Functional Characterization of the Antibiotic Resistance Microflora

Science 325, 1128-1131 DOI: 10.1126/science.1176950

Citation Report

#	Article	IF	CITATIONS
1	New Ways of Killing the Beast: Prospects for Inorganic–Organic Hybrid Nanomaterials as Antibacterial Agents. ChemBioChem, 2009, 10, 2847-2850.	1.3	31
4	Resistance carrying plasmid in a traumatic wound. Journal of Wound Care, 2010, 19, 306-310.	0.5	3
5	Review: Postnatal development of the mucosal immune system and consequences on health in adulthood. Canadian Journal of Animal Science, 2010, 90, 129-136.	0.7	4
6	Origins and Evolution of Antibiotic Resistance. Microbiology and Molecular Biology Reviews, 2010, 74, 417-433.	2.9	4,061
7	Antibiotic resistance and its cost: is it possible to reverse resistance?. Nature Reviews Microbiology, 2010, 8, 260-271.	13.6	1,855
8	Activity of berberine on Shigella dysenteriae investigated by microcalorimetry and multivariate analysis. Journal of Thermal Analysis and Calorimetry, 2010, 102, 331-336.	2.0	38
9	The fixed period. Evolutionary Anthropology, 2010, 19, 4-8.	1.7	2
10	Viewing the human microbiome through three-dimensional glasses: integrating structural and functional studies to better define the properties of myriad carbohydrate-active enzymes. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1261-1264.	0.7	26
11	Construction and characterization of Enterococcus faecalis CG110/gfp/pRE25*, a tool for monitoring horizontal gene transfer in complex microbial ecosystems. FEMS Microbiology Letters, 2010, 313, 111-119.	0.7	14
12	Natural evolution of TEM-1 β-lactamase: experimental reconstruction and clinical relevance. FEMS Microbiology Reviews, 2010, 34, 1015-1036.	3.9	240
13	Antibiotic resistance in faecal microbiota of Greek healthy infants. Beneficial Microbes, 2010, 1, 297-306.	1.0	26
14	Predicting Plasmid Promiscuity Based on Genomic Signature. Journal of Bacteriology, 2010, 192, 6045-6055.	1.0	162
15	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. Virulence, 2010, 1, 299-303.	1.8	166
16	<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> fermented milk product reduces inflammation by altering a niche for colitogenic microbes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18132-18137.	3.3	196
17	A functional metagenomic approach for expanding the synthetic biology toolbox for biomass conversion. Molecular Systems Biology, 2010, 6, 360.	3.2	64
18	The Human Microbiome Project, Personalized Medicine and the Birth of Pharmacomicrobiomics. Current Pharmacogenomics and Personalized Medicine, 2010, 8, 182-193.	0.2	72
19	The human gut mobile metagenome. Gut Microbes, 2010, 1, 415-431.	4.3	36
20	The antibiotic resistome. Expert Opinion on Drug Discovery, 2010, 5, 779-788.	2.5	83

ARTICLE

IF CITATIONS

Long-term impacts of antibiotic exposure on the human intestinal microbiota. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf

22	Antimicrobial Susceptibility Testing Using High Surface-to-Volume Ratio Microchannels. Analytical Chemistry, 2010, 82, 1012-1019.	3.2	128
23	Horizontal gene transfer and the genomics of enterococcal antibiotic resistance. Current Opinion in Microbiology, 2010, 13, 632-639.	2.3	247
24	Antibiotic resistance in the environment: a link to the clinic?. Current Opinion in Microbiology, 2010, 13, 589-594.	2.3	638
25	Innate immunity and gut–microbe mutualism in Drosophila. Developmental and Comparative Immunology, 2010, 34, 369-376.	1.0	144
26	Prudent use of antimicrobial agents: Revisiting concepts and estimating perspectives in a global world. Enfermedades Infecciosas Y MicrobiologÃa ClÂnica, 2010, 28, 487-488.	0.3	7
27	The global need for effective antibiotics: challenges and recent advances. Trends in Pharmacological Sciences, 2010, 31, 509-515.	4.0	182
28	Compensation of Fitness Costs and Reversibility of Antibiotic Resistance Mutations. Antimicrobial Agents and Chemotherapy, 2010, 54, 2085-2095.	1.4	144
29	The population genetics of antibiotic resistance: integrating molecular mechanisms and treatment contexts. Nature Reviews Genetics, 2010, 11, 405-414.	7.7	181
30	Oral biofilms: a reservoir of transferable, bacterial, antimicrobial resistance. Expert Review of Anti-Infective Therapy, 2010, 8, 1441-1450.	2.0	139
31	Evolving Carbapenemases: Can Medicinal Chemists Advance One Step Ahead of the Coming Storm?. Journal of Medicinal Chemistry, 2010, 53, 3013-3027.	2.9	55
32	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. Molecular Oral Microbiology, 2010, 25, 391-405.	1.3	78
33	The Evolution of Antibiotic Resistance. , 2011, , 305-337.		6
34	Ecology and Evolution as Targets: the Need for Novel Eco-Evo Drugs and Strategies To Fight Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2011, 55, 3649-3660.	1.4	171
35	Bacteriophages as vehicles of the resistome in cystic fibrosis. Journal of Antimicrobial Chemotherapy, 2011, 66, 2444-2447.	1.3	63
36	Broad Dissemination of Plasmid-Mediated Quinolone Resistance Genes in Sediments of Two Urban Coastal Wetlands. Environmental Science & Technology, 2011, 45, 447-454.	4.6	101
37	Tertiary-Treated Municipal Wastewater is a Significant Point Source of Antibiotic Resistance Genes into Duluth-Superior Harbor. Environmental Science & Technology, 2011, 45, 9543-9549.	4.6	335
40	Antibiotic Resistance in Waste Water and Surface Water and Human Health Implications. Handbook of Environmental Chemistry, 2011, , 173-212.	0.2	7

	CITATION	Report	
#	Article	IF	CITATIONS
41	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. Briefings in Functional Genomics, 2011, 10, 322-333.	1.3	41
42	A Biosensor Platform for Rapid Antimicrobial Susceptibility Testing Directly From Clinical Samples. Journal of Urology, 2011, 185, 148-153.	0.2	90
43	Description and validation of coupling high performance liquid chromatography with resonance Rayleigh scattering in aminoglycosides determination. Analytica Chimica Acta, 2011, 706, 199-204.	2.6	18
44	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. Current Opinion in Pharmacology, 2011, 11, 439-445.	1.7	80
45	Antibiotics and the resistant microbiome. Current Opinion in Microbiology, 2011, 14, 556-563.	2.3	140
46	Bacterial community characteristics under long-term antibiotic selection pressures. Water Research, 2011, 45, 6063-6073.	5.3	116
47	Population biological principles of drug-resistance evolution in infectious diseases. Lancet Infectious Diseases, The, 2011, 11, 236-247.	4.6	220
48	Structure and antimicrobial properties of multivalent short peptides. MedChemComm, 2011, 2, 308.	3.5	34
49	Acceleration of Emergence of Bacterial Antibiotic Resistance in Connected Microenvironments. Science, 2011, 333, 1764-1767.	6.0	472
50	Crystal ball – 2011. Environmental Microbiology Reports, 2011, 3, 1-26.	1.0	9
51	Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4554-4561.	3.3	1,912
52	The Human Microbiome and Host–Pathogen Interactions. , 2011, , 43-61.		5
53	Functional Metagenomic Investigations of the Human Intestinal Microbiota. Frontiers in Microbiology, 2011, 2, 188.	1.5	44
54	Functional Metagenomics Reveals Previously Unrecognized Diversity of Antibiotic Resistance Genes in Gulls. Frontiers in Microbiology, 2011, 2, 238.	1.5	46
59	Catabolic pathway for 2â€nitroimidazole involves a novel nitrohydrolase that also confers drug resistance. Environmental Microbiology, 2011, 13, 1010-1017.	1.8	16
60	Analysis of antibiotic resistance regions in Gram-negative bacteria. FEMS Microbiology Reviews, 2011, 35, 820-855.	3.9	290
61	Persistence of antibiotic resistance in bacterial populations. FEMS Microbiology Reviews, 2011, 35, 901-911.	3.9	325
62	Identification of bacterial plasmids based on mobility and plasmid population biology. FEMS Microbiology Reviews, 2011, 35, 936-956.	3.9	187

#	ARTICLE	IF	CITATIONS
63	Origins of bacterial diversity through horizontal genetic transfer and adaptation to new ecological niches. FEMS Microbiology Reviews, 2011, 35, 957-976.	3.9	517
64	Combinatorial events of insertion sequences and ICE in Gram-negative bacteria. FEMS Microbiology Reviews, 2011, 35, 912-935.	3.9	164
65	Monitoring horizontal antibiotic resistance gene transfer in a colonic fermentation model. FEMS Microbiology Ecology, 2011, 78, 210-219.	1.3	39
66	The Human Oral Metagenome. , 2011, , 165-173.		2
67	Antibiotic resistance is ancient. Nature, 2011, 477, 457-461.	13.7	1,967
68	Microbial Genomics and Infectious Diseases. New England Journal of Medicine, 2011, 365, 347-357.	13.9	156
69	Screening for novel antibacterial agents based on the activities of compounds on metabolism of Escherichia coli: A microcalorimetric study. Journal of Hazardous Materials, 2011, 185, 346-352.	6.5	32
70	Antifungal evaluation of cholic acid and its derivatives on Candida albicans by microcalorimetry and chemometrics. Analytica Chimica Acta, 2011, 689, 250-256.	2.6	23
71	Antimicrobial strategies for limiting bacterial contaminants in fuel bioethanol fermentations. Progress in Energy and Combustion Science, 2011, 37, 351-370.	15.8	92
72	Characterization of antibiotic resistance determinants in oral biofilms. Journal of Microbiology, 2011, 49, 595-602.	1.3	40
73	Current Concepts of the Intestinal Microbiota and the Pathogenesis of Infection. Current Infectious Disease Reports, 2011, 13, 28-34.	1.3	89
74	A spatial approach for the epidemiology of antibiotic use and resistance in community-based studies: the emergence of urban clusters of Escherichia coli quinolone resistance in Sao Paulo, Brasil. International Journal of Health Geographics, 2011, 10, 17.	1.2	44
75	Skin microbiota: Microbial community structure and its potential association with health and disease. Infection, Genetics and Evolution, 2011, 11, 839-848.	1.0	174
76	Selective Advantage of Resistant Strains at Trace Levels of Antibiotics: a Simple and Ultrasensitive Color Test for Detection of Antibiotics and Genotoxic Agents. Antimicrobial Agents and Chemotherapy, 2011, 55, 1204-1210.	1.4	138
77	Antibiotic Resistance Is Prevalent in an Isolated Cave Microbiome. PLoS ONE, 2012, 7, e34953.	1.1	541
78	Functional Cloning and Characterization of Antibiotic Resistance Genes from the Chicken Gut Microbiome. Applied and Environmental Microbiology, 2012, 78, 3028-3032.	1.4	40
79	Wide Variation in Antibiotic Resistance Proteins Identified by Functional Metagenomic Screening of a Soil DNA Library. Applied and Environmental Microbiology, 2012, 78, 1708-1714.	1.4	61
80	Diversity of Individual Dynamic Patterns of Emergence of Resistance to Quinolones in Escherichia coli From the Fecal Flora of Healthy Volunteers Exposed to Ciprofloxacin. Journal of Infectious Diseases, 2012, 206, 1399-1406.	1.9	31

