

Kat Holt

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

217 papers	15,217 citations	61 h-index	120 g-index
261 ext. papers	23,460 ext. citations	9 avg, IF	7.14 L-index

#	Paper	IF	Citations
217	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. <i>PLoS Computational Biology</i> , 2017 , 13, e1005595	5	2223
216	Bandage: interactive visualization of de novo genome assemblies. <i>Bioinformatics</i> , 2015 , 31, 3350-2	7.2	794
215	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , 2013 , 45, 1176-82	36.3	676
214	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014 , 6, 90	14.4	603
213	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in Klebsiella pneumoniae, an urgent threat to public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3574-81	11.5	588
212	The infant nasopharyngeal microbiome impacts severity of lower respiratory infection and risk of asthma development. <i>Cell Host and Microbe</i> , 2015 , 17, 704-15	23.4	512
211	Performance of neural network basecalling tools for Oxford Nanopore sequencing. <i>Genome Biology</i> , 2019 , 20, 129	18.3	490
210	High-throughput sequencing provides insights into genome variation and evolution in Salmonella Typhi. <i>Nature Genetics</i> , 2008 , 40, 987-93	36.3	398
209	Epidemic multiple drug resistant Salmonella Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. <i>Genome Research</i> , 2009 , 19, 2279-87	9.7	374
208	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015 , 47, 632-9	36.3	305
207	Evolutionary dynamics of Clostridium difficile over short and long time scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7527-32	11.5	291
206	Completing bacterial genome assemblies with multiplex MinION sequencing. <i>Microbial Genomics</i> , 2017 , 3, e000132	4.4	268
205	Identification of capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016 , 2, e000102	4.4	216
204	Shigella sonnei genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012 , 44, 1056-9	36.3	203
203	Gastrointestinal Carriage Is a Major Reservoir of Klebsiella pneumoniae Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , 2017 , 65, 208-215	11.6	193
202	Population genomics of Klebsiella pneumoniae. <i>Nature Reviews Microbiology</i> , 2020 , 18, 344-359	22.2	166
201	Klebsiella pneumoniae as a key trafficker of drug resistance genes from environmental to clinically important bacteria. <i>Current Opinion in Microbiology</i> , 2018 , 45, 131-139	7.9	159

200	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017 , 358, 785-789	33.3	157
199	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018 , 360, 733-738	33.3	146
198	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016 , 2, e000094	4.4	135
197	<i>Klebsiella pneumoniae</i> Population Genomics and Antimicrobial-Resistant Clones. <i>Trends in Microbiology</i> , 2016 , 24, 944-956	12.4	130
196	Kaptive Web: User-Friendly Capsule and Lipopolysaccharide Serotype Prediction for <i>Klebsiella</i> Genomes. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	126
195	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , 2009 , 10, 36	4.5	120
194	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	6	115
193	Genomic insights to control the emergence of vancomycin-resistant enterococci. <i>MBio</i> , 2013 , 4,	7.8	112
192	On the origin of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <i>BMC Genomics</i> , 2012 , 13, 258	4.5	111
191	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018 , 4,	4.4	106
190	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	17.4	104
189	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, 2171-6	9.7	104
188	The diversity of surface polysaccharides. <i>Microbial Genomics</i> , 2016 , 2, e000073	4.4	101
187	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, 1230-40	11.6	96
186	Emergence of a globally dominant IncHI1 plasmid type associated with multiple drug resistant typhoid. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1245	4.8	95
185	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	36.3	94
184	Microbial mercury methylation in Antarctic sea ice. <i>Nature Microbiology</i> , 2016 , 1, 16127	26.6	92
183	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, 17522-7	11.5	89

