

Kat Holt

List of Publications by Year in descending order

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201
papers

28,839
citations

10388

72
h-index

8393

147
g-index

261
all docs

261
docs citations

261
times ranked

26126
citing authors

#	ARTICLE	IF	CITATIONS
1	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. PLoS Computational Biology, 2017, 13, e1005595.	3.2	5,135
2	Performance of neural network basecalling tools for Oxford Nanopore sequencing. Genome Biology, 2019, 20, 129.	8.8	1,971
3	Bandage: interactive visualization of <i>de novo</i> genome assemblies. Bioinformatics, 2015, 31, 3350-3352.	4.1	1,671
4	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. Genome Medicine, 2014, 6, 90.	8.2	953
5	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3574-81.	7.1	942
6	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. Nature Genetics, 2013, 45, 1176-1182.	21.4	900
7	The Infant Nasopharyngeal Microbiome Impacts Severity of Lower Respiratory Infection and Risk of Asthma Development. Cell Host and Microbe, 2015, 17, 704-715.	11.0	721
8	Completing bacterial genome assemblies with multiplex MinION sequencing. Microbial Genomics, 2017, 3, e000132.	2.0	559
9	Population genomics of <i>Klebsiella pneumoniae</i> . Nature Reviews Microbiology, 2020, 18, 344-359.	28.6	510
10	Epidemic multiple drug resistant <i>Salmonella</i> Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. Genome Research, 2009, 19, 2279-2287.	5.5	504
11	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. Nature Genetics, 2008, 40, 987-993.	21.4	453
12	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	21.4	403
13	A genomic surveillance framework and genotyping tool for <i>Klebsiella pneumoniae</i> and its related species complex. Nature Communications, 2021, 12, 4188.	12.8	394
14	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. Clinical Infectious Diseases, 2017, 65, 208-215.	5.8	381
15	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. Microbial Genomics, 2016, 2, e000102.	2.0	372
16	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532.	7.1	346
17	<i>Klebsiella pneumoniae</i> as a key trafficker of drug resistance genes from environmental to clinically important bacteria. Current Opinion in Microbiology, 2018, 45, 131-139.	5.1	337
18	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. Nature Genetics, 2012, 44, 1056-1059.	21.4	278

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19	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	12.6	255
20	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018, 360, 733-738.	12.6	254
21	Kaptive Web: User-Friendly Capsule and Lipopolysaccharide Serotype Prediction for <i>Klebsiella</i> Genomes. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	239
22	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008114.	3.5	228
23	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	2.0	224
24	<i>Klebsiella pneumoniae</i> Population Genomics and Antimicrobial-Resistant Clones. <i>Trends in Microbiology</i> , 2016, 24, 944-956.	7.7	217
25	Polypolish: Short-read polishing of long-read bacterial genome assemblies. <i>PLoS Computational Biology</i> , 2022, 18, e1009802.	3.2	210
26	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	12.8	205
27	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018, 4, .	2.0	197
28	FastSpar: rapid and scalable correlation estimation for compositional data. <i>Bioinformatics</i> , 2019, 35, 1064-1066.	4.1	190
29	The diversity of <i>Klebsiella pneumoniae</i> surface polysaccharides. <i>Microbial Genomics</i> , 2016, 2, e000073.	2.0	185
30	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from South and Southeast Asia. <i>Genome Medicine</i> , 2020, 12, 11.	8.2	178
31	Trycycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	8.8	175
32	Deepbiner: Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006583.	3.2	171
33	Frequent transmission of the <i>Mycobacterium tuberculosis</i> Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam. <i>Nature Genetics</i> , 2018, 50, 849-856.	21.4	167
34	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , 2009, 10, 36.	2.8	161
35	Microbial mercury methylation in Antarctic sea ice. <i>Nature Microbiology</i> , 2016, 1, 16127.	13.3	158
36	Five decades of genome evolution in the globally distributed, extensively antibiotic-resistant <i>Acinetobacter baumannii</i> global clone 1. <i>Microbial Genomics</i> , 2016, 2, e000052.	2.0	155