#	Article	IF	CITATIONS
81	Bottlenecks in the Transferability of Antibiotic Resistance from Natural Ecosystems to Human Bacterial Pathogens. Frontiers in Microbiology, 2011, 2, 265.	1.5	74
82	Evolutionary, ecological and biotechnological perspectives on plasmids resident in the human gut mobile metagenome. Bioengineered, 2012, 3, 13-31.	1.4	27
83	Bacterial symbioses of the medicinal leech Hirudo verbana. Gut Microbes, 2012, 3, 322-331.	4.3	34
84	A public resource facilitating clinical use of genomes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11920-11927.	3.3	194
85	Enzymatic resistance to the lipopeptide surfactin as identified through imaging mass spectrometry of bacterial competition. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13082-13087.	3.3	92
86	Bacterial recombination promotes the evolution of multi-drug-resistance in functionally diverse populations. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1477-1484.	1.2	64
87	Natural Antibiotic Resistance and Contamination by Antibiotic Resistance Determinants: The Two Ages in the Evolution of Resistance to Antimicrobials. Frontiers in Microbiology, 2012, 3, 1.	1.5	936
88	Isolation, identification and characterization of human intestinal bacteria with the ability to utilize chloramphenicol as the sole source of carbon and energy. FEMS Microbiology Ecology, 2012, 82, 703-712.	1.3	36
89	Functional screening of antibiotic resistance genes from human gut microbiota reveals a novel gene fusion. FEMS Microbiology Letters, 2012, 336, 11-16.	0.7	60
90	Defining a Healthy Human Gut Microbiome: Current Concepts, Future Directions, and Clinical Applications. Cell Host and Microbe, 2012, 12, 611-622.	5.1	615
91	Computational tools for viral metagenomics and their application in clinical research. Virology, 2012, 434, 162-174.	1.1	59
92	Staphylococcus epidermidis pan-genome sequence analysis reveals diversity of skin commensal and hospital infection-associated isolates. Genome Biology, 2012, 13, R64.	13.9	206
93	Long-Term Exposure to Antibiotics Has Caused Accumulation of Resistance Determinants in the Gut Microbiota of Honeybees. MBio, 2012, 3, .	1.8	161
94	Evolutionary medicine: its scope, interest and potential. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4305-4321.	1.2	113
95	In-feed antibiotic effects on the swine intestinal microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1691-1696.	3.3	942
96	Prevalence of Clinically Relevant Antibiotic Resistance Genes in Surface Water Samples Collected from Germany and Australia. Environmental Science & amp; Technology, 2012, 46, 9716-9726.	4.6	178
97	Bottled mineral water as a potential source of antibiotic resistant bacteria. Water Research, 2012, 46, 3612-3622.	5.3	76
98	The Shared Antibiotic Resistome of Soil Bacteria and Human Pathogens. Science, 2012, 337, 1107-1111.	6.0	1,314

#	Article	IF	CITATIONS
99	Metagenomic epidemiology: a public health need for the control of antimicrobial resistance. Clinical Microbiology and Infection, 2012, 18, 67-73.	2.8	38
100	Metagenomics and antibiotics. Clinical Microbiology and Infection, 2012, 18, 27-31.	2.8	45
101	Emergence of antibiotic resistance: need for a new paradigm. Clinical Microbiology and Infection, 2012, 18, 615-616.	2.8	47
102	The Impact of the Gut Microbiota on Human Health: An Integrative View. Cell, 2012, 148, 1258-1270.	13.5	2,920
103	The Origins of Antibiotic Resistance. Handbook of Experimental Pharmacology, 2012, , 13-30.	0.9	32
104	Insights into antibiotic resistance through metagenomic approaches. Future Microbiology, 2012, 7, 73-89.	1.0	251
105	Droplet microfluidics for high-throughput biological assays. Lab on A Chip, 2012, 12, 2146.	3.1	854
106	Correlation Between Upstream Human Activities and Riverine Antibiotic Resistance Genes. Environmental Science & Technology, 2012, 46, 11541-11549.	4.6	435
107	Inhibition of Staphylococcus aureus adherence to Caco-2 cells by lactobacilli andÂcell surface properties that influence attachment. Anaerobe, 2012, 18, 508-515.	1.0	54
108	Antibiotic resistance genes in anaerobic bacteria isolated from primary dental root canal infections. Anaerobe, 2012, 18, 576-580.	1.0	32
109	Context matters $\hat{a} \in $ the complex interplay between resistome genotypes and resistance phenotypes. Current Opinion in Microbiology, 2012, 15, 577-582.	2.3	97
110	Insect Immunology. , 2012, , 480-512.		7
111	Effect of berberine on Escherichia coli, Bacillus subtilis, and their mixtures as determined by isothermal microcalorimetry. Applied Microbiology and Biotechnology, 2012, 96, 503-510.	1.7	39
113	Compareads: comparing huge metagenomic experiments. BMC Bioinformatics, 2012, 13, S10.	1.2	32
114	Inferring Dynamic Signatures of Microbes in Complex Host Ecosystems. PLoS Computational Biology, 2012, 8, e1002624.	1.5	54
115	Deep Sequencing Analyses of Low Density Microbial Communities: Working at the Boundary of Accurate Microbiota Detection. PLoS ONE, 2012, 7, e32942.	1.1	160
116	Pseudomonas aeruginosa Overrides the Virulence Inducing Effect of Opioids When It Senses an Abundance of Phosphate. PLoS ONE, 2012, 7, e34883.	1.1	64
117	16S rRNA Gene Pyrosequencing Reveals Bacterial Dysbiosis in the Duodenum of Dogs with Idiopathic Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39333.	1.1	187

ARTICLE IF CITATIONS # Metagenomic Profiling of Microbial Composition and Antibiotic Resistance Determinants in Puget 118 1.1 50 Sound. PLoS ONE, 2012, 7, e48000. Pollution Impacts on Bacterioplankton Diversity in a Tropical Urban Coastal Lagoon System. PLoS ONE, 1.1 2012, 7, e51175. Excretion of Antibiotic Resistance Genes by Dairy Calves Fed Milk Replacers with Varying Doses of 120 50 1.5 Antibiotics. Frontiers in Microbiology, 2012, 3, 139. Assessment of Antibiotic Resistance in Probiotic Lactobacilli., 0,,. 121 The Human Microbiome: Our Second Genome. Annual Review of Genomics and Human Genetics, 2012, 13, 122 2.5 498 151-170. 124 Human Microbiome: A Genetic Bazaar for Microbes?. Current Biology, 2012, 22, R20-R22. 1.8 Human health implications of clinically relevant bacteria in wastewater habitats. Environmental 125 2.7 78 Science and Pollution Research, 2013, 20, 3550-3569. The tetA gene decreases tigecycline sensitivity of Salmonella enterica isolates. International Journal 1.1 49 of Antimicrobial Agents, 2013, 42, 133-140. 128 Replenishing our defensive microbes. BioEssays, 2013, 35, 810-817. 1.2 39 Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. 129 5.8 Nature Communications, 2013, 4, 2151. Le microbiote intestinal est l'avenir de la multirésistance bactérienne. Journal Des Anti-infectieux, 130 2 0.1 2013, 15, 166-177. Antibiotic resistance: Origins, mechanisms, approaches to counter. Applied Biochemistry and Microbiology, 2013, 49, 665-671. Developing a metagenomic view of xenobiotic metabolism. Pharmacological Research, 2013, 69, 21-31. 132 3.1 159 Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut. Annual Review of Microbiology, 2013, 67, 459-475. 39 Targeting agr- and agr-Like Quorum Sensing Systems for Development of Common Therapeutics to 134 2.1 100 Treat Multiple Gram-Positive Bacterial Infections. Sensors, 2013, 13, 5130-5166. Tracing antibacterial compounds from Acalypha australis Linn. by spectrum-effect relationships and semi-preparative HPLC. Journal of Separation Science, 2013, 36, 1667-1676. Microbiota's 'little helpers': bacteriophages and antibiotic-associated responses in the gut 136 13.9 14 microbiome. Genome Biology, 2013, 14, 127. Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 2.4 1163-1169.

ARTICLE IF CITATIONS Large plasmids of Escherichia coli and Salmonella encode highly diverse arrays of accessory genes on 138 0.4 31 common replicon families. Plasmid, 2013, 69, 36-48. Resistance to selective decontamination: the jury is still out. Lancet Infectious Diseases, The, 2013, 13, 4.6 282-283. 140 Conjugative Plasmids in Anthropogenic Soils., 2013, , 215-247. 0 Investigation of antibiotic resistance in the genomic era of multidrug-resistant Gram-negative bacilli, especiallyEnterobacteriaceae,PseudomonasandAcinetobacter. Expert Review of Anti-Infective Therapy, 141 24 2013, 11, 277-296. 'Blooming' in the gut: how dysbiosis might contribute to pathogen evolution. Nature Reviews 142 13.6 314 Microbiology, 2013, 11, 277-284. Detection of antibiotic resistance genes in samples from acute and chronic endodontic infections and after treatment. Archives of Oral Biology, 2013, 58, 1123-1128. 0.8 The human microbiome is a source of therapeutic drug targets. Current Opinion in Chemical Biology, 144 2.8 56 2013, 17, 379-384. Intrinsic antibiotic resistance: Mechanisms, origins, challenges and solutions. International Journal 145 1.5 434 of Medical Microbiology, 2013, 303, 287-292. Galleria Mellonella as a Model Host to Study Gut Microbe Homeostasis and Brain Infection by the 146 Human Pathogen Listeria Monocytogenes. Advances in Biochemical Engineering/Biotechnology, 2013, 0.6 26 135, 27-39. Heterologous viral expression systems in fosmid vectors increase the functional analysis potential of 1.6 metagenomic libraries. Scientific Reports, 2013, 3, 1107. Metagenomic Profiles of Antibiotic Resistance Genes (ARGs) between Human Impacted Estuary and Deep 148 329 4.6 Ocean Sediments. Environmental Science & amp; Technology, 2013, 47, 12753-12760. Pyrosequencing estimates of the diversity of antibiotic resistant bacteria in a wastewater system. 1.2 Water Science and Technology, 2013, 67, 1534-1543. Food and human gut as reservoirs of transferable antibiotic resistance encoding genes. Frontiers in 150 1.5 184 Microbiology, 2013, 4, 173. Mining Metagenomic Datasets for Antibiotic Resistance Genes., 2013, , 1-7. 152 Bacterial sex in dental plaque. Journal of Oral Microbiology, 2013, 5, 20736. 1.2 27 Mobile genetic elements of the human gastrointestinal tract. Gut Microbes, 2013, 4, 271-280. 129 From Germ Theory to Germ Therapy. Plastic and Reconstructive Surgery, 2013, 132, 854e-861e. 154 0.7 44 The antibiotic resistance "mobilome†searching for the link between environment and clinic. 1.5 221 Frontiers in Microbiology, 2013, 4, 138.

#	Article	IF	CITATIONS
156	Novel resistance functions uncovered using functional metagenomic investigations of resistance reservoirs. Frontiers in Microbiology, 2013, 4, 145.	1.5	79
157	Environmental and Public Health Implications of Water Reuse: Antibiotics, Antibiotic Resistant Bacteria, and Antibiotic Resistance Genes. Antibiotics, 2013, 2, 367-399.	1.5	100
158	Antibiotic resistance shaping multi-level population biology of bacteria. Frontiers in Microbiology, 2013, 4, 15.	1.5	153
159	Concentration-dependent activity in natural environments. Frontiers in Microbiology, 2013, 4, 20.	1.5	197
160	Antibiotic Resistance in and from Nature. Microbiology Spectrum, 2013, 1, .	1.2	3
161	Comparative Genome Analysis of Megasphaera sp. Reveals Niche Specialization and Its Potential Role in the Human Gut. PLoS ONE, 2013, 8, e79353.	1.1	120
162	Differential Effects of Antibiotic Therapy on the Structure and Function of Human Gut Microbiota. PLoS ONE, 2013, 8, e80201.	1.1	194
163	In Silico Assigned Resistance Genes Confer Bifidobacterium with Partial Resistance to Aminoglycosides but Not to l'-Lactams. PLoS ONE, 2013, 8, e82653.	1.1	17
164	Mobile elements, zoonotic pathogens and commensal bacteria: conduits for the delivery of resistance genes into humans, production animals and soil microbiota. Frontiers in Microbiology, 2013, 4, 86.	1.5	103
165	The human microbiome as a reservoir of antimicrobial resistance. Frontiers in Microbiology, 2013, 4, 87.	1.5	237
166	Causes, consequences, and perspectives in the variations of intestinal density of colonization of multidrug-resistant enterobacteria. Frontiers in Microbiology, 2013, 4, 129.	1.5	33
167	Horizontal gene transfer in the human gastrointestinal tract: potential spread of antibiotic resistance genes. Infection and Drug Resistance, 2014, 7, 167.	1.1	377
168	Identification of Aminoglycoside and β-Lactam Resistance Genes from within an Infant Gut Functional Metagenomic Library. PLoS ONE, 2014, 9, e108016.	1.1	48
169	Application of Microarray and Functional-Based Screening Methods for the Detection of Antimicrobial Resistance Genes in the Microbiomes of Healthy Humans. PLoS ONE, 2014, 9, e86428.	1.1	62
170	Human Intestinal Cells Modulate Conjugational Transfer of Multidrug Resistance Plasmids between Clinical Escherichia coli Isolates. PLoS ONE, 2014, 9, e100739.	1.1	22
171	The design of novel classes of macrolides for neutrophil-dominated inflammatory diseases. Future Medicinal Chemistry, 2014, 6, 657-674.	1.1	8
172	The abundance of antibiotic resistance genes in human guts has correlation to the consumption of antibiotics in animal. Gut Microbes, 2014, 5, 245-249.	4.3	57
173	Emergence and spread of antibiotic resistance: setting a parameter space. Upsala Journal of Medical Sciences, 2014, 119, 68-77.	0.4	120

