

Antti Valter Karkman

List of Publications by Year in descending order

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33
papers

4,063
citations

279701

23
h-index

395590

33
g-index

36
all docs

36
docs citations

36
times ranked

5373
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic-Resistance Genes in Waste Water. Trends in Microbiology, 2018, 26, 220-228.	3.5	627
2	Fecal pollution can explain antibiotic resistance gene abundances in anthropogenically impacted environments. Nature Communications, 2019, 10, 80.	5.8	378
3	Community-led, integrated, reproducible multi-omics with anvio™. Nature Microbiology, 2021, 6, 3-6.	5.9	370
4	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. Science Advances, 2019, 5, eaau9124.	4.7	346
5	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. Nature Communications, 2018, 9, 3891.	5.8	313
6	Tetracycline Resistance Genes Persist at Aquaculture Farms in the Absence of Selection Pressure. Environmental Science & Technology, 2011, 45, 386-391.	4.6	273
7	High-throughput quantification of antibiotic resistance genes from an urban wastewater treatment plant. FEMS Microbiology Ecology, 2016, 92, fiw014.	1.3	167
8	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. FEMS Microbiology Ecology, 2018, 94, .	1.3	148
9	Abundances of Tetracycline, Sulphonamide and Beta-Lactam Antibiotic Resistance Genes in Conventional Wastewater Treatment Plants (WWTPs) with Different Waste Load. PLoS ONE, 2014, 9, e103705.	1.1	144
10	Aquaculture changes the profile of antibiotic resistance and mobile genetic element associated genes in Baltic Sea sediments. FEMS Microbiology Ecology, 2016, 92, fiw052.	1.3	142
11	Influence of Manure Application on the Environmental Resistome under Finnish Agricultural Practice with Restricted Antibiotic Use. Environmental Science & Technology, 2017, 51, 5989-5999.	4.6	142
12	Seasonality of antibiotic prescriptions for outpatients and resistance genes in sewers and wastewater treatment plant outflow. FEMS Microbiology Ecology, 2016, 92, fiw060.	1.3	124
13	Sulphonamide and Trimethoprim Resistance Genes Persist in Sediments at Baltic Sea Aquaculture Farms but Are Not Detected in the Surrounding Environment. PLoS ONE, 2014, 9, e92702.	1.1	108
14	Significant disparities in allergy prevalence and microbiota between the young people in Finnish and Russian Karelia. Clinical and Experimental Allergy, 2017, 47, 665-674.	1.4	97
15	Patterns in the skin microbiota differ in children and teenagers between rural and urban environments. Scientific Reports, 2017, 7, 45651.	1.6	93
16	The ecology of human microbiota: dynamics and diversity in health and disease. Annals of the New York Academy of Sciences, 2017, 1399, 78-92.	1.8	88
17	“Every Gene Is Everywhere but the Environment Selects” Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. Genome Biology and Evolution, 2016, 8, 1388-1400.	1.1	82
18	Differences in bacterial community composition in Baltic Sea sediment in response to fish farming. Aquaculture, 2011, 313, 15-23.	1.7	51

#	ARTICLE	IF	CITATIONS
19	Cold temperature decreases bacterial species richness in nitrogen-removing bioreactors treating inorganic mine waters. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2876-2883.	1.7	51
20	Evaluating the mobility potential of antibiotic resistance genes in environmental resistomes without metagenomics. <i>Scientific Reports</i> , 2016, 6, 35790.	1.6	46
21	Long-term application of Swedish sewage sludge on farmland does not cause clear changes in the soil bacterial resistome. <i>Environment International</i> , 2020, 137, 105339.	4.8	38
22	Predicting clinical resistance prevalence using sewage metagenomic data. <i>Communications Biology</i> , 2020, 3, 711.	2.0	37
23	Holistic View on Health: Two Protective Layers of Biodiversity. <i>Annales Zoologici Fennici</i> , 2017, 54, 39-49.	0.2	35
24	<i>Enterococcus rivorum</i> sp. nov., from water of pristine brooks. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2169-2173.	0.8	22
25	Discovery of bacterial polyhydroxyalkanoate synthase (PhaC)-encoding genes from seasonal Baltic Sea ice and cold estuarine waters. <i>Extremophiles</i> , 2015, 19, 197-206.	0.9	21
26	Immune-microbiota interaction in Finnish and Russian Karelia young people with high and low allergy prevalence. <i>Clinical and Experimental Allergy</i> , 2020, 50, 1148-1158.	1.4	19
27	An active bacterial community linked to high chl- <i>a</i> concentrations in Antarctic winter-pack ice and evidence for the development of an anaerobic sea-ice bacterial community. <i>ISME Journal</i> , 2017, 11, 2345-2355.	4.4	16
28	Contrasting microbiotas between Finnish and Estonian infants: Exposure to <i>Acinetobacter</i> may contribute to the allergy gap. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2342-2351.	2.7	16
29	Cyanobacteria as a Source for Novel Anti-Leukemic Compounds. <i>Current Pharmaceutical Biotechnology</i> , 2015, 17, 78-91.	0.9	15
30	Nature-oriented daycare diversifies skin microbiota in children—No robust association with allergies. <i>Pediatric Allergy and Immunology</i> , 2018, 29, 318-321.	1.1	13
31	Fish Farming Affects the Abundance and Diversity of the Mercury Resistance Gene <i>merA</i> in Marine Sediments. <i>Microbes and Environments</i> , 2011, 26, 205-211.	0.7	11
32	Bacterial communities in Arctic first-year drift ice during the winter/spring transition. <i>Environmental Microbiology Reports</i> , 2016, 8, 527-535.	1.0	10
33	Interplay between skin microbiota and immunity in atopic individuals. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1280-1284.	2.7	5