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37	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018, 10, 77.	8.2	153
38	Airway Microbiota Dynamics Uncover a Critical Window for Interplay of Pathogenic Bacteria and Allergy in Childhood Respiratory Disease. <i>Cell Host and Microbe</i> , 2018, 24, 341-352.e5.	11.0	146
39	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , 2016, 7, 12827.	12.8	145
40	The genomic signatures of <i>Shigella</i> evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , 2016, 14, 235-250.	28.6	142
41	On the origin of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <i>BMC Genomics</i> , 2012, 13, 258.	2.8	139
42	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 577-581.	3.0	137
43	Genomic Insights to Control the Emergence of Vancomycin-Resistant Enterococci. <i>MBio</i> , 2013, 4, .	4.1	136
44	Typhoid in Kenya Is Associated with a Dominant Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhi Haplotype That Is Also Widespread in Southeast Asia. <i>Journal of Clinical Microbiology</i> , 2010, 48, 2171-2176.	3.9	133
45	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , 2017, 8, 15483.	12.8	132
46	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018, 4, eaat5869.	10.3	130
47	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019, 8, 2138.	1.6	128
48	An Outpatient, Ambulant-Design, Controlled Human Infection Model Using Escalating Doses of <i>Salmonella</i> Typhi Challenge Delivered in Sodium Bicarbonate Solution. <i>Clinical Infectious Diseases</i> , 2014, 58, 1230-1240.	5.8	126
49	Novel Subclone of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 with Enhanced Virulence and Transmissibility, China. <i>Emerging Infectious Diseases</i> , 2020, 26, 289-297.	4.3	126
50	Tracking the establishment of local endemic populations of an emergent enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17522-17527.	7.1	124
51	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , 2015, 16, 667.	2.8	119
52	Identification of <i>Acinetobacter baumannii</i> loci for capsular polysaccharide (KL) and lipooligosaccharide outer core (OCL) synthesis in genome assemblies using curated reference databases compatible with Kaptive. <i>Microbial Genomics</i> , 2020, 6, .	2.0	118
53	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019, 8, 2138.	1.6	115
54	Emergence of a Globally Dominant IncHI1 Plasmid Type Associated with Multiple Drug Resistant Typhoid. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1245.	3.0	114

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55	Comparative genomics of Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> . <i>Gut</i> , 2017, 66, 1382-1389.	12.1	114
56	Beginner's guide to comparative bacterial genome analysis using next-generation sequence data. <i>Microbial Informatics and Experimentation</i> , 2013, 3, 2.	7.6	113
57	Combined high-resolution genotyping and geospatial analysis reveals modes of endemic urban typhoid fever transmission. <i>Open Biology</i> , 2011, 1, 110008.	3.6	112
58	A novel ciprofloxacin-resistant subclade of H58 <i>Salmonella</i> Typhi is associated with fluoroquinolone treatment failure. <i>ELife</i> , 2016, 5, e14003.	6.0	111
59	In silico serotyping of <i>E. coli</i> from short read data identifies limited novel O-loci but extensive diversity of O:H serotype combinations within and between pathogenic lineages. <i>Microbial Genomics</i> , 2016, 2, e000064.	2.0	110
60	Are <i>Escherichia coli</i> Pathotypes Still Relevant in the Era of Whole-Genome Sequencing?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 141.	3.9	110
61	Antimicrobial-Resistant <i>Klebsiella pneumoniae</i> Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. <i>Clinical Infectious Diseases</i> , 2018, 67, 161-170.	5.8	108
62	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the <i>Klebsiella pneumoniae</i> Clonal Group 258. <i>Genome Biology and Evolution</i> , 2015, 7, 1267-1279.	2.5	99
63	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
64	The sensitivity of real-time PCR amplification targeting invasive <i>Salmonella</i> serovars in biological specimens. <i>BMC Infectious Diseases</i> , 2010, 10, 125.	2.9	94
65	Convergence of virulence and MDR in a single plasmid vector in MDR <i>Klebsiella pneumoniae</i> ST15. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1218-1222.	3.0	93
66	Dynamics of antimicrobial resistance in intestinal <i>Escherichia coli</i> from children in community settings in South Asia and sub-Saharan Africa. <i>Nature Microbiology</i> , 2018, 3, 1063-1073.	13.3	89
67	Differential host susceptibility and bacterial virulence factors driving <i>Klebsiella</i> liver abscess in an ethnically diverse population. <i>Scientific Reports</i> , 2016, 6, 29316.	3.3	87
68	Short read sequence typing (SRST): multi-locus sequence types from short reads. <i>BMC Genomics</i> , 2012, 13, 338.	2.8	84
69	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant <i>Shigella sonnei</i> : A Cross-Sectional Study. <i>PLoS Medicine</i> , 2016, 13, e1002055.	8.4	84
70	A GC1 <i>Acinetobacter baumannii</i> isolate carrying AbaR3 and the aminoglycoside resistance transposon TnaphA6 in a conjugative plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 955-958.	3.0	83
71	Diversity-Generating Machines: Genetics of Bacterial Sugar-Coating. <i>Trends in Microbiology</i> , 2018, 26, 1008-1021.	7.7	83
72	Inducible colistin resistance via a disrupted plasmid-borne <i>mcr-1</i> gene in a 2008 Vietnamese <i>Shigella sonnei</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2314-2317.	3.0	82