#	Article	IF	CITATIONS
174	Antimicrobial resistance characteristics and fitness of Gram-negative fecal bacteria from volunteers treated with minocycline or amoxicillin. Frontiers in Microbiology, 2014, 5, 722.	1.5	31
175	Characterization and comparative analysis of antibiotic resistance plasmids isolated from a wastewater treatment plant. Frontiers in Microbiology, 2014, 5, 558.	1.5	37
176	Molecular Identification and Quantification of Tetracycline and Erythromycin Resistance Genes in Spanish and Italian Retail Cheeses. BioMed Research International, 2014, 2014, 1-10.	0.9	48
177	Draft Genome Sequences of Antibiotic-Resistant Commensal Escherichia coli. Genome Announcements, 2014, 2, .	0.8	1
178	Commet: Comparing and combining multiple metagenomic datasets. , 2014, , .		24
179	High Rates of Antimicrobial Drug Resistance Gene Acquisition after International Travel, the Netherlands. Emerging Infectious Diseases, 2014, 20, 649-657.	2.0	112
180	Coselection for resistance to multiple late-generation human therapeutic antibiotics encoded on tetracycline resistance plasmids captured from uncultivated stream and soil bacteria. Journal of Applied Microbiology, 2014, 117, 380-389.	1.4	24
181	Forces shaping the antibiotic resistome. BioEssays, 2014, 36, 1179-1184.	1.2	56
182	In and out: an analysis of epibiotic vs periplasmic bacterial predators. ISME Journal, 2014, 8, 625-635.	4.4	63
183	Effects of Decontamination of the Oropharynx and Intestinal Tract on Antibiotic Resistance in ICUs. JAMA - Journal of the American Medical Association, 2014, 312, 1429.	3.8	146
184	The Ellis Island Effect. Mobile Genetic Elements, 2014, 4, e29801.	1.8	20
185	Does the change on gastrointestinal tract microbiome affects host?. Brazilian Journal of Infectious Diseases, 2014, 18, 660-663.	0.3	4
186	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	9.4	482
187	A degenerate PCR-based strategy as a means of identifying homologues of aminoglycoside and β-lactam resistance genes in the gut microbiota. BMC Microbiology, 2014, 14, 25.	1.3	18
188	Functional metagenomic characterization of antibiotic resistance genes in agricultural soils from China. Environment International, 2014, 65, 9-15.	4.8	149
189	Antibiotic treatments and microbes in the gut. Environmental Microbiology, 2014, 16, 919-924.	1.8	48
190	General principles of antibiotic resistance in bacteria. Drug Discovery Today: Technologies, 2014, 11, 33-39.	4.0	157
191	Antibiotic Resistance is Widespread in Urban Aquatic Environments of Rio de Janeiro, Brazil. Microbial Ecology, 2014, 68, 441-452.	1.4	33

#	ARTICLE	IF	CITATIONS
192	Metagenomic insights into the human gut resistome and the forces that shape it. BioEssays, 2014, 36, 316-329.	1.2	76
193	Bacterial diversity and antibiotic resistance in water habitats: searching the links with the human microbiome. FEMS Microbiology Reviews, 2014, 38, 761-778.	3.9	288
194	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. Nature Communications, 2014, 5, 4714.	5.8	123
195	Antibiotic resistance genes in bacterial and bacteriophage fractions of Tunisian and Spanish wastewaters as markers to compare the antibiotic resistance patterns in each population. Environment International, 2014, 73, 167-175.	4.8	76
196	Environmental and public health implications of antibiotic-resistance genes in municipal wastewaters. Pravention Und Gesundheitsforderung, 2014, 9, 175-179.	1.5	4
197	Effects of selective digestive decontamination (SDD) on the gut resistome. Journal of Antimicrobial Chemotherapy, 2014, 69, 2215-2223.	1.3	90
198	Genomic Heterogeneity and Ecological Speciation within One Subspecies of Bacillus subtilis. Applied and Environmental Microbiology, 2014, 80, 4842-4853.	1.4	44
199	Biogeography and individuality shape function in the human skin metagenome. Nature, 2014, 514, 59-64.	13.7	869
200	In vitro microbial culture models and their application in drug development. Advanced Drug Delivery Reviews, 2014, 69-70, 217-224.	6.6	5
201	The Yin and Yang of Bacterial Resilience in the Human Gut Microbiota. Journal of Molecular Biology, 2014, 426, 3866-3876.	2.0	58
202	Human Skin Buffering Capacity: An Updated Overview. , 2014, , 171-176.		2
203	Antibiotics and the gut microbiota. Journal of Clinical Investigation, 2014, 124, 4212-4218.	3.9	529
204	Prevalence and Antibiogram Profiling of Escherichia coli Pathotypes Isolated from the Kat River and the Fort Beaufort Abstraction Water. International Journal of Environmental Research and Public Health, 2014, 11, 8213-8227.	1.2	39
206	DNA microarray analysis reveals that antibiotic resistance-gene diversity in human gut microbiota is age related. Scientific Reports, 2014, 4, 4302.	1.6	60
207	The commensal infant gut meta-mobilome as a potential reservoir for persistent multidrug resistance integrons. Scientific Reports, 2015, 5, 15317.	1.6	32
208	Gut resistome development in healthy twin pairs in the first year of life. Microbiome, 2015, 3, 27.	4.9	88
209	A survey on the developmental intestinal microbiota research in <scp>C</scp> hina: The history, funding, and frontiers of gut bacteria. Journal of Digestive Diseases, 2015, 16, 421-430.	0.7	3
210	Ecology and Evolution of the Human Microbiota: Fire, Farming and Antibiotics. Genes, 2015, 6, 841-857.	1.0	61

#	Article	IF	CITATIONS
211	Biotechnological applications of functional metagenomics in the food and pharmaceutical industries. Frontiers in Microbiology, 2015, 6, 672.	1.5	83
212	Characterization of antibiotic resistance in commensal bacteria from an aquaculture ecosystem. Frontiers in Microbiology, 2015, 6, 914.	1.5	56
213	Next-generation sequencing (NGS) for assessment of microbial water quality: current progress, challenges, and future opportunities. Frontiers in Microbiology, 2015, 6, 1027.	1.5	200
214	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. PLoS ONE, 2015, 10, e0069533.	1.1	202
215	Screening Currency Notes for Microbial Pathogens and Antibiotic Resistance Genes Using a Shotgun Metagenomic Approach. PLoS ONE, 2015, 10, e0128711.	1.1	25
216	Impact of Ciprofloxacin and Clindamycin Administration on Gram-Negative Bacteria Isolated from Healthy Volunteers and Characterization of the Resistance Genes They Harbor. Antimicrobial Agents and Chemotherapy, 2015, 59, 4410-4416.	1.4	39
217	Application of metagenomics in the human gut microbiome. World Journal of Gastroenterology, 2015, 21, 803.	1.4	292
218	Highly Efficient and Excitation Tunable Two-Photon Luminescence Platform For Targeted Multi-Color MDRB Imaging Using Graphene Oxide. Scientific Reports, 2014, 4, 6090.	1.6	35
219	Relocating the History of Science. Boston Studies in the Philosophy and History of Science, 2015, , .	0.4	2
220	The Newest "Omicsâ€â€"Metagenomics and Metabolomics—Enter the Battle against the Neglected Tropical Diseases. PLoS Neglected Tropical Diseases, 2015, 9, e0003382.	1.3	44
221	Environment, dysbiosis, immunity and sex-specific susceptibility: A translational hypothesis for regressive autism pathogenesis. Nutritional Neuroscience, 2015, 18, 145-161.	1.5	57
222	New insight into the gut microbiome through metagenomics. Advances in Genomics and Genetics, 0, , 77.	0.8	10
223	Same Exposure but Two Radically Different Responses to Antibiotics: Resilience of the Salivary Microbiome versus Long-Term Microbial Shifts in Feces. MBio, 2015, 6, e01693-15.	1.8	333
224	Ultrahigh-throughput discovery of promiscuous enzymes by picodroplet functional metagenomics. Nature Communications, 2015, 6, 10008.	5.8	225
225	Identification of a New Tetracycline Resistance Determinant tet47 from Fish Intestine. Journal of Food Protection, 2015, 78, 1581-1585.	0.8	4
226	Antimicrobial peptide-conjugated graphene oxide membrane for efficient removal and effective killing of multiple drug resistant bacteria. RSC Advances, 2015, 5, 18881-18887.	1.7	99
228	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. MBio, 2015, 6, .	1.8	357
229	Functional genomic and metagenomic approaches to understanding gut microbiota–animal mutualism. Current Opinion in Microbiology, 2015, 24, 38-46.	2.3	48

#	Article	IF	CITATIONS
230	Proteomics as the final step in the functional metagenomics study of antimicrobial resistance. Frontiers in Microbiology, 2015, 6, 172.	1.5	20
231	Antibiotics and the developing infant gut microbiota and resistome. Current Opinion in Microbiology, 2015, 27, 51-56.	2.3	184
232	The hidden resistome of retail chicken meat. Journal of Global Antimicrobial Resistance, 2015, 3, 44-46.	0.9	4
233	MetaRank: Ranking Microbial Taxonomic Units or Functional Groups for Comparative Analysis of Metagenomes. , 2015, , 442-447.		0
234	Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. Scientific Reports, 2015, 5, 11981.	1.6	50
235	Genomics, evolution, and molecular epidemiology of the Streptococcus bovis / Streptococcus equinus complex (SBSEC). Infection, Genetics and Evolution, 2015, 33, 419-436.	1.0	91
236	The potential impact of coinfection on antimicrobial chemotherapy and drug resistance. Trends in Microbiology, 2015, 23, 537-544.	3.5	36
237	Antimicrobial resistance in humans, livestock and the wider environment. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140083.	1.8	461
238	Antimicrobial resistance determinants of Escherichia coli isolates recovered from some rivers in Osun State, South-Western Nigeria: Implications for public health. Science of the Total Environment, 2015, 523, 82-94.	3.9	73
239	Antibiotic Discovery: Combatting Bacterial Resistance in Cells and in Biofilm Communities. Molecules, 2015, 20, 5286-5298.	1.7	276
240	Resistance Genes and Genetic Elements Associated with Antibiotic Resistance in Clinical and Commensal Isolates of Streptococcus salivarius. Applied and Environmental Microbiology, 2015, 81, 4155-4163.	1.4	38
241	The microbiome of uncontacted Amerindians. Science Advances, 2015, 1, .	4.7	721
242	The human gut resistome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140087.	1.8	275
243	Influence of the amoxicillin concentration on organics removal and microbial community structure in an anaerobic EGSB reactor treating with antibiotic wastewater. Chemical Engineering Journal, 2015, 274, 94-101.	6.6	77
244	The Oral Microbiome and Its Relationship to Genomics and Oral Disease. , 2015, , 35-65.		1
245	Improving microbial fitness in the mammalian gut by in vivo temporal functional metagenomics. Molecular Systems Biology, 2015, 11, 788.	3.2	26
246	Fighting microbial drug resistance: a primer on the role of evolutionary biology in public health. Evolutionary Applications, 2015, 8, 211-222.	1.5	34
247	The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents. Antimicrobial Agents and Chemotherapy, 2015, 59, 6551-6560.	1.4	155

