifer Microbial Communities. <i>Ground Water</i> , 2014, 52, 737-747.	0.7	6
43	Early diagenetic processes generate iron and manganese oxide layers in the sediments of Lake Baikal, Siberia. <i>Environmental Sciences: Processes and Impacts</i> , 2014, 16, 879-889.	1.7	37
44	Wastewater as a point source of antibiotic-resistance genes in the sediment of a freshwater lake. <i>ISME Journal</i> , 2014, 8, 1381-1390.	4.4	354
45	Bacterial structures and ecosystem functions in glaciated floodplains: contemporary states and potential future shifts. <i>ISME Journal</i> , 2013, 7, 2361-2373.	4.4	49
46	Chemical Extraction of Microorganisms from Water-Saturated, Packed Sediment. <i>Water Environment Research</i> , 2013, 85, 503-513.	1.3	4
47	A brief multi-disciplinary review on antimicrobial resistance in medicine and its linkage to the global environmental microbiota. <i>Frontiers in Microbiology</i> , 2013, 4, 96.	1.5	246
48	Response of lotic microbial communities to altered water source and nutritional state in a glaciated alpine floodplain. <i>Limnology and Oceanography</i> , 2013, 58, 951-965.	1.6	17
49	Impact of particulate organic matter composition and degradation state on the vertical structure of particle-associated and planktonic lacustrine bacteria. <i>Aquatic Microbial Ecology</i> , 2013, 69, 81-92.	0.9	7
50	Increased Levels of Multiresistant Bacteria and Resistance Genes after Wastewater Treatment and Their Dissemination into Lake Geneva, Switzerland. <i>Frontiers in Microbiology</i> , 2012, 3, 106.	1.5	314
51	Fundamentals of Microbial Community Resistance and Resilience. <i>Frontiers in Microbiology</i> , 2012, 3, 417.	1.5	1,131
52	Contribution of bacterial cells to lacustrine organic matter based on amino sugars and d-amino acids. <i>Geochimica Et Cosmochimica Acta</i> , 2012, 89, 159-172.	1.6	26
53	Simple Absolute Quantification Method Correcting for Quantitative PCR Efficiency Variations for Microbial Community Samples. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4481-4489.	1.4	179
54	Bacterial Chitin Hydrolysis in Two Lakes with Contrasting Trophic Statuses. <i>Applied and Environmental Microbiology</i> , 2012, 78, 695-704.	1.4	23

#	ARTICLE	IF	CITATIONS
55	Local Conditions Structure Unique Archaeal Communities in the Anoxic Sediments of Meromictic Lake Kivu. <i>Microbial Ecology</i> , 2012, 64, 291-310.	1.4	34
56	Response of sediment microbial community structure in a freshwater reservoir to manipulations in oxygen availability. <i>FEMS Microbiology Ecology</i> , 2012, 80, 248-263.	1.3	23
57	Methane Formation and Future Extraction in Lake Kivu. , 2012, , 165-180.		13
58	Methane sources and sinks in Lake Kivu. <i>Journal of Geophysical Research</i> , 2011, 116, .	3.3	96
59	Analysis of sulfur-related transcription by <i>Roseobacter</i> communities using a taxon-specific functional gene microarray. <i>Environmental Microbiology</i> , 2011, 13, 453-467.	1.8	22
60	Regime Shift and Microbial Dynamics in a Sequencing Batch Reactor for Nitrification and Anammox Treatment of Urine. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5897-5907.	1.4	75
61	Changes in Dimethylsulfoniopropionate Demethylase Gene Assemblages in Response to an Induced Phytoplankton Bloom. <i>Applied and Environmental Microbiology</i> , 2011, 77, 524-531.	1.4	45
62	Methane Oxidation (Aerobic). <i>Encyclopedia of Earth Sciences Series</i> , 2011, , 575-578.	0.1	11
63	High Diversity of Diazotrophs in the Forefield of a Receding Alpine Glacier. <i>Microbial Ecology</i> , 2009, 57, 179-190.	1.4	124
64	Microbial communities in contrasting freshwater marsh microhabitats. <i>FEMS Microbiology Ecology</i> , 2009, 69, 84-97.	1.3	33
65	Large iron isotope fractionation at the oxic-anoxic boundary in Lake Nyos. <i>Earth and Planetary Science Letters</i> , 2009, 285, 52-60.	1.8	70
66	Progress in the Ecological Genetics and Biodiversity of Freshwater Bacteria. <i>BioScience</i> , 2008, 58, 103-113.	2.2	33
67	Detection and Quantification of <i>Dehalococcoides</i> -Related Bacteria in a Chlorinated Ethene-Contaminated Aquifer Undergoing Natural Attenuation. <i>Bioremediation Journal</i> , 2008, 12, 193-209.	1.0	6
68	Transcriptional response of <i>Silicibacter pomeroyi</i> DSS-3 to dimethylsulfoniopropionate (DMSP). <i>Environmental Microbiology</i> , 2007, 9, 2742-2755.	1.8	54
69	Effects of pioneering plants on microbial structures and functions in a glacier forefield. <i>Biology and Fertility of Soils</i> , 2007, 44, 289-297.	2.3	56
70	Variation in Microbial Community Composition and Culturability in the Rhizosphere of <i>Leucanthemopsis alpina</i> (L.) Heywood and Adjacent Bare Soil Along an Alpine Chronosequence. <i>Microbial Ecology</i> , 2006, 52, 679-692.	1.4	66
71	Bacterial Taxa That Limit Sulfur Flux from the Ocean. <i>Science</i> , 2006, 314, 649-652.	6.0	296
72	Effects of model root exudates on structure and activity of a soil diazotroph community. <i>Environmental Microbiology</i> , 2005, 7, 1711-1724.	1.8	166

#	ARTICLE	IF	CITATIONS
73	New Molecular Screening Tools for Analysis of Free-Living Diazotrophs in Soil. <i>Applied and Environmental Microbiology</i> , 2004, 70, 240-247.	1.4	138
74	Endophytic nifH gene diversity in African sweet potato. <i>Canadian Journal of Microbiology</i> , 2003, 49, 549-555.	0.8	87
75	mRNA Extraction and Reverse Transcription-PCR Protocol for Detection of nifH Gene Expression by <i>Azotobacter vinelandii</i> in Soil. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1928-1935.	1.4	148
76	A strategy for optimizing quality and quantity of DNA extracted from soil. <i>Journal of Microbiological Methods</i> , 2001, 45, 7-20.	0.7	260
77	Trait-Based Model Reproduces Patterns of Population Structure and Diversity of Methane Oxidizing Bacteria in a Stratified Lake. <i>Frontiers in Environmental Science</i> , 0, 10, .	1.5	1