Helmut Brgmann

List of Publications by Citations

76 papers	5,804 citations	32 h-index	76 g-index
83 ext. papers	7,325 ext. citations	7 avg, IF	5.55 L-index

#	Paper	IF	Citations
76	Tackling antibiotic resistance: the environmental framework. *Nature Reviews Microbiology*, **2015**, 13, 310-7	22.2	1092
75	Fundamentals of microbial community resistance and resilience. *Frontiers in Microbiology*, **2012**, 3, 417	5.7	759
74	Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. *Frontiers in Microbiology*, **2016**, 7, 214	5.7	321
73	Wastewater as a point source of antibiotic-resistance genes in the sediment of a freshwater lake. *ISME Journal*, **2014**, 8, 1381-90	11.9	269
72	Increased levels of multiresistant bacteria and resistance genes after wastewater treatment and their dissemination into lake geneva, Switzerland. *Frontiers in Microbiology*, **2012**, 3, 106	5.7	249
71	Bacterial taxa that limit sulfur flux from the ocean. *Science*, **2006**, 314, 649-52	33.3	247
70	A strategy for optimizing quality and quantity of DNA extracted from soil. *Journal of Microbiological Methods*, **2001**, 45, 7-20	2.8	221
69	A brief multi-disciplinary review on antimicrobial resistance in medicine and its linkage to the global environmental microbiota. *Frontiers in Microbiology*, **2013**, 4, 96	5.7	189
68	Does human activity impact the natural antibiotic resistance background? Abundance of antibiotic resistance genes in 21 Swiss lakes. *Environment International*, **2015**, 81, 45-55	12.9	145
67	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. *Environmental Science & Technology*, **2017**, 51, 13061-13069	10.3	144
66	Effects of model root exudates on structure and activity of a soil diazotroph community. *Environmental Microbiology*, **2005**, 7, 1711-24	5.2	140
65	mRNA extraction and reverse transcription-PCR protocol for detection of nifH gene expression by Azotobacter vinelandii in soil. *Applied and Environmental Microbiology*, **2003**, 69, 1928-35	4.8	138
64	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes. *ISME Journal*, **2019**, 13, 346-360	11.9	135
63	Simple absolute quantification method correcting for quantitative PCR efficiency variations for microbial community samples. *Applied and Environmental Microbiology*, **2012**, 78, 4481-9	4.8	126
62	Inactivation of Antibiotic Resistant Bacteria and Resistance Genes by Ozone: From Laboratory Experiments to Full-Scale Wastewater Treatment. *Environmental Science & Technology*, **2016**, 50, 11862-11871	10.3	123
61	New molecular screening tools for analysis of free-living diazotrophs in soil. *Applied and Environmental Microbiology*, **2004**, 70, 240-7	4.8	123
60	Strong impact of anthropogenic contamination on the co-occurrence patterns of a riverine microbial community. *Environmental Microbiology*, **2017**, 19, 4993-5009	5.2	110