#	Article	IF	CITATIONS
248	Limited dissemination of the wastewater treatment plant core resistome. Nature Communications, 2015, 6, 8452.	5.8	173
249	The Ocean as a Global Reservoir of Antibiotic Resistance Genes. Applied and Environmental Microbiology, 2015, 81, 7593-7599.	1.4	177
250	Characterization and Detection of a Widely Distributed Gene Cluster That Predicts Anaerobic Choline Utilization by Human Gut Bacteria. MBio, 2015, 6, .	1.8	173
251	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. Antimicrobial Agents and Chemotherapy, 2015, 59, 7335-7345.	1.4	61
252	Elucidating the Role of Residue 67 in IMP-Type Metallo-β-Lactamase Evolution. Antimicrobial Agents and Chemotherapy, 2015, 59, 7299-7307.	1.4	19
253	High-throughput bacterial functional genomics in the sequencing era. Current Opinion in Microbiology, 2015, 27, 86-95.	2.3	35
254	deFUME: Dynamic exploration of functional metagenomic sequencing data. BMC Research Notes, 2015, 8, 328.	0.6	9
255	Recovery of Plasmid pEMB1, Whose Toxin-Antitoxin System Stabilizes an Ampicillin Resistance-Conferring β-Lactamase Gene in Escherichia coli, from Natural Environments. Applied and Environmental Microbiology, 2015, 81, 40-47.	1.4	11
256	Oral Gram-negative anaerobic bacilli as a reservoir of β-lactam resistance genes facilitating infections with multiresistant bacteria. International Journal of Antimicrobial Agents, 2015, 45, 99-105.	1.1	31
257	What is a resistance gene? Ranking risk in resistomes. Nature Reviews Microbiology, 2015, 13, 116-123.	13.6	698
259	The human microbiota associated with overall health. Critical Reviews in Biotechnology, 2015, 35, 129-140.	5.1	20
260	Bacterial Strain Diversity Within Wounds. Advances in Wound Care, 2015, 4, 12-23.	2.6	10
261	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. ISME Journal, 2015, 9, 207-216.	4.4	540
262	Survival and Evolution of a Large Multidrug Resistance Plasmid in New Clinical Bacterial Hosts. Molecular Biology and Evolution, 2016, 33, 2860-2873.	3.5	212
263	Antibiotics and the Human Gut Microbiome: Dysbioses and Accumulation of Resistances. Frontiers in Microbiology, 2015, 6, 1543.	1.5	613
264	Study of the Aminoglycoside Subsistence Phenotype of Bacteria Residing in the Gut of Humans and Zoo Animals. Frontiers in Microbiology, 2015, 6, 1550.	1.5	15
265	Dissemination of Antimicrobial Resistance in Microbial Ecosystems through Horizontal Gene Transfer. Frontiers in Microbiology, 2016, 7, 173.	1.5	1,018
266	Breaking the Spell: Combating Multidrug Resistant â€~Superbugs'. Frontiers in Microbiology, 2016, 7, 174.	1.5	98

	Charles		
		I.	CITATIONS
#	ARTICLE	IF	CITATIONS
267	Escherichia coli Î ² -Lactamases: What Really Matters. Frontiers in Microbiology, 2016, 7, 417.	1.5	71
268	Composition and Functional Characterization of Microbiome Associated with Mucus of the Coral Fungia echinata Collected from Andaman Sea. Frontiers in Microbiology, 2016, 7, 936.	1.5	44
269	Hospital Effluents Are One of Several Sources of Metal, Antibiotic Resistance Genes, and Bacterial Markers Disseminated in Sub-Saharan Urban Rivers. Frontiers in Microbiology, 2016, 7, 1128.	1.5	99
270	Sponge Microbiota Are a Reservoir of Functional Antibiotic Resistance Genes. Frontiers in Microbiology, 2016, 7, 1848.	1.5	15
271	Evaluation of Machine Learning and Rules-Based Approaches for Predicting Antimicrobial Resistance Profiles in Gram-negative Bacilli from Whole Genome Sequence Data. Frontiers in Microbiology, 2016, 7, 1887.	1.5	88
272	Expanding the Repertoire of Carbapenem-Hydrolyzing Metallo-ß-Lactamases by Functional Metagenomic Analysis of Soil Microbiota. Frontiers in Microbiology, 2016, 7, 1985.	1.5	18
273	Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. PLoS Computational Biology, 2016, 12, e1004977.	1.5	434
274	Parallel Mapping of Antibiotic Resistance Alleles in Escherichia coli. PLoS ONE, 2016, 11, e0146916.	1.1	15
275	Detection of Novel Integrons in the Metagenome of Human Saliva. PLoS ONE, 2016, 11, e0157605.	1.1	21
276	The effect of habitual and experimental antiperspirant and deodorant product use on the armpit microbiome. PeerJ, 2016, 4, e1605.	0.9	49
278	Antibiotics/antimicrobials: systemic and local administration in the therapy of mild to moderately advanced periodontitis. Periodontology 2000, 2016, 71, 82-112.	6.3	204
279	Role of Gut Microbiome in the Modulation of Environmental Toxicants and Therapeutic Agents. , 2016, , 491-518.		2
280	Crowdsourced Data Indicate Widespread Multidrug Resistance in Skin Flora of Healthy Young Adults. Journal of Microbiology and Biology Education, 2016, 17, 172-182.	0.5	7
281	Metagenomic Insights into Transferable Antibiotic Resistance in Oral Bacteria. Journal of Dental Research, 2016, 95, 969-976.	2.5	48
282	Clinical metagenomics for the management of hospital- and healthcare-acquired pneumonia. Future Microbiology, 2016, 11, 427-439.	1.0	29
283	The gut resistome is highly dynamic during the first months of life. Future Microbiology, 2016, 11, 501-510.	1.0	15
284	Graph mining for next generation sequencing: leveraging the assembly graph for biological insights. BMC Genomics, 2016, 17, 340.	1.2	2
285	Metagenomic Analysis Revealing Antibiotic Resistance Genes (ARGs) and Their Genetic Compartments in the Tibetan Environment. Environmental Science & amp; Technology, 2016, 50, 6670-6679.	4.6	155

#	Article		CITATIONS
286	Changes of resistome, mobilome and potential hosts of antibiotic resistance genes during the transformation of anaerobic digestion from mesophilic to thermophilic. Water Research, 2016, 98, 261-269.		184
287	Antibiotic-Induced Changes in the Intestinal Microbiota and Disease. Trends in Molecular Medicine, 2016, 22, 458-478.	3.5	630
288	Interconnected microbiomes and resistomes in low-income human habitats. Nature, 2016, 533, 212-216.	13.7	425
289	The Bacterial Mobile Resistome Transfer Network Connecting the Animal and Human Microbiomes. Applied and Environmental Microbiology, 2016, 82, 6672-6681.	1.4	258
290	Functional mining of transporters using synthetic selections. Nature Chemical Biology, 2016, 12, 1015-1022.	3.9	64
291	Contemporary challenges and opportunities in the diagnosis and outbreak detection of multidrug-resistant infectious disease. Expert Review of Molecular Diagnostics, 2016, 16, 1163-1175.	1.5	6
292	Identification, antimicrobial resistance and molecular characterization of the human emerging pathogen Streptococcus gallolyticus subsp. pasteurianus. Diagnostic Microbiology and Infectious Disease, 2016, 86, 329-335.	0.8	14
293	Prevalence and dissemination of antibiotic resistance genes and coselection of heavy metals in Chinese dairy farms. Journal of Hazardous Materials, 2016, 320, 10-17.	6.5	120
294	High frequencies of antibiotic resistance genes in infants' meconium and early fecal samples. Journal of Developmental Origins of Health and Disease, 2016, 7, 35-44.	0.7	61
295	A novel Direct MIC-gradient Strip Method to screen for antibiotic-resistant faecal Enterobacteriaceae. Journal of Microbiological Methods, 2016, 129, 94-97.	0.7	2
296	Insights into human evolution from ancient and contemporary microbiome studies. Current Opinion in Genetics and Development, 2016, 41, 14-26.	1.5	49
297	Exploring divergent antibiotic resistance genes in ancient metagenomes and discovery of a novel betaâ€lactamase family. Environmental Microbiology Reports, 2016, 8, 886-895.	1.0	16
299	Comparison of antimicrobial resistant genes in chicken gut microbiome grown on organic and conventional diet. Veterinary and Animal Science, 2016, 1-2, 9-14.	0.6	21
300	Mobile genes in the human microbiome are structured from global to individual scales. Nature, 2016, 535, 435-439.	13.7	233
301	Antibiotics and the Intestinal MicrobiomeIntestinal microbiome : Individual Responses, Resilience of the Ecosystem, and the Susceptibility to Infections. Current Topics in Microbiology and Immunology, 2016, 398, 123-146.	0.7	27
302	Antimicrobial Drug Efflux Genes and Pumps in Bacteria of Animal and Environmental Origin. , 2016, , 561-593.		2
303	Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children. Scientific Reports, 2016, 6, 24030.	1.6	33
304	Long-Term Implications of Antibiotic Use on Gut Health and Microbiota in Populations Including Patients With Cystic Fibrosis. , 2016, , 223-259.		1

#	Article		CITATIONS
305	Impact of 4-epi-oxytetracycline on the gut microbiota and blood metabolomics of Wistar rats. Scientific Reports, 2016, 6, 23141.	1.6	12
306	Developmental dynamics of the preterm infant gut microbiota and antibiotic resistome. Nature Microbiology, 2016, 1, 16024.	5.9	346
307	How Should We Be Determining Background and Baseline Antibiotic Resistance Levels in Agroecosystem Research?. Journal of Environmental Quality, 2016, 45, 420-431.	1.0	42
308	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. Future Medicinal Chemistry, 2016, 8, 1133-1151.	1.1	17
309	Programmable biomaterials for dynamic and responsive drug delivery. Experimental Biology and Medicine, 2016, 241, 1127-1137.	1.1	9
310	Plasmid metagenomics reveals multiple antibiotic resistance gene classes among the gut microbiomes of hospitalised patients. Journal of Clobal Antimicrobial Resistance, 2016, 6, 57-66.	0.9	13
311	Lethal neonatal meningoencephalitis caused by multi-drug resistant, highly virulent <i>Escherichia coli</i> . Infectious Diseases, 2016, 48, 461-466.	1.4	19
312	High Diversity of CTX-M Extended-Spectrum β-Lactamases in Municipal Wastewater and Urban Wetlands. Microbial Drug Resistance, 2016, 22, 312-320.	0.9	11
313	Antibiotic resistance in Enterobacteriaceae: mechanisms and clinical implications. BMJ, The, 2016, 352, h6420.	3.0	236
314	The human microbiota: novel targets for hospital-acquired infections and antibiotic resistance. Annals of Epidemiology, 2016, 26, 342-347.	0.9	35
315	Fecal Microbiota Transplantation Inhibits Multidrug-Resistant Gut Pathogens: Preliminary Report Performed in an Immunocompromised Host. Archivum Immunologiae Et Therapiae Experimentalis, 2016, 64, 255-258.	1.0	57
316	Endless resistance. Endless antibiotics?. MedChemComm, 2016, 7, 37-49.	3.5	39
317	Indirect resistance to several classes of antibiotics in cocultures with resistant bacteria expressing antibiotic-modifying or -degrading enzymes. Journal of Antimicrobial Chemotherapy, 2016, 71, 100-110.	1.3	64
318	Antibiotic Resistance and the Biology of History. Body and Society, 2016, 22, 19-52.	0.3	236
319	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. ISME Journal, 2017, 11, 237-247.	4.4	298
320	Oral Fluid as a Biological Material for Antemortem Detection of Oxytetracycline in Pigs by Liquid Chromatography–Tandem Mass Spectrometry. Journal of Agricultural and Food Chemistry, 2017, 65, 494-500.	2.4	18
321	Rapid resistome mapping using nanopore sequencing. Nucleic Acids Research, 2017, 45, gkw1328.	6.5	62
322	Inflammatory disease caused by intestinal pathobionts. Current Opinion in Microbiology, 2017, 35, 64-69.	2.3	60

#	Article		CITATIONS
323	Environmental and genetic modulation of the phenotypic expression of antibiotic resistance. FEMS Microbiology Reviews, 2017, 41, 374-391.	3.9	112
324	The antibiotic resistome: gene flow in environments, animals and human beings. Frontiers of Medicine, 2017, 11, 161-168.	1.5	84
325	The Threat of Antimicrobial Resistance on the Human Microbiome. Microbial Ecology, 2017, 74, 1001-1008.	1.4	102
326	Reduction in fecal microbiota diversity and short-chain fatty acid producers in Methicillin-resistant Staphylococcus aureus infected individuals as revealed by PacBio single molecule, real-time sequencing technology. European Journal of Clinical Microbiology and Infectious Diseases, 2017, 36, 1463-1472.	1.3	20
327	Fingerprinting microbiomes towards screening for microbial antibiotic resistance. Integrative Biology (United Kingdom), 2017, 9, 406-417.	0.6	30
328	TCDD influences reservoir of antibiotic resistance genes in murine gut microbiome. FEMS Microbiology Ecology, 2017, 93, .	1.3	32
329	Tackling the Antibiotic Resistance: The "Gut―Feeling. , 2017, , 325-338.		2
330	Contact Precautions for Preventing Nosocomial Transmission of Extended-Spectrum β Lactamase–Producing Escherichia coli: A Point/Counterpoint Review. Clinical Infectious Diseases, 2017, 65, 342-347.	2.9	87
331	Long-term use of antibiotics and risk of colorectal adenoma. Gut, 2018, 67, gutjnl-2016-313413.	6.1	125
332	Next-generation approaches to understand and combat the antibiotic resistome. Nature Reviews Microbiology, 2017, 15, 422-434.	13.6	438
334	The Evolution of Antibiotic Resistance. , 2017, , 257-284.		3
335	Can Consideration of the Microbiome Improve Antimicrobial Utilization and Treatment Outcomes in the Oncology Patient?. Clinical Cancer Research, 2017, 23, 3263-3268.	3.2	30
336	On-site removal of antibiotics and antibiotic resistance genes from leachate by aged refuse bioreactor: Effects of microbial community and operational parameters. Chemosphere, 2017, 178, 486-495.	4.2	50
337	Drug Resistance in Bacteria, Fungi, Malaria, and Cancer. , 2017, , .		13
338	Application of genomic technologies to measure and monitor antibiotic resistance in animals. Annals of the New York Academy of Sciences, 2017, 1388, 121-135.	1.8	41
339	Geographically widespread honeybeeâ€gut symbiont subgroups show locally distinct antibioticâ€resistant patterns. Molecular Ecology, 2017, 26, 6590-6607.	2.0	26
341	Metagenomic Cosmid Libraries Suitable for Functional Screening in Proteobacteria. , 2017, , 1-11.		2
342	Human Gut Metagenomics: Success and Limits of the Activity-Based Approaches. , 2017, , 161-178.		0

