

# Ester M Eckert

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47  
papers

1,277  
citations

19  
h-index

35  
g-index

49  
ext. papers

1,810  
ext. citations

6.8  
avg. IF

4.84  
L-index

#	Paper	IF	Citations
47	Co-occurrence of integrase 1, antibiotic and heavy metal resistance genes in municipal wastewater treatment plants. <i>Water Research</i> , <b>2016</b> , 94, 208-214	12.5	270
46	Microplastics increase impact of treated wastewater on freshwater microbial community. <i>Environmental Pollution</i> , <b>2018</b> , 234, 495-502	9.3	132
45	Rapid successions affect microbial N-acetyl-glucosamine uptake patterns during a lacustrine spring phytoplankton bloom. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 794-806	5.2	74
44	Rainfall increases the abundance of antibiotic resistance genes within a riverine microbial community. <i>Environmental Pollution</i> , <b>2017</b> , 226, 473-478	9.3	63
43	Constitutive presence of antibiotic resistance genes within the bacterial community of a large subalpine lake. <i>Molecular Ecology</i> , <b>2015</b> , 24, 3888-900	5.7	63
42	Co-selection of antibiotic and heavy metal resistance in freshwater bacteria. <i>Journal of Limnology</i> , <b>2016</b> , 75,	1.5	55
41	Assessing the Influence of Vegan, Vegetarian and Omnivore Oriented Westernized Dietary Styles on Human Gut Microbiota: A Cross Sectional Study. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 317	5.7	52
40	Effluents of wastewater treatment plants promote the rapid stabilization of the antibiotic resistome in receiving freshwater bodies. <i>Water Research</i> , <b>2019</b> , 158, 72-81	12.5	50
39	Bacterial epibionts of Daphnia: a potential route for the transfer of dissolved organic carbon in freshwater food webs. <i>ISME Journal</i> , <b>2014</b> , 8, 1808-19	11.9	49
38	Network of Interactions Between Ciliates and Phytoplankton During Spring. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1289	5.7	37
37	Impact of industrial wastewater on the dynamics of antibiotic resistance genes in a full-scale urban wastewater treatment plant. <i>Science of the Total Environment</i> , <b>2019</b> , 646, 1204-1210	10.2	32
36	The role of metal contamination in shaping microbial communities in heavily polluted marine sediments. <i>Environmental Pollution</i> , <b>2020</b> , 265, 114823	9.3	31
35	Persistence of antibiotic resistance genes in large subalpine lakes: the role of anthropogenic pollution and ecological interactions. <i>Hydrobiologia</i> , <b>2018</b> , 824, 93-108	2.4	28
34	Daphnia as a refuge for an antibiotic resistance gene in an experimental freshwater community. <i>Science of the Total Environment</i> , <b>2016</b> , 571, 77-81	10.2	28
33	Grazing resistant freshwater bacteria profit from chitin and cell-wall-derived organic carbon. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 2019-30	5.2	28
32	Antibiotic disturbance affects aquatic microbial community composition and food web interactions but not community resilience. <i>Molecular Ecology</i> , <b>2019</b> , 28, 1170-1182	5.7	23
31	High-quality treated wastewater causes remarkable changes in natural microbial communities and int11 gene abundance. <i>Water Research</i> , <b>2019</b> , 167, 114895	12.5	23

