

Patrick Munk

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1827184/publications.pdf>

Version: 2024-02-01

25
papers

2,109
citations

471509
17
h-index

552781
26
g-index

36
all docs

36
docs citations

36
times ranked

2904
citing authors

#	ARTICLE	IF	CITATIONS
1	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	12.8	612
2	Clades of huge phages from across Earth's ecosystems. Nature, 2020, 578, 425-431.	27.8	331
3	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908.	13.3	230
4	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. MSys, 2016, 1, .	3.8	153
5	Megaphages infect Prevotella and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700.	13.3	141
6	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. Journal of Antimicrobial Chemotherapy, 2017, 72, 385-392.	3.0	89
7	Farm dust resistomes and bacterial microbiomes in European poultry and pig farms. Environment International, 2020, 143, 105971.	10.0	66
8	The antimicrobial resistome in relation to antimicrobial use and biosecurity in pig farming, a metagenome-wide association study in nine European countries. Journal of Antimicrobial Chemotherapy, 2019, 74, 865-876.	3.0	63
9	Associations between antimicrobial use and the faecal resistome on broiler farms from nine European countries. Journal of Antimicrobial Chemotherapy, 2019, 74, 2596-2604.	3.0	49
10	Setting a baseline for global urban virome surveillance in sewage. Scientific Reports, 2020, 10, 13748.	3.3	39
11	Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers: A metagenome-wide cross-sectional study. Environment International, 2020, 143, 105939.	10.0	33
12	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. Communications Biology, 2020, 3, 155.	4.4	33
13	Genomic evolution of antimicrobial resistance in Escherichia coli. Scientific Reports, 2021, 11, 15108.	3.3	33
14	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. MBio, 2021, 12, e0052121.	4.1	30
15	Secrets of the Hospital Underbelly: Patterns of Abundance of Antimicrobial Resistance Genes in Hospital Wastewater Vary by Specific Antimicrobial and Bacterial Family. Frontiers in Microbiology, 2021, 12, 703560.	3.5	26
16	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	2.5	24
17	Extended-spectrum beta-lactamase-producing Escherichia coli and antimicrobial resistance in municipal and hospital wastewaters in Czech Republic: Culture-based and metagenomic approaches. Environmental Research, 2021, 193, 110487.	7.5	24
18	The association between measurements of antimicrobial use and resistance in the faeces microbiota of finisher batches. Epidemiology and Infection, 2017, 145, 2827-2837.	2.1	18

#	ARTICLE	IF	CITATIONS
19	Global Distribution of <i>mcr</i> Gene Variants in 214K Metagenomic Samples. <i>MSystems</i> , 2022, 7, e0010522.	3.8	17
20	Predicting effects of changed antimicrobial usage on the abundance of antimicrobial resistance genes in finisherâ€™ gut microbiomes. <i>Preventive Veterinary Medicine</i> , 2020, 174, 104853.	1.9	16
21	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. <i>Frontiers in Public Health</i> , 2020, 8, 38.	2.7	11
22	Antimicrobial resistance in hospital wastewater in Scotland: a cross-sectional metagenomics study. <i>Lancet, The</i> , 2019, 394, S1.	13.7	9
23	Risk Factors for Antimicrobial Resistance in Turkey Farms: A Cross-Sectional Study in Three European Countries. <i>Antibiotics</i> , 2021, 10, 820.	3.7	8
24	Robustness in quantifying the abundance of antimicrobial resistance genes in pooled faeces samples from batches of slaughter pigs using metagenomics analysis. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 24, 398-402.	2.2	7
25	Validation of the register-based lifetime antimicrobial usage measurement for finisher batches based on comparison with recorded antimicrobial usage at farm level. <i>Epidemiology and Infection</i> , 2018, 146, 515-523.	2.1	4