#	Article	IF	CITATIONS
343	Functional Metagenomics and Antimicrobial Resistance. , 2017, , 243-253.		1
344	Clinical metagenomics of bone and joint infections: a proof of concept study. Scientific Reports, 2017, 7, 7718.	1.6	97
345	Antibiotic-Resistant Environmental Bacteria and Their Role as Reservoirs in Disease. Advances in Environmental Microbiology, 2017, , 187-212.	0.1	3
346	Prediction of antibiotic resistance: time for a new preclinical paradigm?. Nature Reviews Microbiology, 2017, 15, 689-696.	13.6	221
347	A pilot study demonstrating the altered gut microbiota functionality in stable adults with Cystic Fibrosis. Scientific Reports, 2017, 7, 6685.	1.6	35
348	Antimicrobial resistance of Lactobacillus spp. from fermented foods and human gut. LWT - Food Science and Technology, 2017, 86, 201-208.	2.5	21
349	Prudent use and regulatory guidelines for veterinary antibiotics—politics or science?. Journal of Applied Microbiology, 2017, 123, 1373-1380.	1.4	10
350	FARME DB: a functional antibiotic resistance element database. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw165.	1.4	40
352	Evolutionary Trajectories to Antibiotic Resistance. Annual Review of Microbiology, 2017, 71, 579-596.	2.9	179
353	Using metagenomics to investigate human and environmental resistomes. Journal of Antimicrobial Chemotherapy, 2017, 72, 2690-2703.	1.3	87
354	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. Indian Journal of Microbiology, 2017, 57, 23-38.	1.5	21
355	Antibiotics: Pharmacokinetics, toxicity, resistance and multidrug efflux pumps. Biochemical Pharmacology, 2017, 133, 43-62.	2.0	110
356	Translational metagenomics and the human resistome: confronting the menace of the new millennium. Journal of Molecular Medicine, 2017, 95, 41-51.	1.7	20
357	Genomic and functional techniques to mine the microbiome for novel antimicrobials and antimicrobial resistance genes. Annals of the New York Academy of Sciences, 2017, 1388, 42-58.	1.8	38
358	Genomics and the evolution of antibiotic resistance. Annals of the New York Academy of Sciences, 2017, 1388, 92-107.	1.8	50
359	HuMiChip2 for strain level identification and functional profiling of human microbiomes. Applied Microbiology and Biotechnology, 2017, 101, 423-435.	1.7	16
360	Characterization of the binding of neomycin/paromomycin sulfate with DNA using acridine orange as fluorescence probe and molecular docking technique. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2077-2089.	2.0	11
361	Plasmid-mediated colistin resistance in animals: current status and future directions. Animal Health Research Reviews, 2017, 18, 136-152.	1.4	34

#	Article		CITATIONS
362	Factors influencing horizontal gene transfer in the intestine. Animal Health Research Reviews, 2017, 18, 153-159.		32
363	A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds. Journal of Antimicrobial Chemotherapy, 2017, 72, 385-392.	1.3	89
364	Impact of anthropogenic activities on the dissemination of antibiotic resistance across ecological boundaries. Essays in Biochemistry, 2017, 61, 11-21.	2.1	50
365	The oral microbiome. Emerging Topics in Life Sciences, 2017, 1, 287-296.	1.1	4
366	The Role of the Food Chain in the Spread of Antimicrobial Resistance (AMR). , 2017, , 23-47.		9
367	Evolutionary Biology Needs Wild Microbiomes. Frontiers in Microbiology, 2017, 8, 725.	1.5	179
368	Tetracycline Resistance Genes Identified from Distinct Soil Environments in China by Functional Metagenomics. Frontiers in Microbiology, 2017, 8, 1406.	1.5	37
369	MinION Nanopore Sequencing Enables Correlation between Resistome Phenotype and Genotype of Coliform Bacteria in Municipal Sewage. Frontiers in Microbiology, 2017, 8, 2105.	1.5	39
370	The Bacillus subtilis Conjugative Plasmid pLS20 Encodes Two Ribbon-Helix-Helix Type Auxiliary Relaxosome Proteins That Are Essential for Conjugation. Frontiers in Microbiology, 2017, 8, 2138.	1.5	10
371	Detection of antibiotic resistance genes in the feces of young adult Japanese. Bioscience of Microbiota, Food and Health, 2017, 36, 151-154.	0.8	4
372	Effect of antibiotics on bacterial populations: a multi-hierarchical selection process. F1000Research, 2017, 6, 51.	0.8	75
373	Discovery of a new family of relaxases in Firmicutes bacteria. PLoS Genetics, 2017, 13, e1006586.	1.5	49
374	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. Microbiome, 2017, 5, 84.	4.9	247
375	Comparative gut microbiota and resistome profiling of intensive care patients receiving selective digestive tract decontamination and healthy subjects. Microbiome, 2017, 5, 88.	4.9	90
376	Clonality, virulence and antimicrobial resistance of enteroaggregative Escherichia coli from Mirzapur, Bangladesh. Journal of Medical Microbiology, 2017, 66, 1429-1435.	0.7	19
377	Metagenomic Insights into Environmental Microbiome and Their Application in Food/Pharmaceutical Industry. , 2018, , 23-38.		3
378	Engineering chemical interactions in microbial communities. Chemical Society Reviews, 2018, 47, 1705-1729.	18.7	25
379	Microbiota–drug interactions: Impact on metabolism and efficacy of therapeutics. Maturitas, 2018, 112, 53-63.	1.0	71

#	Article		CITATIONS
380	Biochemical mechanisms determine the functional compatibility of heterologous genes. Nature Communications, 2018, 9, 522.	5.8	59
381	Diarrheagenic Escherichia coli and Acute Gastroenteritis in Children in Davidson County, Tennessee, United States: A Case-control Study. Pediatric Infectious Disease Journal, 2018, 37, 543-548.	1.1	17
382	An inÂvitro study to assess the impact of tetracycline on the human intestinal microbiome. Anaerobe, 2018, 49, 85-94.	1.0	32
383	Functional metagenomics reveals a novel carbapenem-hydrolyzing mobile beta-lactamase from Indian river sediments contaminated with antibiotic production waste. Environment International, 2018, 112, 279-286.	4.8	60
384	MetaCherchant: analyzing genomic context of antibiotic resistance genes in gut microbiota. Bioinformatics, 2018, 34, 434-444.	1.8	31
385	The antibiotic resistome and microbiota landscape of refugees from Syria, Iraq and Afghanistan in Germany. Microbiome, 2018, 6, 37.	4.9	21
386	Effect of biochar amendment on the alleviation of antibiotic resistance in soil and phyllosphere of Brassica chinensis L Soil Biology and Biochemistry, 2018, 119, 74-82.	4.2	105
387	Reduced Susceptibility to Antiseptics Is Conferred by Heterologous Housekeeping Genes. Microbial Drug Resistance, 2018, 24, 105-112.	0.9	11
388	Environmental factors influencing the development and spread of antibiotic resistance. FEMS Microbiology Reviews, 2018, 42, .	3.9	612
389	The Search for â€ ⁻ Evolution-Proof' Antibiotics. Trends in Microbiology, 2018, 26, 471-483.	3.5	68
390	Antibiotic Resistance Gene Detection in the Microbiome Context. Microbial Drug Resistance, 2018, 24, 542-546.	0.9	14
391	Antibiotic resistome in a largeâ€scale healthy human gut microbiota deciphered by metagenomic and network analyses. Environmental Microbiology, 2018, 20, 355-368.	1.8	141
392	Human Resistome Study with Metagenomic Sequencing Data. Hanyang Medical Reviews, 2018, 38, 73.	0.4	1
393	Metagenomics of Antimicrobial Resistance in Gut Microbiome. , 2018, , .		0
394	Human microbiomes and antibiotic resistance. Human Microbiome Journal, 2018, 10, 43-52.	3.8	84
395	Microbiome as a tool and a target in the effort to address antimicrobial resistance. Proceedings of the United States of America, 2018, 115, 12902-12910.	3.3	72
396	Bifidobacterial Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. MSphere, 2018, 3, .	1.3	71
397	Rapidly mitigating antibiotic resistant risks in chicken manure by <scp><i>Hermetia illucens</i></scp> bioconversion with intestinal microflora. Environmental Microbiology, 2018, 20, 4051-4062.	1.8	46

#	Article		CITATIONS
398	The Role of Phage in the Adaptation of Bacteria to New Environmental Niches. Grand Challenges in Biology and Biotechnology, 2018, , 267-306.	2.4	4
399	Integrative metagenomic and biochemical studies on rifamycin ADP-ribosyltransferases discovered in the sediment microbiome. Scientific Reports, 2018, 8, 12143.	1.6	7
400	A Population-Based Surveillance Study of Shared Genotypes of Escherichia coli Isolates from Retail Meat and Suspected Cases of Urinary Tract Infections. MSphere, 2018, 3, .	1.3	75
401	Detection of the antimicrobial resistance genes blaTEM-1, cfxA, tetQ, tetM, tetW and ermC in endodontic infections of a Mexican population. Journal of Global Antimicrobial Resistance, 2018, 15, 20-24.	0.9	10
402	The host microbiome and impact of tuberculosis chemotherapy. Tuberculosis, 2018, 113, 26-29.	0.8	19
403	Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system. FEMS Microbiology Ecology, 2018, 94, .	1.3	72
404	Characterization of Wild and Captive Baboon Gut Microbiota and Their Antibiotic Resistomes. MSystems, 2018, 3, .	1.7	51
405	Impact of the Use and Type of Antibiotics on Acute Graft-versus-Host Disease. Biology of Blood and Marrow Transplantation, 2018, 24, 2178-2183.	2.0	28
406	Resistance to Enediyne Antitumor Antibiotics by Sequestration. Cell Chemical Biology, 2018, 25, 1075-1085.e4.	2.5	21
407	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. Cell Reports, 2018, 24, 1190-1202.e5.	2.9	56
408	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908.	5.9	230
409	Evolution of Plasmid-Mediated Antibiotic Resistance in the Clinical Context. Trends in Microbiology, 2018, 26, 978-985.	3.5	284
410	Long-term organic fertilization increased antibiotic resistome in phyllosphere of maize. Science of the Total Environment, 2018, 645, 1230-1237.	3.9	97
411	Functional Repertoire of Antibiotic Resistance Genes in Antibiotic Manufacturing Effluents and Receiving Freshwater Sediments. Frontiers in Microbiology, 2017, 8, 2675.	1.5	40
412	The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variants—but not always. Microbiome, 2018, 6, 125.	4.9	39
413	Safety Evaluations of Bifidobacterium bifidum BCN4 and Bifidobacterium longum BORI. International Journal of Molecular Sciences, 2018, 19, 1422.	1.8	83
414	The evolving interface between synthetic biology and functional metagenomics. Nature Chemical Biology, 2018, 14, 752-759.	3.9	44
415	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	4.9	115