59	High diversity of diazotrophs in the forefield of a receding alpine glacier. *Microbial Ecology*, **2009**, 57, 179-90	4.4	110
58	Endophytic nifH gene diversity in African sweet potato. *Canadian Journal of Microbiology*, **2003**, 49, 549-55	3.2	70
57	Methane sources and sinks in Lake Kivu. *Journal of Geophysical Research*, **2011**, 116,		68
56	Large iron isotope fractionation at the oxic–anoxic boundary in Lake Nyos. *Earth and Planetary Science Letters*, **2009**, 285, 52-60	5.3	65
55	Water and sanitation: an essential battlefront in the war on antimicrobial resistance. *FEMS Microbiology Ecology*, **2018**, 94,	4.3	64
54	Regime shift and microbial dynamics in a sequencing batch reactor for nitrification and anammox treatment of urine. *Applied and Environmental Microbiology*, **2011**, 77, 5897-907	4.8	64
53	Variation in microbial community composition and culturability in the rhizosphere of Leucanthemopsis alpina (L.) Heywood and adjacent bare soil along an alpine chronosequence. *Microbial Ecology*, **2006**, 52, 679-92	4.4	57
52	Estimating bacterial diversity for ecological studies: methods, metrics, and assumptions. *PLoS ONE*, **2015**, 10, e0125356	3.7	55
51	Effects of pioneering plants on microbial structures and functions in a glacier forefield. *Biology and Fertility of Soils*, **2007**, 44, 289-297	6.1	51
50	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. *ISME Journal*, **2018**, 12, 1344-1359	11.9	47
49	Transcriptional response of Silicibacter pomeroyi DSS-3 to dimethylsulfoniopropionate (DMSP). *Environmental Microbiology*, **2007**, 9, 2742-55	5.2	47
48	Growth of Nitrosococcus-Related Ammonia Oxidizing Bacteria Coincides with Extremely Low pH Values in Wastewater with High Ammonia Content. *Environmental Science & Technology*, **2017**, 51, 6857-6866	10.3	36
47	Bacterial structures and ecosystem functions in glaciated floodplains: contemporary states and potential future shifts. *ISME Journal*, **2013**, 7, 2361-73	11.9	35
46	Changes in dimethylsulfoniopropionate demethylase gene assemblages in response to an induced phytoplankton bloom. *Applied and Environmental Microbiology*, **2011**, 77, 524-31	4.8	35
45	Local conditions structure unique archaeal communities in the anoxic sediments of meromictic Lake Kivu. *Microbial Ecology*, **2012**, 64, 291-310	4.4	33
44	Microbial communities in contrasting freshwater marsh microhabitats. *FEMS Microbiology Ecology*, **2009**, 69, 84-97	4.3	31
43	Early diagenetic processes generate iron and manganese oxide layers in the sediments of Lake Baikal, Siberia. *Environmental Sciences: Processes and Impacts*, **2014**, 16, 879-89	4.3	27
42	Progress in the Ecological Genetics and Biodiversity of Freshwater Bacteria. *BioScience*, **2008**, 58, 103-113	3.7	26

41	Bacteria-induced mixing in natural waters. *Geophysical Research Letters*, **2017**, 44, 9424-9432	4.9	24
40	Niche partitioning of methane-oxidizing bacteria along the oxygen-methane counter gradient of stratified lakes. *ISME Journal*, **2020**, 14, 274-287	11.9	22
39	Analysis of sulfur-related transcription by Roseobacter communities using a taxon-specific functional gene microarray. *Environmental Microbiology*, **2011**, 13, 453-67	5.2	21
38	Growth and rapid succession of methanotrophs effectively limit methane release during lake overturn. *Communications Biology*, **2020**, 3, 108	6.7	20
37	Response of sediment microbial community structure in a freshwater reservoir to manipulations in oxygen availability. *FEMS Microbiology Ecology*, **2012**, 80, 248-63	4.3	19
36	Contribution of bacterial cells to lacustrine organic matter based on amino sugars and d-amino acids. *Geochimica Et Cosmochimica Acta*, **2012**, 89, 159-172	5.5	18
35	A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. *Environment International*, **2020**, 144, 106035	12.9	17
34	Hydrologic linkages drive spatial structuring of bacterial assemblages and functioning in alpine floodplains. *Frontiers in Microbiology*, **2015**, 6, 1221	5.7	16
33	Bacterial chitin hydrolysis in two lakes with contrasting trophic statuses. *Applied and Environmental Microbiology*, **2012**, 78, 695-704	4.8	16
32	Response of lotic microbial communities to altered water source and nutritional state in a glaciated alpine floodplain. *Limnology and Oceanography*, **2013**, 58, 951-965	4.8	15
31	Methane Formation and Future Extraction in Lake Kivu **2012**, 165-180		12
30	Aerobic methane oxidation under copper scarcity in a stratified lake. *Scientific Reports*, **2019**, 9, 4817	4.9	11
29	Spatio-temporal patterns of major bacterial groups in alpine waters. *PLoS ONE*, **2014**, 9, e113524	3.7	11
28	Unraveling the riverine antibiotic resistome: The downstream fate of anthropogenic inputs. *Water Research*, **2021**, 197, 117050	12.5	9
27	Distinct growth stages controlled by the interplay of deterministic and stochastic processes in functional anammox biofilms. *Water Research*, **2021**, 200, 117225	12.5	9
26	Predator-induced changes in dissolved organic carbon dynamics. *Oikos*, **2019**, 128, 430-440	4	9
25	Every fifth published metagenome is not available to science. *PLoS Biology*, **2020**, 18, e3000698	9.7	9
24	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. *Environmental Science & Technology*, **2021**, 55, 10862-10874	10.3	8

