

Antti Valter Karkman

List of Publications by Year in Descending Order

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Version: 2024-04-23

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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.

35
papers

2,327
citations

22
h-index

36
g-index

36
ext. papers

3,276
ext. citations

7.1
avg, IF

5.41
L-index

#	Paper	IF	Citations
35	Community-led, integrated, reproducible multi-omics with anvio. <i>Nature Microbiology</i> , 2021 , 6, 3-6	26.6	62
34	Interplay between skin microbiota and immunity in atopic individuals. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021 , 76, 1280-1284	9.3	2
33	Predicting clinical resistance prevalence using sewage metagenomic data. <i>Communications Biology</i> , 2020 , 3, 711	6.7	11
32	Contrasting microbiotas between Finnish and Estonian infants: Exposure to Acinetobacter may contribute to the allergy gap. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020 , 75, 2342-2351	9.3	17
31	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	12.9	22
30	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	4.1	9
29	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. <i>Science Advances</i> , 2019 , 5, eaau9124	14.3	184
28	Fecal pollution can explain antibiotic resistance gene abundances in anthropogenically impacted environments. <i>Nature Communications</i> , 2019 , 10, 80	17.4	195
27	Nature-oriented daycare diversifies skin microbiota in children-No robust association with allergies. <i>Pediatric Allergy and Immunology</i> , 2018 , 29, 318-321	4.2	8
26	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	82
25	Antibiotic-Resistance Genes in Waste Water. <i>Trends in Microbiology</i> , 2018 , 26, 220-228	12.4	354
24	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018 , 9, 3891	17.4	145
23	Significant disparities in allergy prevalence and microbiota between the young people in Finnish and Russian Karelia. <i>Clinical and Experimental Allergy</i> , 2017 , 47, 665-674	4.1	65
22	Influence of Manure Application on the Environmental Resistome under Finnish Agricultural Practice with Restricted Antibiotic Use. <i>Environmental Science & Technology</i> , 2017 , 51, 5989-5999	10.3	90
21	Patterns in the skin microbiota differ in children and teenagers between rural and urban environments. <i>Scientific Reports</i> , 2017 , 7, 45651	4.9	63
20	The ecology of human microbiota: dynamics and diversity in health and disease. <i>Annals of the New York Academy of Sciences</i> , 2017 , 1399, 78-92	6.5	65
19	High Throughput Method for Analyzing Antibiotic Resistance Genes in Wastewater Treatment Plants 2017 , 253-262		3

18	Holistic View on Health: Two Protective Layers of Biodiversity. <i>Annales Zoologici Fennici</i> , 2017 , 54, 39-49	0.9	24
17	An active bacterial community linked to high chl-a 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	11.9	10
16	Evaluating the mobility potential of antibiotic resistance genes in environmental resistomes without metagenomics. <i>Scientific Reports</i> , 2016 , 6, 35790	4.9	29
15	Aquaculture changes the profile of antibiotic resistance and mobile genetic element associated genes in Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2016 , 92, fiw052	4.3	93
14	High-throughput quantification of antibiotic resistance genes from an urban wastewater treatment plant. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	126
13	Cyanobacteria as a Source For Novel Anti-Leukemic Compounds. <i>Current Pharmaceutical Biotechnology</i> , 2016 , 17, 78-91	2.6	8
12	Bacterial communities in Arctic first-year drift ice during the winter/spring transition. <i>Environmental Microbiology Reports</i> , 2016 , 8, 527-35	3.7	8
11	"Every Gene Is Everywhere but the Environment Selects": Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. <i>Genome Biology and Evolution</i> , 2016 , 8, 1388-400	3.9	55
10	Seasonality of antibiotic prescriptions for outpatients and resistance genes in sewers and wastewater treatment plant outflow. <i>FEMS Microbiology Ecology</i> , 2016 , 92, fiw060	4.3	87
9	Discovery of bacterial polyhydroxyalkanoate synthase (PhaC)-encoding genes from seasonal Baltic Sea ice and cold estuarine waters. <i>Extremophiles</i> , 2015 , 19, 197-206	3	19
8	Abundances of tetracycline, sulphonamide and beta-lactam antibiotic resistance genes in conventional wastewater treatment plants (WWTPs) with different waste load. <i>PLoS ONE</i> , 2014 , 9, e103705	3.7	114
7	Sulphonamide and trimethoprim resistance genes persist in sediments at Baltic Sea aquaculture farms but are not detected in the surrounding environment. <i>PLoS ONE</i> , 2014 , 9, e92702	3.7	75
6	<i>Enterococcus rivorum</i> sp. nov., from water of pristine brooks. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012 , 62, 2169-2173	2.2	17
5	Differences in bacterial community composition in Baltic Sea sediment in response to fish farming. <i>Aquaculture</i> , 2011 , 313, 15-23	4.4	37
4	Tetracycline resistance genes persist at aquaculture farms in the absence of selection pressure. <i>Environmental Science & Technology</i> , 2011 , 45, 386-91	10.3	202
3	Fish farming affects the abundance and diversity of the mercury resistance gene merA in marine sediments. <i>Microbes and Environments</i> , 2011 , 26, 205-11	2.6	7
2	Cold temperature decreases bacterial species richness in nitrogen-removing bioreactors treating inorganic mine waters. <i>Biotechnology and Bioengineering</i> , 2011 , 108, 2876-83	4.9	46
1	Fecal pollution explains antibiotic resistance gene abundances in anthropogenically impacted environments		3