#	Article		CITATIONS
416	Acid-resistant genes of oral plaque microbiome from the functional metagenomics. Journal of Oral Microbiology, 2018, 10, 1424455.		4
417	CRISPR-Cas antimicrobials: Challenges and future prospects. PLoS Pathogens, 2018, 14, e1006990.	2.1	105
418	High genomic diversity of multi-drug resistant wastewater Escherichia coli. Scientific Reports, 2018, 8, 8928.	1.6	39
419	Fast and efficient inactivation of antibiotic resistant Escherichia coli by iron electrode-activated sodium peroxydisulfate in a galvanic cell. Chemical Engineering Journal, 2019, 355, 150-158.	6.6	28
420	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. , 2019, , 175-223.		3
421	Early-life gut microbiome modulation reduces the abundance of antibiotic-resistant bacteria. Antimicrobial Resistance and Infection Control, 2019, 8, 131.	1.5	63
422	<i>Escherichia coli</i> from Commercial Broiler and Backyard Chickens Share Sequence Types, Antimicrobial Resistance Profiles, and Resistance Genes with Human Extraintestinal Pathogenic <i>Escherichia coli</i> . Foodborne Pathogens and Disease, 2019, 16, 813-822.	0.8	45
423	Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nature Microbiology, 2019, 4, 1432-1442.	5.9	614
424	Pharmacomicrobiomics informs clinical pharmacogenomics. Pharmacogenomics, 2019, 20, 731-739.	0.6	7
425	Antibiotic resistance in Pseudomonas aeruginosa – Mechanisms, epidemiology and evolution. Drug Resistance Updates, 2019, 44, 100640.	6.5	269
427	Pharmaceutical exposure changed antibiotic resistance genes and bacterial communities in soil-surface- and overhead-irrigated greenhouse lettuce. Environment International, 2019, 131, 105031.	4.8	48
428	<p>Evaluation of gut bacterial community composition and antimicrobial resistome in pregnant and non-pregnant women from Saudi population</p> . Infection and Drug Resistance, 2019, Volume 12, 1749-1761.	1.1	18
429	Surface Exclusion Revisited: Function Related to Differential Expression of the Surface Exclusion System of Bacillus subtilis Plasmid pLS20. Frontiers in Microbiology, 2019, 10, 1502.	1.5	11
430	Sewage effluent from an Indian hospital harbors novel carbapenemases and integron-borne antibiotic resistance genes. Microbiome, 2019, 7, 97.	4.9	76
433	Quantifying the impact of treatment history on plasmid-mediated resistance evolution in human gut microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23106-23116.	3.3	19
434	Streptococcal peptides that signal <scp><i>Enterococcus faecalis</i></scp> cells carrying the pheromoneâ€responsive conjugative plasmid pAM373. Molecular Oral Microbiology, 2019, 34, 254-262.	1.3	4
435	The evolution of antibiotic resistance. Science, 2019, 365, 1082-1083.	6.0	322
436	Fecal Transplant in Children With Clostridioides difficile Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. Open Forum Infectious Diseases, 2019, 6, ofz379.	0.4	32

#	Article		CITATIONS
437	The fecal resistome of dairy cattle is associated with diet during nursing. Nature Communications, 2019, 10, 4406.		100
438	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. Nature Communications, 2019, 10, 4538.	5.8	222
439	Anaerobes in cystic fibrosis patients' airways. Critical Reviews in Microbiology, 2019, 45, 103-117.	2.7	19
440	Importance of antibiotic residues in animal food. Food and Chemical Toxicology, 2019, 125, 462-466.	1.8	343
441	High throughput cultivation-based screening on porous aluminum oxide chips allows targeted isolation of antibiotic resistant human gut bacteria. PLoS ONE, 2019, 14, e0210970.	1.1	15
442	Discovery and Characterization of Cas9 Inhibitors Disseminated across Seven Bacterial Phyla. Cell Host and Microbe, 2019, 25, 233-241.e5.	5.1	63
443	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. Nature Communications, 2019, 10, 308.	5.8	33
444	Aminoglycoside Enhances the Delivery of Antisense Morpholino Oligonucleotides InÂVitro and in mdx Mice. Molecular Therapy - Nucleic Acids, 2019, 16, 663-674.	2.3	8
445	Transfer of a lincomycin-resistant plasmid between coagulase-negative staphylococci during soybean fermentation and mouse intestine passage. FEMS Microbiology Letters, 2019, 366, .	0.7	7
446	Gut microbiome interventions in human health and diseases. Medicinal Research Reviews, 2019, 39, 2286-2313.	5.0	52
447	Antibiotic Treatment Drives the Diversification of the Human Gut Resistome. Genomics, Proteomics and Bioinformatics, 2019, 17, 39-51.	3.0	51
448	Nasal Resistome Development in Infants With Cystic Fibrosis in the First Year of Life. Frontiers in Microbiology, 2019, 10, 212.	1.5	10
449	VERA: agent-based modeling transmission of antibiotic resistance between human pathogens and gut microbiota. Bioinformatics, 2019, 35, 3803-3811.	1.8	4
450	Two Component Regulatory Systems and Antibiotic Resistance in Gram-Negative Pathogens. International Journal of Molecular Sciences, 2019, 20, 1781.	1.8	111
451	Metagenome analysis and interpretation. , 2019, , 139-160.		5
453	Identification and reconstruction of novel antibiotic resistance genes from metagenomes. Microbiome, 2019, 7, 52.	4.9	84
454	Metagenomic characterization of antibiotic resistance genes in Antarctic soils. Ecotoxicology and Environmental Safety, 2019, 176, 300-308.	2.9	58
455	Comparative Metagenomics and Network Analyses Provide Novel Insights Into the Scope and Distribution of β-Lactamase Homologs in the Environment. Frontiers in Microbiology, 2019, 10, 146.	1.5	18

		CITATION REP	PORT	
#	Article		IF	CITATIONS
456	Rapid molecular detection of macrolide resistance. BMC Infectious Diseases, 2019, 19, 144.		1.3	10
457	Gut microbiota of aquatic organisms: A key endpoint for ecotoxicological studies. Environme Pollution, 2019, 248, 989-999.	ntal	3.7	160
458	Metagenomic Next-Generation Sequencing in Clinical Microbiology. Indian Journal of Medica Microbiology, 2019, 37, 133-140.	l	0.3	12
460	Antimicrobial Resistance, Gut Microbiota, and Health. , 2019, , 902-926.			2
461	Comparative network analysis revealing the mechanisms of antibiotic resistance genes remo leachate recirculation under different hydraulic loadings. Science of the Total Environment, 2 649, 318-326.	val by 019,	3.9	22
462	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the h gut microbiota. Nature Microbiology, 2019, 4, 447-458.	iuman	5.9	68
463	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	?	5.9	129
464	Antibiotics as both friends and foes of the human gut microbiome: The microbial community Drug Development Research, 2019, 80, 86-97.	approach.	1.4	43
465	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchar upregulated expression in the effluent microbiomes. ISME Journal, 2019, 13, 346-360.	ıge, and	4.4	289
466	Within-host heterogeneity and flexibility of mcr-1 transmission in chicken gut. International J of Antimicrobial Agents, 2020, 55, 105806.	ournal	1.1	33
467	Preventive antibiotic treatment of calves: emergence of dysbiosis causing propagation of ob stateâ€associated and mobile multidrug resistanceâ€carrying bacteria. Microbial Biotechnolo 669-682.	ese ogy, 2020, 13,	2.0	18
468	Think before you prescribe: how dentistry contributes to antibiotic resistance. Australian Der Journal, 2020, 65, 21-29.	ntal	0.6	25
469	Chemistry and Enzymology Encoded by the Human Microbiome. , 2020, , 261-286.			0
470	Forensic human identification using skin microbiome genetic signatures. , 2020, , 155-169.			1
471	Gut microbiota and old age: Modulating factors and interventions for healthy longevity. Experimental Gerontology, 2020, 141, 111095.		1.2	61
472	Understanding the impact of antibiotic perturbation on the human microbiome. Genome Me 2020, 12, 82.	dicine,	3.6	148
473	Antimicrobial Resistance in <i>Escherichia coli</i> ., 0, , .			19
474	Antibiotics in Food Chain: The Consequences for Antibiotic Resistance. Antibiotics, 2020, 9, 0	688.	1.5	60

#	Article	IF	CITATIONS
475	Overview. Infectious Disease Clinics of North America, 2020, 34, 649-658.	1.9	22
476	Multidrug-resistant genes and pathogenic bacteria in hospital wastewater. , 2020, , 177-202.		0
477	Antimicrobial Resistance. , 2020, , .		2
478	Widespread transfer of mobile antibiotic resistance genes within individual gut microbiomes revealed through bacterial Hi-C. Nature Communications, 2020, 11, 4379.	5.8	116
479	Emergence of tigecycline- and eravacycline-resistant Tet(X4)-producing Enterobacteriaceae in the gut microbiota of healthy Singaporeans. Journal of Antimicrobial Chemotherapy, 2020, 75, 3480-3484.	1.3	34
480	The Toothbrush Microbiome: Impact of User Age, Period of Use and Bristle Material on the Microbial Communities of Toothbrushes. Microorganisms, 2020, 8, 1379.	1.6	10
481	Human Movement and Transmission of Antimicrobial-Resistant Bacteria. Handbook of Environmental Chemistry, 2020, , 311-344.	0.2	2
482	Antibiotic Resistance in the Environment. Handbook of Environmental Chemistry, 2020, , .	0.2	5
483	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. Scientific Reports, 2020, 10, 18870.	1.6	13
484	Integron gene cassettes harboring novel variants of d-alanine-d-alanine ligase confer high-level resistance to d-cycloserine. Scientific Reports, 2020, 10, 20709.	1.6	4
485	Factors Obscuring the Role of E. coli from Domestic Animals in the Global Antimicrobial Resistance Crisis: An Evidence-Based Review. International Journal of Environmental Research and Public Health, 2020, 17, 3061.	1.2	34
486	Antibiotic resistomes discovered in the gut microbiomes of Korean swine and cattle. GigaScience, 2020, 9, .	3.3	32
487	Defining the oral microbiome by whole-genome sequencing and resistome analysis: the complexity of the healthy picture. BMC Microbiology, 2020, 20, 120.	1.3	152
488	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. Nature Communications, 2020, 11, 2354.	5.8	75
489	Combining metagenomics and metatranscriptomics to study human, animal and environmental resistomes. Medicine in Microecology, 2020, 3, 100014.	0.7	6
490	Personalized Mapping of Drug Metabolism by the Human Gut Microbiome. Cell, 2020, 181, 1661-1679.e22.	13.5	239
491	Combination therapy against multidrug resistance. , 2020, , 39-64.		2
492	Metatranscriptomics Reveals Antibiotic-Induced Resistance Gene Expression in the Murine Gut Microbiota. Frontiers in Microbiology, 2020, 11, 322.	1.5	16

#	Article	IF	CITATIONS
493	The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography. ISME Journal, 2020, 14, 1584-1599.	4.4	78
494	Metagenomic analysis reveals the microbiome and resistome in migratory birds. Microbiome, 2020, 8, 26.	4.9	109
495	Programmable removal of bacterial pathogens using CRISPR-Cas9 system. , 2020, , 39-44.		1
496	Addressing Learning Needs on the Use of Metagenomics in Antimicrobial Resistance Surveillance. Frontiers in Public Health, 2020, 8, 38.	1.3	11
497	What Is Metagenomics Teaching Us, and What Is Missed?. Annual Review of Microbiology, 2020, 74, 117-135.	2.9	54
498	Wastewater treatment plants and release: The vase of Odin for emerging bacterial contaminants, resistance and determinant of environmental wellness. Emerging Contaminants, 2020, 6, 212-224.	2.2	18
499	Microbiome diversity inÂDiaphorina citriÂpopulations from Kenya and Tanzania shows links to China. PLoS ONE, 2020, 15, e0235348.	1.1	9
500	Urbanization drives riverine bacterial antibiotic resistome more than taxonomic community at watershed scale. Environment International, 2020, 137, 105524.	4.8	76
501	Emerging Priorities for Microbiome Research. Frontiers in Microbiology, 2020, 11, 136.	1.5	113
502	Manure fertilization increase antibiotic resistance in soils from typical greenhouse vegetable production bases, China. Journal of Hazardous Materials, 2020, 391, 122267.	6.5	61
503	Mobilizable antibiotic resistance genes are present in dust microbial communities. PLoS Pathogens, 2020, 16, e1008211.	2.1	25
504	From Metagenomes to Molecules: Innovations in Functional Metagenomics Unlock Hidden Chemistry in the Human Microbiome. Biochemistry, 2020, 59, 729-730.	1.2	5
505	Antibiotic resistance: turning evolutionary principles into clinical reality. FEMS Microbiology Reviews, 2020, 44, 171-188.	3.9	154
506	Systematic review of human gut resistome studies revealed variable definitions and approaches. Gut Microbes, 2020, 12, 1700755.	4.3	15
507	Persistence of wastewater antibiotic resistant bacteria and their genes in human fecal material. FEMS Microbiology Ecology, 2020, 96, .	1.3	3
508	The prolonged disruption of a single-course amoxicillin on mice gut microbiota and resistome, and recovery by inulin, Bifidobacterium longum and fecal microbiota transplantation. Environmental Pollution, 2020, 265, 114651.	3.7	23
509	Recombinant lactobacillin PlnK adjusts the gut microbiome distribution in broilers. British Poultry Science, 2020, 61, 390-399.	0.8	9
510	Problems of conventional disinfection and new sterilization methods for antibiotic resistance control. Chemosphere, 2020, 254, 126831.	4.2	85