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73	Variation in <i>Salmonella enterica</i> Serovar Typhi IncHI1 Plasmids during the Global Spread of Resistant Typhoid Fever. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 716-727.	3.2	81
74	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015, 6, e00080.	4.1	81
75	Multidrug-Resistant <i>Salmonella enterica</i> Serovar Paratyphi A Harbors IncHI1 Plasmids Similar to Those Found in Serovar Typhi. <i>Journal of Bacteriology</i> , 2007, 189, 4257-4264.	2.2	80
76	Co-circulation of Multidrug-resistant <i>Shigella</i> Among Men Who Have Sex With Men in Australia. <i>Clinical Infectious Diseases</i> , 2019, 69, 1535-1544.	5.8	77
77	Vitamin D over the first decade and susceptibility to childhood allergy and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 472-481.e9.	2.9	76
78	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , 2021, 15, 1810-1825.	9.8	74
79	Laboratory and molecular surveillance of paediatric typhoidal <i>Salmonella</i> in Nepal: Antimicrobial resistance and implications for vaccine policy. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006408.	3.0	70
80	High-Throughput Genotyping of <i>Salmonella enterica</i> Serovar Typhi Allowing Geographical Assignment of Haplotypes and Pathotypes within an Urban District of Jakarta, Indonesia. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1741-1746.	3.9	69
81	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019, 5, .	2.0	69
82	High-throughput bacterial SNP typing identifies distinct clusters of <i>Salmonella</i> Typhi causing typhoid in Nepalese children. <i>BMC Infectious Diseases</i> , 2010, 10, 144.	2.9	68
83	Evidence of microevolution of <i>Salmonella</i> Typhimurium during a series of egg-associated outbreaks linked to a single chicken farm. <i>BMC Genomics</i> , 2013, 14, 800.	2.8	67
84	A Bioinformatic Strategy for the Detection, Classification and Analysis of Bacterial Autotransporters. <i>PLoS ONE</i> , 2012, 7, e43245.	2.5	65
85	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	13.3	65
86	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2021, 12, 2684.	12.8	65
87	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	2.0	65
88	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012, 13, R103.	9.6	62
89	Informal genomic surveillance of regional distribution of <i>Salmonella</i> Typhi genotypes and antimicrobial resistance via returning travellers. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007620.	3.0	62
90	The STRATAA study protocol: a programme to assess the burden of enteric fever in Bangladesh, Malawi and Nepal using prospective population census, passive surveillance, serological studies and healthcare utilisation surveys. <i>BMJ Open</i> , 2017, 7, e016283.	1.9	61

