

# 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

471061

17  
h-index

552369

26  
g-index

36  
all docs

36  
docs citations

36  
times ranked

2904  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Distribution of <i>mcr</i> Gene Variants in 214K Metagenomic Samples. <i>MSystems</i> , 2022, 7, e0010522.	1.7	17
2	Extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> and antimicrobial resistance in municipal and hospital wastewaters in Czech Republic: Culture-based and metagenomic approaches. <i>Environmental Research</i> , 2021, 193, 110487.	3.7	24
3	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.	0.9	7
4	Risk Factors for Antimicrobial Resistance in Turkey Farms: A Cross-Sectional Study in Three European Countries. <i>Antibiotics</i> , 2021, 10, 820.	1.5	8
5	Genomic evolution of antimicrobial resistance in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2021, 11, 15108.	1.6	33
6	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. <i>MBio</i> , 2021, 12, e0052121.	1.8	30
7	Secrets of the Hospital Underbelly: Patterns of Abundance of Antimicrobial Resistance Genes in Hospital Wastewater Vary by Specific Antimicrobial and Bacterial Family. <i>Frontiers in Microbiology</i> , 2021, 12, 703560.	1.5	26
8	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.	0.7	16
9	Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers: A metagenome-wide cross-sectional study. <i>Environment International</i> , 2020, 143, 105939.	4.8	33
10	Farm dust resistomes and bacterial microbiomes in European poultry and pig farms. <i>Environment International</i> , 2020, 143, 105971.	4.8	66
11	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
12	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. <i>Communications Biology</i> , 2020, 3, 155.	2.0	33
13	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. <i>Frontiers in Public Health</i> , 2020, 8, 38.	1.3	11
14	Clades of huge phages from across Earthâ€™s ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
15	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. <i>PLoS ONE</i> , 2019, 14, e0222531.	1.1	24
16	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
17	Associations between antimicrobial use and the faecal resistome on broiler farms from nine European countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2596-2604.	1.3	49
18	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612

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19	Antimicrobial resistance in hospital wastewater in Scotland: a cross-sectional metagenomics study. <i>Lancet, The</i> , 2019, 394, S1.	6.3	9
20	The antimicrobial resistome in relation to antimicrobial use and biosecurity in pig farming, a metagenome-wide association study in nine European countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 865-876.	1.3	63
21	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.	1.0	4
22	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. <i>Nature Microbiology</i> , 2018, 3, 898-908.	5.9	230
23	The association between measurements of antimicrobial use and resistance in the faeces microbiota of finisher batches. <i>Epidemiology and Infection</i> , 2017, 145, 2827-2837.	1.0	18
24	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 385-392.	1.3	89
25	Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition. <i>MSystems</i> , 2016, 1, .	1.7	153