

Interconnected microbiomes and resistomes in low-inc

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The structure and diversity of human, animal and environmental resistomes. <i>Microbiome</i> , 2016, 4, 54.	11.1	355
2	Insights into human evolution from ancient and contemporary microbiome studies. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 14-26.	3.3	49
3	Polydopamine Nanocoating for Effective Photothermal Killing of Bacteria and Fungus upon Near-Infrared Irradiation. <i>Advanced Materials Interfaces</i> , 2016, 3, 1600767.	3.7	99
4	Rapid resistome mapping using nanopore sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw1328.	14.5	62
5	Antibiotic resistance in the food supply chain: where can sequencing and metagenomics aid risk assessment?. <i>Current Opinion in Food Science</i> , 2017, 14, 66-71.	8.0	76
6	The Threat of Antimicrobial Resistance on the Human Microbiome. <i>Microbial Ecology</i> , 2017, 74, 1001-1008.	2.8	102
7	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. <i>Nature Communications</i> , 2017, 8, 15784.	12.8	287
8	The <i>tet39</i> Determinant and the <i>msrE-mphE</i> Genes in <i>Acinetobacter</i> Plasmids Are Each Part of Discrete Modules Flanked by Inversely Oriented <i>p dif</i> (<i>XerC-XerD</i>) Sites. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	98
9	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	248
10	Different drugs for bad bugs: antivirulence strategies in the age of antibiotic resistance. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 457-471.	46.4	570
11	Next-generation approaches to understand and combat the antibiotic resistome. <i>Nature Reviews Microbiology</i> , 2017, 15, 422-434.	28.6	438
12	Antibiotic Resistance Genes and Associated Microbial Community Conditions in Aging Landfill Systems. <i>Environmental Science & Technology</i> , 2017, 51, 12859-12867.	10.0	154
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15	Changes in the intestinal microbiota following the administration of azithromycin in a randomised placebo-controlled trial among infants in south India. <i>Scientific Reports</i> , 2017, 7, 9168.	3.3	55
16	Prevalence, antimicrobial susceptibility, and molecular characterization of <i>Staphylococcus aureus</i> isolated from dairy herds in northern China. <i>Journal of Dairy Science</i> , 2017, 100, 8796-8803.	3.4	85
17	PAHs accelerate the propagation of antibiotic resistance genes in coastal water microbial community. <i>Environmental Pollution</i> , 2017, 231, 1145-1152.	7.5	80
18	Comparison of Fecal Microbial Composition and Antibiotic Resistance Genes from Swine, Farm Workers and the Surrounding Villagers. <i>Scientific Reports</i> , 2017, 7, 4965.	3.3	18

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19	Global acquisition of genetic material from different bacteria into the staphylococcal cassette chromosome elements of a <i>Staphylococcus epidermidis</i> isolate. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 581-587.	2.5	10
20	Global epidemiology of CTX-M β -lactamases: temporal and geographical shifts in genotype. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2145-2155.	3.0	561
21	Genomic and functional techniques to mine the microbiome for novel antimicrobials and antimicrobial resistance genes. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 42-58.	3.8	38
22	Genomics and the evolution of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 92-107.	3.8	50
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29	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. <i>Microbiome</i> , 2017, 5, 84.	11.1	247
30	Microbial phylogeny determines transcriptional response of resistome to dynamic composting processes. <i>Microbiome</i> , 2017, 5, 103.	11.1	60
31	Comparative gut microbiota and resistome profiling of intensive care patients receiving selective digestive tract decontamination and healthy subjects. <i>Microbiome</i> , 2017, 5, 88.	11.1	90
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36	Vision: Rods See in Bright Light. <i>Current Biology</i> , 2018, 28, R364-R366.	3.9	16

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40	Bacterial community structure and abundances of antibiotic resistance genes in heavy metals contaminated agricultural soil. <i>Environmental Science and Pollution Research</i> , 2018, 25, 9547-9555.	5.3	39
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50	Microbial Community Composition and Antibiotic Resistance Genes within a North Carolina Urban Water System. <i>Water (Switzerland)</i> , 2018, 10, 1539.	2.7	13
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88	Deciphering extracellular antibiotic resistance genes (eARGs) in activated sludge by metagenome. <i>Water Research</i> , 2019, 161, 610-620.	11.3	97
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118	Metagenomic Analysis Reveals the Distribution of Antibiotic Resistance Genes in a Large-Scale Population of Healthy Individuals and Patients With Varied Diseases. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 590018.	3.5	17
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120	Tackling Multidrug Resistance in Streptococci " From Novel Biotherapeutic Strategies to Nanomedicines. <i>Frontiers in Microbiology</i> , 2020, 11, 579916.	3.5	24
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122	Gut microbiome: Current development, challenges, and perspectives. , 2020, , 227-241.		1
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130	Quantifying the transmission of antimicrobial resistance at the human and livestock interface with genomics. <i>Clinical Microbiology and Infection</i> , 2020, 26, 1612-1616.	6.0	39
131	The soil in our microbial DNA informs about environmental interfaces across host and subsistence modalities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190577.	4.0	4
132	Impact of investigational microbiota therapeutic RBX2660 on the gut microbiome and resistome revealed by a placebo-controlled clinical trial. <i>Microbiome</i> , 2020, 8, 125.	11.1	41
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134	A Review of Antimicrobial Resistance in Poultry Farming within Low-Resource Settings. <i>Animals</i> , 2020, 10, 1264.	2.3	103
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136	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. <i>Scientific Reports</i> , 2020, 10, 18870.	3.3	13
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138	Community-Acquired Antimicrobial Resistant Enterobacteriaceae in Central America: A One Health Systematic Review. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 7622.	2.6	9
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142	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	9.8	22
143	A survey of within-host and between-hosts modelling for antibiotic resistance. <i>BioSystems</i> , 2020, 196, 104182.	2.0	8
144	Comparative assessment of faecal microbial composition and metabonome of swine, farmers and human control. <i>Scientific Reports</i> , 2020, 10, 8997.	3.3	14
145	Coexistence of Antibiotic Resistance Genes and Virulence Factors Deciphered by Large-Scale Complete Genome Analysis. <i>MSystems</i> , 2020, 5, .	3.8	46

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148	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	12.8	133
149	Metatranscriptomics Reveals Antibiotic-Induced Resistance Gene Expression in the Murine Gut Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 322.	3.5	16
150	The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography. <i>ISME Journal</i> , 2020, 14, 1584-1599.	9.8	78
151	Correlation between antimicrobial resistance and faecal contamination in small urban streams and bathing waters. <i>Science of the Total Environment</i> , 2020, 739, 140242.	8.0	25
152	Wastewater treatment plants and release: The vase of Odin for emerging bacterial contaminants, resistance and determinant of environmental wellness. <i>Emerging Contaminants</i> , 2020, 6, 212-224.	4.9	18
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156	Instruction of microbiome taxonomic profiling based on 16S rRNA sequencing. <i>Journal of Microbiology</i> , 2020, 58, 193-205.	2.8	20
157	ARGminer: a web platform for the crowdsourcing-based curation of antibiotic resistance genes. <i>Bioinformatics</i> , 2020, 36, 2966-2973.	4.1	37
158	Molecular characterization of Extended-spectrum β lactamase- producing <i>E. coli</i> recovered from community-acquired urinary tract infections in Upper Egypt. <i>Scientific Reports</i> , 2020, 10, 2772.	3.3	41
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