#	Article	IF	CITATIONS
511	Dental plaque microbiota of pet owners and their dogs as a shared source and reservoir of antimicrobial resistance genes. Journal of Global Antimicrobial Resistance, 2020, 21, 285-290.	0.9	13
512	Resident microbial communities inhibit growth and antibiotic-resistance evolution of Escherichia coli in human gut microbiome samples. PLoS Biology, 2020, 18, e3000465.	2.6	47
513	Two genes involved in clindamycin resistance of Bacillus licheniformis and Bacillus paralicheniformis identified by comparative genomic analysis. PLoS ONE, 2020, 15, e0231274.	1.1	15
514	Geographic pattern of antibiotic resistance genes in the metagenomes of the giant panda. Microbial Biotechnology, 2021, 14, 186-197.	2.0	28
515	Evaluation of recreational risks due to exposure of antibiotic-resistance bacteria from environmental water: A proposed framework. Journal of Environmental Management, 2021, 279, 111626.	3.8	11
516	Is the term "anti-anaerobic―still relevant?. International Journal of Infectious Diseases, 2021, 102, 178-180.	1.5	9
517	Human Gut Microbiome: A Potential Prospective to Counter Antibiotic-Resistant Pathogens. , 2022, , 368-368.		2
518	Intestinal Dysbiosis in Infectious Diseases. , 2022, , 501-514.		0
519	Functional Metagenomic Screening for Antimicrobial Resistance in the. Methods in Molecular Biology, 2021, 2327, 31-50.	0.4	2
521	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. Gut Microbes, 2021, 13, 1-19.	4.3	24
522	Futuristic Non-antibiotic Therapies to Combat Antibiotic Resistance: A Review. Frontiers in Microbiology, 2021, 12, 609459.	1.5	93
523	Gut microbiome and <i>Clostridioides difficile</i> infection: a closer look at the microscopic interface. Therapeutic Advances in Gastroenterology, 2021, 14, 175628482199473.	1.4	31
525	Role prediction of Gram-negative species in the resistome of raw cow's milk. International Journal of Food Microbiology, 2021, 340, 109045.	2.1	6
526	Characterization of the human skin resistome and identification of two microbiota cutotypes. Microbiome, 2021, 9, 47.	4.9	42
528	HMD-ARG: hierarchical multi-task deep learning for annotating antibiotic resistance genes. Microbiome, 2021, 9, 40.	4.9	48
529	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. Microbiome, 2021, 9, 49.	4.9	81
530	Fecal Microbiome and Resistome Profiling of Healthy and Diseased Pakistani Individuals Using Next-Generation Sequencing. Microorganisms, 2021, 9, 616.	1.6	5
531	Antibiotic resistome from the One-Health perspective: understanding and controlling antimicrobial resistance transmission. Experimental and Molecular Medicine, 2021, 53, 301-309.	3.2	113

#	Article	IF	CITATIONS
532	Removal of antibiotic resistance genes from swine wastewater by membrane filtration treatment. Ecotoxicology and Environmental Safety, 2021, 210, 111885.	2.9	77
533	Novel class 1 integron harboring antibiotic resistance genes in wastewater-derived bacteria as revealed by functional metagenomics. Plasmid, 2021, 114, 102563.	0.4	4
535	Experimental systems biology approaches reveal interaction mechanisms in model multispecies communities. Trends in Microbiology, 2021, 29, 1083-1094.	3.5	9
536	A novel bipartite antitermination system widespread in conjugative elements of Gram-positive bacteria. Nucleic Acids Research, 2021, 49, 5553-5567.	6.5	5
537	Insights into Emergence of Antibiotic Resistance in Acid-Adapted Enterohaemorrhagic Escherichia coli. Antibiotics, 2021, 10, 522.	1.5	10
538	Antioxidant Molecules as a Source of Mitigation of Antibiotic Resistance Gene Dissemination. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	8
539	Metagenomics and Other Omics Approaches to Bacterial Communities and Antimicrobial Resistance Assessment in Aquacultures. Antibiotics, 2021, 10, 787.	1.5	7
540	Colistin Selection of the Mcr-1 Gene in Broiler Chicken Intestinal Microbiota. Antibiotics, 2021, 10, 677.	1.5	1
541	Mosaic Ends Tagmentation (METa) Assembly for Highly Efficient Construction of Functional Metagenomic Libraries. MSystems, 2021, 6, e0052421.	1.7	2
542	Characterization of Extended-Spectrum Cephalosporin (ESC) Resistance in Salmonella Isolated from Chicken and Identification of High Frequency Transfer of blaCMY-2 Gene Harboring Plasmid In Vitro and In Vivo. Animals, 2021, 11, 1778.	1.0	2
543	Metagenomics analysis revealed the distinctive ruminal microbiome and resistive profiles in dairy buffaloes. Animal Microbiome, 2021, 3, 44.	1.5	11
544	Targeting the gut microbiome: An emerging trend in hematopoietic stem cell transplantation. Blood Reviews, 2021, 48, 100790.	2.8	28
545	Linking plasmid-based beta-lactamases to their bacterial hosts using single-cell fusion PCR. ELife, 2021, 10, .	2.8	18
546	Tracking the transition to agriculture in Southern Europe through ancient DNA analysis of dental calculus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	29
547	Probiotics impact the antibiotic resistance gene reservoir along the human GI tract in a person-specific and antibiotic-dependent manner. Nature Microbiology, 2021, 6, 1043-1054.	5.9	109
548	Antibiotic Resistance Decreases the Efficacy of Endodontic Filling Pastes for Root Canal Treatment in Children′s Teeth. Children, 2021, 8, 692.	0.6	6
549	Phylum barrier and Escherichia coli intra-species phylogeny drive the acquisition of antibiotic-resistance genes. Microbial Genomics, 2021, 7, .	1.0	9
550	Embracing Metagenomic Complexity with a Genome-Free Approach. MSystems, 2021, 6, e0081621.	1.7	9

#	Article	IF	CITATIONS
551	Characteristics of phytoplankton-zooplankton communities and the roles in the transmission of antibiotic resistance genes under the pressure of river contamination. Science of the Total Environment, 2021, 780, 146452.	3.9	14
552	Metagenomics-Based Analysis of the Age-Related Cumulative Effect of Antibiotic Resistance Genes in Gut Microbiota. Antibiotics, 2021, 10, 1006.	1.5	12
553	Occurrence of Mycoplasma spp. in wild birds: phylogenetic analysis and potential factors affecting distribution. Scientific Reports, 2021, 11, 17065.	1.6	6
554	More diversified antibiotic resistance genes in chickens and workers of the live poultry markets. Environment International, 2021, 153, 106534.	4.8	41
555	Genome-Scale Metabolic Models and Machine Learning Reveal Genetic Determinants of Antibiotic Resistance in Escherichia coli and Unravel the Underlying Metabolic Adaptation Mechanisms. MSystems, 2021, 6, e0091320.	1.7	26
556	Antibiotic resistance genes on the Qinghai-Tibet Plateau above an elevation of 5,000 m. Environmental Science and Pollution Research, 2022, 29, 4508-4518.	2.7	4
557	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.	1.5	26
558	Microbiomes and Resistomes in Biopsy Tissue and Intestinal Lavage Fluid of Colorectal Cancer. Frontiers in Cell and Developmental Biology, 2021, 9, 736994.	1.8	9
559	The Human Gut Resistome up to Extreme Longevity. MSphere, 2021, 6, e0069121.	1.3	12
560	Gastric acid suppression, lifestyle factors and intestinal carriage of ESBL and carbapenemase-producing Enterobacterales: a nationwide population-based study. Journal of Antimicrobial Chemotherapy, 2021, 77, 237-245.	1.3	6
561	Extended-Spectrum β-Lactamase-Producing and <i>mcr-1</i> -Positive Escherichia coli from the Gut Microbiota of Healthy Singaporeans. Applied and Environmental Microbiology, 2021, 87, e0048821.	1.4	10
562	Carbon source type can affect tetracycline removal by Pseudomonas sp. TC952 through regulation of extracellular polymeric substances composition and production. Science of the Total Environment, 2022, 804, 149907.	3.9	12
565	Metagenomics of the Human Body. , 2011, , .		18
566	Recent Progress in Engineering Human-Associated Microbiomes. Methods in Molecular Biology, 2014, 1151, 3-25.	0.4	15
567	Bioprospecting for β-lactam resistance genes using a metagenomics-guided strategy. Applied Microbiology and Biotechnology, 2017, 101, 6253-6260.	1.7	2
568	Antibiotic-contaminated wastewater irrigated vegetables pose resistance selection risks to the gut microbiome. Environmental Pollution, 2020, 264, 114752.	3.7	66
569	Streptococcus gordonii pheromone s.g.cAM373 may influence the reservoir of antibiotic resistance determinants of Enterococcus faecalis origin in the oral metagenome. Journal of Medical Microbiology, 2017, 66, 1635-1639.	0.7	5
570	Excess body weight and age associated with the carriage of fluoroquinolone and third-generation cephalosporin resistance genes in commensal Escherichia coli from a cohort of urban Vietnamese children. Journal of Medical Microbiology, 2018, 67, 1457-1466.	0.7	8

#	Article	IF	Citations
577	Novel Computational Protocols for Functionally Classifying and Characterising Serine Beta-Lactamases. PLoS Computational Biology, 2016, 12, e1004926.	1.5	24
578	The Genome of Akkermansia muciniphila, a Dedicated Intestinal Mucin Degrader, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876.	1.1	328
579	The Gut as Reservoir of Antibiotic Resistance: Microbial Diversity of Tetracycline Resistance in Mother and Infant. PLoS ONE, 2011, 6, e21644.	1.1	111
580	Pediatric Fecal Microbiota Harbor Diverse and Novel Antibiotic Resistance Genes. PLoS ONE, 2013, 8, e78822.	1.1	150
581	In Silico Analysis of Antibiotic Resistance Genes in the Gut Microflora of Individuals from Diverse Geographies and Age-Groups. PLoS ONE, 2013, 8, e83823.	1.1	74
582	Development of HuMiChip for Functional Profiling of Human Microbiomes. PLoS ONE, 2014, 9, e90546.	1.1	18
583	Impact of extensive antibiotic treatment on faecal carriage of antibiotic-resistant enterobacteria in children in a low resistance prevalence setting. PLoS ONE, 2017, 12, e0187618.	1.1	14
584	How to Fight Back Against Antibiotic Resistance. American Scientist, 2014, 102, 42.	0.1	51
585	Diverse Distribution of Resistomes in the Human and Environmental Microbiomes. Current Genomics, 2018, 19, 701-711.	0.7	10
586	Personal genomes in progress: from the Human Genome Project to the Personal Genome Project. Dialogues in Clinical Neuroscience, 2010, 12, 47-60.	1.8	64
588	ENDOECOLOGICAL ASPECTS OF ANTIBIOTIC RESISTANCE: A LITERATURE REVIEW. Ekologiya Cheloveka (Human Ecology), 2020, , 31-36.	0.2	2
589	Mikrobiyota, prebiyotik ve probiyotikler. Anadolu Güncel Tıp Dergisi, 2019, 1, 68-71.	0.0	6
590	The human gut resistome: Current concepts & future prospects. Indian Journal of Medical Research, 2019, 150, 345.	0.4	28
591	Resistance Is Mobile: The Accelerating Evolution of Mobile Genetic Elements Encoding Resistance. Journal of Evolutionary Medicine, 2014, 2, 1-3.	0.5	5
592	Commensal Staphylococcus spp., Acinetobacter spp. and Stenotrophomonas maltophilia as reservoirs of antibiotic resistance genes. African Journal of Biotechnology, 2012, 11, .	0.3	1
593	Dissemination of antibiotic resistance genes associated with the sporobiota in sediments impacted by wastewater. PeerJ, 2018, 6, e4989.	0.9	12
594	Human gut resistome can be country-specific. PeerJ, 2019, 7, e6389.	0.9	13
595	Applying a Novel Fuzzy-PI Controller on the Model of Continuous Stirred Tank Reactor. International Journal of Machine Learning and Computing, 2011, , 218-223.	0.8	3