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91	Developmental patterns in the nasopharyngeal microbiome during infancy are associated with asthma risk. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1683-1691.	2.9	61
92	Evolution of atypical enteropathogenic <i>E. coli</i> by repeated acquisition of LEE pathogenicity island variants. <i>Nature Microbiology</i> , 2016, 1, 15010.	13.3	60
93	The Burden and Characteristics of Enteric Fever at a Healthcare Facility in a Densely Populated Area of Kathmandu. <i>PLoS ONE</i> , 2010, 5, e13988.	2.5	58
94	Genome and Transcriptome Adaptation Accompanying Emergence of the Definitive Type 2 Host-Restricted <i>Salmonella enterica</i> Serovar Typhimurium Pathovar. <i>MBio</i> , 2013, 4, e00565-13.	4.1	57
95	A conjugative plasmid carrying the carbapenem resistance gene blaOXA-23 in AbaR4 in an extensively resistant GC1 <i>Acinetobacter baumannii</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2625-2628.	3.0	57
96	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella Typhi</i> at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	12.8	56
97	Navigating the future of bacterial molecular epidemiology. <i>Current Opinion in Microbiology</i> , 2010, 13, 640-645.	5.1	54
98	Kaptive 2.0: updated capsule and lipopolysaccharide locus typing for the <i>Klebsiella pneumoniae</i> species complex. <i>Microbial Genomics</i> , 2022, 8, .	2.0	52
99	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	12.8	51
100	WGS Analysis and Interpretation in Clinical and Public Health Microbiology Laboratories: What Are the Requirements and How Do Existing Tools Compare?. <i>Pathogens</i> , 2014, 3, 437-458.	2.8	50
101	Genomic resistance island AGI1 carrying a complex class 1 integron in a multiply antibiotic-resistant ST25 <i>Acinetobacter baumannii</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2519-2523.	3.0	50
102	Empirical ways to identify novel Bedaquiline resistance mutations in AtpE. <i>PLoS ONE</i> , 2019, 14, e0217169.	2.5	50
103	Evolution of carbapenem resistance in <i>Acinetobacter baumannii</i> during a prolonged infection. <i>Microbial Genomics</i> , 2018, 4, .	2.0	49
104	Evolution of a clade of <i>Acinetobacter baumannii</i> global clone 1, lineage 1 via acquisition of carbapenem- and aminoglycoside-resistance genes and dispersion of ISAbal. <i>Microbial Genomics</i> , 2019, 5, .	2.0	49
105	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , 2016, 3, 71-82.	6.2	48
106	Temporal Fluctuation of Multidrug Resistant <i>Salmonella Typhi</i> Haplotypes in the Mekong River Delta Region of Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e929.	3.0	47
107	Rapid Genomic Characterization and Global Surveillance of <i>Klebsiella</i> Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , 2021, 73, S325-S335.	5.8	47
108	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	3.0	46

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109	Variants of AbGRI3 carrying the <i>armA</i> gene in extensively antibiotic-resistant <i>Acinetobacter baumannii</i> from Singapore. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw542.	3.0	45
110	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021, 7, .	2.0	44
111	Impact of insertion sequences on convergent evolution of <i>Shigella</i> species. <i>PLoS Genetics</i> , 2020, 16, e1008931.	3.5	43
112	Carbapenem and amikacin resistance on a large conjugative <i>Acinetobacter baumannii</i> plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1259-1261.	3.0	42
113	Burden of enteric fever at three urban sites in Africa and Asia: a multicentre population-based study. <i>The Lancet Global Health</i> , 2021, 9, e1688-e1696.	6.3	42
114	A <i>Salmonella</i> Typhimurium-Typhi Genomic Chimera: A Model to Study Vi Polysaccharide Capsule Function In Vivo. <i>PLoS Pathogens</i> , 2011, 7, e1002131.	4.7	41
115	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	12.8	41
116	Detecting SNPs and estimating allele frequencies in clonal bacterial populations by sequencing pooled DNA. <i>Bioinformatics</i> , 2009, 25, 2074-2075.	4.1	40
117	Adaptive Change Inferred from Genomic Population Analysis of the ST93 Epidemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 366-378.	2.5	40
118	The Molecular and Spatial Epidemiology of Typhoid Fever in Rural Cambodia. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004785.	3.0	40
119	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacteriales. <i>ISME Journal</i> , 2020, 14, 1713-1730.	9.8	40
120	pCERC3 from a commensal ST95 <i>Escherichia coli</i> : A ColV virulence-multiresistance plasmid carrying a <i>sul3</i> -associated class 1 integron. <i>Plasmid</i> , 2016, 84-85, 11-19.	1.4	39
121	Silent spread of mobile colistin resistance gene <i>mcr-9.1</i> on IncHI2 superplasmids in clinical carbapenem-resistant Enterobacteriales. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1856.e7-1856.e13.	6.0	37
122	A multiplex single nucleotide polymorphism typing assay for detecting mutations that result in decreased fluoroquinolone susceptibility in <i>Salmonella enterica</i> serovars Typhi and Paratyphi A. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1631-1641.	3.0	36
123	Prediction of antibiotic resistance from antibiotic resistance genes detected in antibiotic-resistant commensal <i>Escherichia coli</i> using PCR or WGS. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 72, dkw511.	3.0	36
124	Five Years of GenoTyphi: Updates to the Global <i>Salmonella</i> Typhi Genotyping Framework. <i>Journal of Infectious Diseases</i> , 2021, 224, S775-S780.	4.0	36
125	Identification of a marker for two lineages within the GC1 clone of <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 557-558.	3.0	35
126	Multiple Genetic Mutations Associated with Polymyxin Resistance in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7899-7902.	3.2	35