182	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , 2016 , 7, 12827	17.4	88
181	The genomic signatures of <i>Shigella</i> evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , 2016 , 14, 235-50	22.2	88
180	Beginner's guide to comparative bacterial genome analysis using next-generation sequence data. <i>Microbial Informatics and Experimentation</i> , 2013 , 3, 2		87
179	Deepbiner: Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks. <i>PLoS Computational Biology</i> , 2018 , 14, e1006583	5	87
178	Combined high-resolution genotyping and geospatial analysis reveals modes of endemic urban typhoid fever transmission. <i>Open Biology</i> , 2011 , 1, 110008	7	85
177	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018 , 10, 77	14.4	83
176	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , 2015 , 16, 667	4.5	81
175	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	23.4	80
174	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , 2017 , 8, 15483	17.4	79
173	A novel ciprofloxacin-resistant subclade of H58 <i>Salmonella</i> Typhi is associated with fluoroquinolone treatment failure. <i>ELife</i> , 2016 , 5, e14003	8.9	79
172	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	5.1	75
171	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	14.4	74
170	A genomic surveillance framework and genotyping tool for <i>Klebsiella pneumoniae</i> and its related species complex. <i>Nature Communications</i> , 2021 , 12, 4188	17.4	74
169	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, 1267-79	3.9	73
168	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, 716-27	5.9	73
167	Are Pathotypes Still Relevant in the Era of Whole-Genome Sequencing?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 141	5.9	73
166	Global expansion of lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018 , 4, eaat5869	14.3	71
165	serotyping of 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	4.4	69

164	FastSpar: rapid and scalable correlation estimation for compositional data. <i>Bioinformatics</i> , 2019 , 35, 1064-1066	68
163	The sensitivity of real-time PCR amplification targeting invasive Salmonella serovars in biological specimens. <i>BMC Infectious Diseases</i> , 2010 , 10, 125	4 68
162	Five decades of genome evolution in the globally distributed, extensively antibiotic-resistant global clone 1. <i>Microbial Genomics</i> , 2016 , 2, e000052	4.4 68
161	Inducible colistin resistance via a disrupted plasmid-borne mcr-1 gene in a 2008 Vietnamese Shigella sonnei isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 2314-7	5.1 67
160	Short read sequence typing (SRST): multi-locus sequence types from short reads. <i>BMC Genomics</i> , 2012 , 13, 338	4.5 67
159	Comparative genomics of Crohn's disease-associated adherent-invasive. <i>Gut</i> , 2017 , 66, 1382-1389	19.2 64
158	Multidrug-resistant Salmonella enterica serovar paratyphi A harbors IncHI1 plasmids similar to those found in serovar typhi. <i>Journal of Bacteriology</i> , 2007 , 189, 4257-64	3.5 64
157	High-throughput bacterial SNP typing identifies distinct clusters of Salmonella Typhi causing typhoid in Nepalese children. <i>BMC Infectious Diseases</i> , 2010 , 10, 144	4 61
156	Convergence of virulence and MDR in a single plasmid vector in MDR Klebsiella pneumoniae ST15. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 1218-1222	5.1 59
155	Antimicrobial-Resistant Klebsiella pneumoniae Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. <i>Clinical Infectious Diseases</i> , 2018 , 67, 161-170	11.6 57
154	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant Shigella sonnei: A Cross-Sectional Study. <i>PLoS Medicine</i> , 2016 , 13, e1002055	11.6 56
153	Differential host susceptibility and bacterial virulence factors driving Klebsiella liver abscess in an ethnically diverse population. <i>Scientific Reports</i> , 2016 , 6, 29316	4.9 55
152	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	11.5 55
151	A bioinformatic strategy for the detection, classification and analysis of bacterial autotransporters. <i>PLoS ONE</i> , 2012 , 7, e43245	3.7 55
150	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019 , 8, 2138	3.6 53
149	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018 , 9, 5094	17.4 53
148	Novel Subclone of Carbapenem-Resistant Klebsiella pneumoniae Sequence Type 11 with Enhanced Virulence and Transmissibility, China. <i>Emerging Infectious Diseases</i> , 2020 , 26, 289-297	10.2 52
147	Evidence of microevolution of Salmonella Typhimurium during a series of egg-associated outbreaks linked to a single chicken farm. <i>BMC Genomics</i> , 2013 , 14, 800	4.5 52