#	Article	IF	CITATIONS
596	High level of intrinsic phenotypic antimicrobial resistance in enterobacteria from terrestrial wildlife in Gabonese national parks. PLoS ONE, 2021, 16, e0257994.	1.1	7
597	Microbiome research potential for developing holistic approaches to improve refugee health. Journal of Global Health Reports, 0, , .	1.0	0
599	Mobile Metagenome. , 2012, , 1-15.		0
600	Potential Adverse Microbiological Effects of Antimicrobials. Issues in Toxicology, 2012, , 403-428.	0.2	0
601	A proposed model for understanding human-bacterial interactions: Space-time approach on community <i>Escherichia coli</i> occurrence and resistance phenomenon. Advances in Bioscience and Biotechnology (Print), 2013, 04, 505-508.	0.3	0
602	Metagenome. , 2014, , 1-3.		Ο
604	Antibiotic Resistance in and from Nature. , 0, , 183-194.		1
605	Metagenome. , 2015, , 1525-1526.		0
606	Can Science Make Peace with the Environment? Science, Power, Exploitation. Boston Studies in the Philosophy and History of Science, 2015, , 367-383.	0.4	0
607	Mining Metagenomic Datasets for Antibiotic Resistance Genes. , 2015, , 487-492.		0
610	Evolutionary Biology of Drug Resistance. , 2017, , 9-36.		2
615	The gut microbiota resistome provides development of drug resistance in causative agents of human infectious diseases. Nauchno-prakticheskii Zhurnal «Patogenez», 2017, , 20-32.	0.2	2
617	Fire in the Forest: Adverse Effects of Antibiotics on the Healthy Human Gut Microbiome. International Journal of Medical Reviews, 2018, 5, 19-26.	0.4	1
621	The use of lactulose and lignin in the complex treatment of patients with dysbiotic vaginal processes. Reproductive Endocrinology, 2018, .	0.0	0
622	Résistance aux antibiotiques et mécanismes d'action des huiles essentielles contre les bactéries. Phytotherapie, 2018, 16, S173-S183.	0.1	1
623	Are Ancient Remedies the New Answer to Fighting Infections?. , 2019, , 351-394.		0
630	Antimicrobial resistance of Escherichia coli, isolated from children's intestinal microbiota. Klinichescheskaya Laboratornaya Diagnostika, 2020, 65, 638-644.	0.2	1
631	Identification, Characterization, and Antioxidant Potential of Bifidobacterium longum subsp. longum Strains Isolated From Feces of Healthy Infants. Frontiers in Microbiology, 2021, 12, 756519.	1.5	11

#	Article	IF	CITATIONS
632	Influence of Antimicrobials on the Gut Microbiota. , 2020, , 53-79.		0
633	<i>Burkholderiaceae</i> and Multidrug Resistance Genes Are Key Players in Resistome Development in a Germfree Soil Model. MSystems, 2021, 6, e0098821.	1.7	7
635	Antibacterial activity and mechanism of berberine against Streptococcus agalactiae. International Journal of Clinical and Experimental Pathology, 2015, 8, 5217-23.	0.5	60
636	Molecular Surveillance of Carbapenem-Resistant Gram-Negative Bacteria in Liver Transplant Candidates. Frontiers in Microbiology, 2021, 12, 791574.	1.5	4
637	A One Health Review of Community-Acquired Antimicrobial-Resistant Escherichia coli in India. International Journal of Environmental Research and Public Health, 2021, 18, 12089.	1.2	5
638	Cross-regional scale pollution of freshwater biofilms unveiled by antibiotic resistance genes. Science of the Total Environment, 2022, 818, 151835.	3.9	11
639	Gene Amplification Uncovers Large Previously Unrecognized Cryptic Antibiotic Resistance Potential in E. coli. Microbiology Spectrum, 2021, 9, e0028921.	1.2	11
640	Safety assessment of Streptococcus salivarius M18 a probiotic for oral health. Beneficial Microbes, 2022, 13, 47-60.	1.0	10
641	Impact of antibiotics on the human microbiome and consequences for host health. MicrobiologyOpen, 2022, 11, e1260.	1.2	169
642	Classic studies of microbial evolution (antibiotic, metal). , 2022, , 293-314.		0
644	Targeted (PCR-based) screening of antibiotic resistance genes' prevalence in the gut microbiota of tribal people of Nabarangpur, Odisha, India. Letters in Applied Microbiology, 2022, 74, 577-585.	1.0	1
645	Bacteroidales species in the human gut are a reservoir of antibiotic resistance genes regulated by invertible promoters. Npj Biofilms and Microbiomes, 2022, 8, 1.	2.9	22
646	Using metagenomic data to boost protein structure prediction and discovery. Computational and Structural Biotechnology Journal, 2022, 20, 434-442.	1.9	3
647	UHPLC-MS/MS Analysis of Antibiotics Transfer and Concentrations in Porcine Oral Fluid after Intramuscular Application. Pharmaceuticals, 2022, 15, 225.	1.7	3
648	Whole Genome Analysis of 335 New Bacterial Species from Human Microbiota Reveals a Huge Reservoir of Transferable Antibiotic Resistance Determinants. International Journal of Molecular Sciences, 2022, 23, 2137.	1.8	0
649	Good microbes, bad genes? The dissemination of antimicrobial resistance in the human microbiome. Gut Microbes, 2022, 14, 2055944.	4.3	50
650	Gut Commensal Escherichia coli, a High-Risk Reservoir of Transferable Plasmid-Mediated Antimicrobial Resistance Traits. Infection and Drug Resistance, 2022, Volume 15, 1077-1091.	1.1	12
651	Non-caloric artificial sweeteners exhibit antimicrobial activity against bacteria and promote bacterial evolution of antibiotic tolerance. Journal of Hazardous Materials, 2022, 433, 128840.	6.5	15

#	Article	IF	CITATIONS
652	Legacy and Emerging Pollutants in an Urban River Stretch and Effects on the Bacterioplankton Community. Water (Switzerland), 2021, 13, 3402.	1.2	7
653	Topical Versus Oral Metronidazole After Excisional Hemorrhoidectomy: A Double-Blind Randomized Controlled Trial. Diseases of the Colon and Rectum, 2022, 65, 1362-1372.	0.7	2
654	A Novel Efficient L-Lysine Exporter Identified by Functional Metagenomics. Frontiers in Microbiology, 2022, 13, 855736.	1.5	7
670	Genomic Tools for the Impact Assessment of 'Hotspots' for Early Warning of MDR Threats. Biomedical and Environmental Sciences, 2016, 29, 656-674.	0.2	3
671	Safety and Efficacy of an AIEC-targeted Bacteriophage Cocktail in a Mice Colitis Model. Journal of Crohn's and Colitis, 2022, 16, 1617-1627.	0.6	9
672	Metagenomics Reveals the Diversity and Taxonomy of Carbohydrate-Active Enzymes and Antibiotic Resistance Genes in Suancai Bacterial Communities. Genes, 2022, 13, 773.	1.0	3
674	Activation of class 1 integron integrase is promoted in the intestinal environment. PLoS Genetics, 2022, 18, e1010177.	1.5	8
675	Evolution of the murine gut resistome following broad-spectrum antibiotic treatment. Nature Communications, 2022, 13, 2296.	5.8	16
676	Metagenomic exploration of antibiotic resistance genes and their hosts in aquaculture waters of the semi-closed Dongshan Bay (China). Science of the Total Environment, 2022, 838, 155784.	3.9	12
677	Dysbiosis and Restoration Dynamics of the Gut Microbiome Following Therapeutic Exposure to Florfenicol in Snubnose Pompano (Trachinotus blochii) to Aid in Sustainable Aquaculture Production Strategies. Frontiers in Microbiology, 2022, 13, .	1.5	3
678	Antibiotic resistance in chronic respiratory diseases: from susceptibility testing to the resistome. European Respiratory Review, 2022, 31, 210259.	3.0	10
679	Antibiotic treatments to mothers during the perinatal period leaving hidden trouble on infants. European Journal of Pediatrics, 2022, 181, 3459-3471.	1.3	2
681	Glucosylated nanoparticles for the oral delivery of antibiotics to the proximal small intestine protect mice from gut dysbiosis. Nature Biomedical Engineering, 2022, 6, 867-881.	11.6	28
682	Microenvironmental Factors that Shape Bacterial Metabolites in Inflammatory Bowel Disease. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	5
683	Molecular Factors and Mechanisms Driving Multidrug Resistance in Uropathogenic Escherichia coli—An Update. Genes, 2022, 13, 1397.	1.0	19
684	Antibiotic resistance genes are differentially mobilized according to resistance mechanism. GigaScience, 2022, 11, .	3.3	11
685	Emergence of antibiotic resistance in gut microbiota and its effect on human health. , 2022, , 211-232.		0
686	Potency of Netilmicin against Staphylococci Compared to Other Ophthalmic Antibiotics. , 0, ,		1

ARTICLE IF CITATIONS # Antimicrobial resistance: new insights and therapeutic implications. Applied Microbiology and 687 1.7 9 Biotechnology, 2022, 106, 6427-6440. Antibiotics and probiotics impact gut antimicrobial resistance gene reservoir in COVID-19 patients. Gut 4.3 Microbes, 2022, 14, . Human Erysipelothrix rhusiopathiae infection via bath water – case report and genome 690 0 1.8 announcement. Frontiers in Cellular and Infection Microbiology, 0, 12, . Multidrug Drug Resistance of & amp; lt; i& amp; gt; Escherichia coli& amp; lt; / i& amp; gt; and <i&gt;Klebsiella&lt;/i&gt; Isolated from Iraqi Patients and Microbiota. Journal of Biosciences and Medicines, 2022, 10, 240-252. 691 0.1 Antibiotic Resistance and the Biology of History. Revue D'Anthropologie Des Connaissances, 2021, 15, . 692 0.1 5 Antimicrobial Resistance and Virulence of <i>Escherichia coli</i> in the Purview of Public Health Monitoring., 0,,. Defining the Benefits of Antibiotic Resistance in Commensals and the Scope for Resistance 694 1.8 2 Optimization. MBio, 2023, 14, . Non-caloric artificial sweeteners modulate conjugative transfer of multi-drug resistance plasmid in 4.3 the gut microbiota. Gut Microbes, 2023, 15, . Longitudinal fluctuations of common antimicrobial resistance genes in the gut microbiomes of 696 2 1.1 healthy Dutch individuals. International Journal of Antimicrobial Agents, 2023, 61, 106716. Metagenomic analysis of gut microbiota and antibiotic-resistant genes in Anser erythropus wintering 1.5 at Shengjin and Caizi Lakes in China. Frontiers in Microbiology, 0, 13, . Metabolic engineering of Escherichia coli for high-level production of free lipoic acid. Metabolic 698 3.6 1 Engineering, 2023, 76, 39-49. Functional metagenomics reveals wildlife as natural reservoirs of novel Î2-lactamases. Science of the 699 Total Environment, 2023, 868, 161505. Differential response to prolonged amoxicillin treatment: long-term resilience of the microbiome 701 4.3 7 versus long-lasting perturbations in the gut resistome. Gut Microbes, 2023, 15, . Environment as Sink for Antimicrobial Resistance and Genes., 2023, , 1-18. The Impact of Non-Pathogenic Bacteria on the Spread of Virulence and Resistance Genes. International 703 1.8 7 Journal of Molecular Sciences, 2023, 24, 1967. Characterization of antibiotic resistomes by reprogrammed bacteriophage-enabled functional 704 5.9 metagenomics in clinical strains. Nature Microbiology, 2023, 8, 410-423. Antimicrobial resistomes in food chain microbiomes. Critical Reviews in Food Science and Nutrition, 705 5.42 0, , 1-22. The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the 1.3 Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. MSphere, 2023, 8, .

#	Article	IF	CITATIONS
707	Alterations in faecal microbiome and resistome in Chinese international travellers: a metagenomic analysis. Journal of Travel Medicine, 2023, 30, .	1.4	3
708	Trophic level and proteobacteria abundance drive antibiotic resistance levels inÂfish from coastal New England. Animal Microbiome, 2023, 5, .	1.5	3
709	The honeybee gut resistome and its role in antibiotic resistance dissemination. Integrative Zoology, 2023, 18, 1014-1026.	1.3	5
710	Field ponding water exacerbates the dissemination of manure-derived antibiotic resistance genes from paddy soil to surrounding waterbodies. Frontiers in Microbiology, 0, 14, .	1.5	1
714	Microbiome therapeutics as an alternative to the antibiotics. , 2023, , 421-441.		0
717	Environment as Sink for Antimicrobial Resistance and Genes. , 2023, , 165-182.		0
718	Antibiotic perturbations to the gut microbiome. Nature Reviews Microbiology, 2023, 21, 772-788.	13.6	20
720	Metagenome. , 2023, , 1862-1863.		0
724	Impact of environment on transmission of antibiotic-resistant superbugs in humans and strategies to lower dissemination of antibiotic resistance. Folia Microbiologica, 0, , .	1.1	0
739	The Emerging Role of the Gut Microbiome in Hematopoietic Stem Cell Transplantation. , 2023, , .		0
741	Metagenomics approaches for microbiome analysis. , 2024, , 191-204.		0