30	Defence strategies and antibiotic resistance gene abundance in enterococci under stress by exposure to low doses of peracetic acid. <i>Chemosphere</i> , <b>2017</b> , 185, 480-488	8.4	23
29	Tracing particulate matter and associated microorganisms in freshwaters. <i>Hydrobiologia</i> , <b>2017</b> , 800, 145-154	15.4	21
28	The mesopelagic anoxic Black Sea as an unexpected habitat for <i>Synechococcus</i> challenges our understanding of global "deep red fluorescence". <i>ISME Journal</i> , <b>2019</b> , 13, 1676-1687	11.9	17
27	Combination of flow cytometry and molecular analysis to monitor the effect of UVC/HO vs UVC/HO/Cu-IDS processes on pathogens and antibiotic resistant genes in secondary wastewater effluents. <i>Water Research</i> , <b>2020</b> , 184, 116194	12.5	16
26	Diverse distribution of Toxin-Antitoxin II systems in <i>Salmonella enterica</i> serovars. <i>Scientific Reports</i> , <b>2016</b> , 6, 28759	4.9	16
25	Contribution of microplastic particles to the spread of resistances and pathogenic bacteria in treated wastewaters. <i>Water Research</i> , <b>2021</b> , 201, 117368	12.5	15
24	Human access impacts biodiversity of microscopic animals in sandy beaches. <i>Communications Biology</i> , <b>2020</b> , 3, 175	6.7	14
23	Does a barcoding gap exist in prokaryotes? Evidences from species delimitation in cyanobacteria. <i>Life</i> , <b>2014</b> , 5, 50-64	3	13
22	Assessing antimicrobial resistance gene load in vegan, vegetarian and omnivore human gut microbiota. <i>International Journal of Antimicrobial Agents</i> , <b>2018</b> , 52, 702-705	14.3	11
21	ddPCR applied on archived Continuous Plankton Recorder samples reveals long-term occurrence of class 1 integrons and a sulphonamide resistance gene in marine plankton communities. <i>Environmental Microbiology Reports</i> , <b>2018</b> , 10, 458-464	3.7	10
20	The microbiome associated with two <i>Synechococcus</i> ribotypes at different levels of ecological interaction. <i>Journal of Phycology</i> , <b>2017</b> , 53, 1151-1158	3	10
19	Archaea and Bacteria in deep lake hypolimnion: in situ dark inorganic carbon uptake. <i>Journal of Limnology</i> , <b>2014</b> , 73,	1.5	10
18	Spatial distribution of antibiotic and heavy metal resistance genes in the Black Sea. <i>Marine Pollution Bulletin</i> , <b>2020</b> , 160, 111635	6.7	9
17	Every fifth published metagenome is not available to science. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000698	9.7	9
16	Freshwater zooplankton microbiome composition is highly flexible and strongly influenced by the environment. <i>Molecular Ecology</i> , <b>2021</b> , 30, 1545-1558	5.7	8
15	Different substrates within a lake harbour connected but specialised microbial communities. <i>Hydrobiologia</i> , <b>2020</b> , 847, 1689-1704	2.4	6
14	An Environmental Strain Is Naturally Competent to Acquire Exogenous DNA. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 574301	5.7	6
13	Comparative phylogeography reveals consistently shallow genetic diversity in a mitochondrial marker in Antarctic bdelloid rotifers. <i>Journal of Biogeography</i> , <b>2021</b> , 48, 1797-1809	4.1	6

12	Genomic Comparison and Spatial Distribution of Different Phylotypes in the Black Sea. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1979	5.7	5
11	The vertical distribution of tetA and intI1 in a deep lake is rather due to sedimentation than to resuspension. <i>FEMS Microbiology Ecology</i> , <b>2020</b> , 96,	4.3	4
10	Seasonality of the antibiotic resistance gene blaCTX-M in temperate Lake Maggiore. <i>Hydrobiologia</i> , <b>2019</b> , 843, 143-153	2.4	3
9	Tossed Wood luckWoins as vectors for anthropogenic pollution into aquatic environment. <i>Environmental Pollution</i> , <b>2020</b> , 259, 113800	9.3	2
8	PET particles raise microbiological concerns for human health while tyre wear microplastic particles potentially affect ecosystem services in waters.. <i>Journal of Hazardous Materials</i> , <b>2022</b> , 429, 128397	12.8	1
7	Lanzarote and Chinijo Islands: An Anchialine UNESCO Global Geopark. <i>Volcanic Tourist Destinations</i> , <b>2019</b> , 109-121	0.1	1
6	Antarctic coastal nanoplankton dynamics revealed by metabarcoding of desalination plant filters: Detection of short-term events and implications for routine monitoring. <i>Science of the Total Environment</i> , <b>2021</b> , 757, 143809	10.2	1
5	The ZVI-Fenton process affects the total load of human pathogenic bacteria in wastewater samples. <i>Journal of Water Process Engineering</i> , <b>2022</b> , 47, 102668	6.7	1
4	Zooplankton as a Transitional Host for in Freshwater.. <i>Applied and Environmental Microbiology</i> , <b>2022</b> , e0252221	4.8	1
3	Contribution of plasmidome, metal resistome and integrases to the persistence of the antibiotic resistome in aquatic environments.. <i>Environmental Pollution</i> , <b>2021</b> , 118774	9.3	0
2	First Record of the Phylum Gnathostomulida in the Southern Ocean. <i>Diversity</i> , <b>2022</b> , 14, 382	2.5	
1	A Metabarcoding Protocol to Analyze Coastal Planktic Communities Collected by Desalination Plant Filters: From Sampling to Bioinformatic Exploratory Analyses. <i>Methods in Molecular Biology</i> , <b>2022</b> , 151-176	1.4	