146	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, 1741-6	9.7	52
145	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, 955-8	5.1	49
144	Navigating the future of bacterial molecular epidemiology. <i>Current Opinion in Microbiology</i> , 2010 , 13, 640-5	7.9	49
143	Evolution of atypical enteropathogenic <i>E. coli</i> by repeated acquisition of LEE pathogenicity island variants. <i>Nature Microbiology</i> , 2016 , 1, 15010	26.6	48
142	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019 , 8, 2138	3.6	48
141	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016 , 1, 16027	26.6	47
140	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	7.8	47
139	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	4.8	47
138	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	3.7	46
137	Convergent adaptation in the dominant global hospital clone ST239 of methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015 , 6, e00080	7.8	44
136	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, 2625-8	5.1	44
135	Diversity-Generating Machines: Genetics of Bacterial Sugar-Coating. <i>Trends in Microbiology</i> , 2018 , 26, 1008-1021	12.4	42
134	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, 437-58	4.5	42
133	Identification of loci for capsular polysaccharide (KL) and lipooligosaccharide outer core (OCL) synthesis in genome assemblies using curated reference databases compatible with. <i>Microbial Genomics</i> , 2020 , 6,	4.4	41
132	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	11.6	41
131	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	26.6	40
130	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012 , 13, R103	18.3	39
129	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, 2519-23	5.1	38

128	Temporal fluctuation of multidrug resistant salmonella typhi haplotypes in the mekong river delta region of Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e929	4.8	38
127	A Salmonella Typhimurium-Typhi genomic chimera: a model to study Vi polysaccharide capsule function in vivo. <i>PLoS Pathogens</i> , 2011 , 7, e1002131	7.6	38
126	Evolution of carbapenem resistance in Acinetobacter baumannii during a prolonged infection. <i>Microbial Genomics</i> , 2018 , 4,	4.4	37
125	Repeated local emergence of carbapenem-resistant in a single hospital ward. <i>Microbial Genomics</i> , 2016 , 2, e000050	4.4	36
124	Detecting SNPs and estimating allele frequencies in clonal bacterial populations by sequencing pooled DNA. <i>Bioinformatics</i> , 2009 , 25, 2074-5	7.2	34
123	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	3	33
122	A multiplex single nucleotide polymorphism typing assay for detecting mutations that result in decreased fluoroquinolone susceptibility in Salmonella enterica serovars Typhi and Paratyphi A. <i>Journal of Antimicrobial Chemotherapy</i> , 2010 , 65, 1631-41	5.1	33
121	Global phylogenomics of multidrug-resistant Salmonella enterica serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019 , 5,	4.4	33
120	Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007620	4.8	29
119	Prediction of antibiotic resistance from antibiotic resistance genes detected in antibiotic-resistant commensal Escherichia coli using PCR or WGS. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 700-704	5.1	29
118	Variants of AbGRI3 carrying the armaA gene in extensively antibiotic-resistant Acinetobacter baumannii from Singapore. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1031-1039	5.1	28
117	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , 2016 , 3, 71-82	10.6	28
116	Empirical ways to identify novel Bedaquiline resistance mutations in AtpE. <i>PLoS ONE</i> , 2019 , 14, e0217169	3.7	27
115	pCERC3 from a commensal ST95 Escherichia coli: A ColV virulence-multiresistance plasmid carrying a sul3-associated class 1 integron. <i>Plasmid</i> , 2016 , 84-85, 11-9	3.3	27
114	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004781	4.8	27
113	The Molecular and Spatial Epidemiology of Typhoid Fever in Rural Cambodia. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004785	4.8	26
112	Trycycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021 , 22, 266	18.3	26
111	Adaptive change inferred from genomic population analysis of the ST93 epidemic clone of community-associated methicillin-resistant Staphylococcus aureus. <i>Genome Biology and Evolution</i> , 2014 , 6, 366-78	3.9	25