23	The effect of top-predator presence and phenotype on aquatic microbial communities. *Ecology and Evolution*, **2017**, 7, 1572-1582	2.8	7
22	Dissemination of antibiotic resistance genes associated with the sporobiota in sediments impacted by wastewater. *PeerJ*, **2018**, 6, e4989	3.1	7
21	In-situ sonication for enhanced recovery of aquifer microbial communities. *Ground Water*, **2014**, 52, 737-47	2.4	6
20	Linking seasonal NO emissions and nitrification failures to microbial dynamics in a SBR wastewater treatment plant. *Water Research X*, **2021**, 11, 100098	8.1	6
19	Temperature modulates stress response in mainstream anammox reactors. *Communications Biology* , **2021**, 4, 23	6.7	6
18	Detection and Quantification of Dehalococcoides-Related Bacteria in a Chlorinated Ethene-Contaminated Aquifer Undergoing Natural Attenuation. *Bioremediation Journal*, **2008**, 12, 193-209	2.3	5
17	Impact of particulate organic matter composition and degradation state on the vertical structure of particle-associated and planktonic lacustrine bacteria. *Aquatic Microbial Ecology*, **2013**, 69, 81-92	1.1	5
16	A historical legacy of antibiotic utilization on bacterial seed banks in sediments. *PeerJ*, **2018**, 6, e4197	3.1	5
15	Lake overturn as a key driver for methane oxidation		5
14	Environmental and Microbial Interactions Shape Methane-Oxidizing Bacterial Communities in a Stratified Lake. *Frontiers in Microbiology*, **2020**, 11, 579427	5.7	5
13	Lake mixing regime selects apparent methane oxidation kinetics of the methanotroph assemblage. *Biogeosciences*, **2020**, 17, 4247-4259	4.6	4
12	Chemical extraction of microorganisms from water-saturated, packed sediment. *Water Environment Research*, **2013**, 85, 503-13	2.8	3
11	Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge.. *Microbiome*, **2022**, 10, 20	16.6	2
10	Microbial methane oxidation efficiency and robustness during lake overturn. *Limnology and Oceanography Letters*, **2021**, 6, 320	7.9	2
9	Wastewater bypass is a major temporary point-source of antibiotic resistance genes and multi-resistance risk factors in a Swiss river. *Water Research*, **2022**, 208, 117827	12.5	2
8	Physical extraction of microorganisms from water-saturated, packed sediment. *Water Environment Research*, **2014**, 86, 407-16	2.8	1
7	Successful mainstream nitritation through NOB inactivation.. *Science of the Total Environment*, **2022** , 822, 153546	10.2	1
6	Microbial Nitrogen Transformation Potential in Sediments of Two Contrasting Lakes Is Spatially Structured but Seasonally Stable.. *MSphere*, **2022**, e0101321	5	1

5	Growth and rapid succession of methanotrophs effectively limit methane release during lake overturn		1
4	Nitrogen isotope effects can be used to diagnose N transformations in wastewater anammox systems. *Scientific Reports*, **2021**, 11, 7850	4.9	1
3	Wastewater Based Epidemiology Enabled Surveillance of Antibiotic Resistance		1
2	Microeukaryotic gut parasites in wastewater treatment plants: diversity, activity, and removal.. *Microbiome*, **2022**, 10, 27	16.6	0
1	Eintrag von Antibiotika und Antibiotikaresistenzen in Wassersysteme der Schweiz. *Pravention Und Gesundheitsforderung*, **2014**, 9, 185-190	0.5	