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127	Gastrointestinal carriage of <i>Klebsiella pneumoniae</i> in a general adult population: a cross-sectional study of risk factors and bacterial genomic diversity. <i>Gut Microbes</i> , 2021, 13, 1939599.	9.8	34
128	Distinct increase in antimicrobial resistance genes among <i>Escherichia coli</i> during 50 years of antimicrobial use in livestock production in China. <i>Nature Food</i> , 2022, 3, 197-205.	14.0	34
129	Insertions in the OCL1 locus of <i>Acinetobacter baumannii</i> lead to shortened lipooligosaccharides. <i>Research in Microbiology</i> , 2014, 165, 472-475.	2.1	33
130	Persistent circulation of a fluoroquinolone-resistant <i>Salmonella enterica</i> Typhi clone in the Indian subcontinent. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 75, 337-341.	3.0	33
131	Genome Sequence of <i>Acinetobacter baumannii</i> Strain D36, an Antibiotic-Resistant Isolate from Lineage 2 of Global Clone 1. <i>Genome Announcements</i> , 2015, 3, .	0.8	32
132	hicap: <i>In Silico</i> Serotyping of the <i>Haemophilus influenzae</i> Capsule Locus. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	32
133	Analysis of <i>Salmonella enterica</i> Serovar Typhimurium Variable-Number Tandem-Repeat Data for Public Health Investigation Based on Measured Mutation Rates and Whole-Genome Sequence Comparisons. <i>Journal of Bacteriology</i> , 2014, 196, 3036-3044.	2.2	31
134	Direct Nanopore Sequencing of mRNA Reveals Landscape of Transcript Isoforms in Apicomplexan Parasites. <i>MSystems</i> , 2021, 6, .	3.8	31
135	A type 2 A/C2 plasmid carrying the <i>aacC4</i> apramycin resistance gene and the <i>erm</i> (42) erythromycin resistance gene recovered from two <i>Salmonella enterica</i> serovars. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1021-1025.	3.0	30
136	Population structure and antimicrobial resistance patterns of <i>Salmonella</i> Typhi isolates in urban Dhaka, Bangladesh from 2004 to 2016. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008036.	3.0	30
137	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	30
138	Genome Sequence of <i>Acinetobacter baumannii</i> Strain A1, an Early Example of Antibiotic-Resistant Global Clone 1. <i>Genome Announcements</i> , 2015, 3, .	0.8	29
139	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , 2021, 10, .	6.0	29
140	Small IncQ1 and Col-Like Plasmids Harboring <i>bla</i> _{KPC-2} and Non-Tn 4401 Elements (NTE <i>bla</i> _{KPC-2} -IId) in High-Risk Lineages of <i>Klebsiella pneumoniae</i> CG258. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	27
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