110	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, 3036-44	3.5	24
109	Carbapenem and amikacin resistance on a large conjugative <i>Acinetobacter baumannii</i> plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1259-61	5.1	23
108	Genome Sequence of <i>Acinetobacter baumannii</i> Strain A1, an Early Example of Antibiotic-Resistant Global Clone 1. <i>Genome Announcements</i> , 2015 , 3,		22
107	A linear plasmid truncation induces unidirectional flagellar phase change in H:z66 positive <i>Salmonella</i> Typhi. <i>Molecular Microbiology</i> , 2007 , 66, 1207-18	4.1	21
106	Insertions in the OCL1 locus of <i>Acinetobacter baumannii</i> lead to shortened lipooligosaccharides. <i>Research in Microbiology</i> , 2014 , 165, 472-5	4	20
105	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	11.5	19
104	High-resolution genotyping of the endemic <i>Salmonella</i> Typhi population during a Vi (typhoid) vaccination trial in Kolkata. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1490	4.8	18
103	Small IncQ1 and Col-Like Plasmids Harboring and Non-Tn Elements (NTE-IId) in High-Risk Lineages of CG258. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	18
102	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019 , 10, 4828	17.4	17
101	hicap: Serotyping of the <i>Haemophilus influenzae</i> Capsule Locus. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	16
100	Multiple Genetic Mutations Associated with Polymyxin Resistance in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 7899-902	5.9	16
99	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	4.8	16
98	Global phylogeny of <i>Shigella sonnei</i> strains from limited single nucleotide polymorphisms (SNPs) and development of a rapid and cost-effective SNP-typing scheme for strain identification by high-resolution melting analysis. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 303-5	9.7	16
97	Cord blood hemopoietic progenitor profiles predict acute respiratory symptoms in infancy. <i>Pediatric Allergy and Immunology</i> , 2008 , 19, 239-47	4.2	16
96	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 ISAb1. <i>Microbial Genomics</i> , 2019 , 5,	4.4	16
95	The complete sequence of <i>Salmonella</i> genomic island SGI1-K. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 305-6	5.1	15
94	Identification of a marker for two lineages within the GC1 clone of <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 557-8	5.1	15
93	A type 2 A/C2 plasmid carrying the aacC4 apramycin resistance gene and the erm(42) erythromycin resistance gene recovered from two <i>Salmonella enterica</i> serovars. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1021-5	5.1	15

92	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , 2021 , 15, 1810-1825	11.9	15
91	Whole Genome Sequence Analysis of Salmonella Typhi Isolated in Thailand before and after the Introduction of a National Immunization Program. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005274	4.8	14
90	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2021 , 8, 2138	3.6	14
89	Trajectories of childhood immune development and respiratory health relevant to asthma and allergy. <i>ELife</i> , 2018 , 7,	8.9	14
88	Correcting index databases improves metagenomic studies		14
87	A small Acinetobacter plasmid carrying the tet39 tetracycline resistance determinant. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 269-71	5.1	13
86	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , 2018 , 18, 95	3	13
85	Persistent circulation of a fluoroquinolone-resistant Salmonella enterica Typhi clone in the Indian subcontinent. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 337-341	5.1	13
84	Elucidation of pathways driving asthma pathogenesis: development of a systems-level analytic strategy. <i>Frontiers in Immunology</i> , 2014 , 5, 447	8.4	13
83	Polypolish: Short-read polishing of long-read bacterial genome assemblies.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009802	5	13
82	The complete sequence of Salmonella genomic island SGI2. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 617-9	5.1	12
81	Genome Sequence of Acinetobacter baumannii Strain D36, an Antibiotic-Resistant Isolate from Lineage 2 of Global Clone 1. <i>Genome Announcements</i> , 2015 , 3,		12
80	The inflated mitochondrial genomes of siphonous green algae reflect processes driving expansion of noncoding DNA and proliferation of introns. <i>PeerJ</i> , 2020 , 8, e8273	3.1	12
79	Clinical and laboratory-induced colistin-resistance mechanisms in Acinetobacter baumannii. <i>Microbial Genomics</i> , 2019 , 5,	4.4	12
78	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. <i>Nature Communications</i> , 2021 , 12, 2879	17.4	12
77	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016 , 16, 115	3	12
76	Impact of insertion sequences on convergent evolution of Shigella species. <i>PLoS Genetics</i> , 2020 , 16, e1008931	10.8	11
75	Morphological, genomic and transcriptomic responses of Klebsiella pneumoniae to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018 , 8, 9868	4.9	11

74	Systems biology and big data in asthma and allergy: recent discoveries and emerging challenges. <i>European Respiratory Journal</i> , 2020 , 55,	13.6	11
73	Investigation of sequential outbreaks of Burkholderia cepacia and multidrug-resistant extended spectrum β -lactamase producing Klebsiella species in a West African tertiary hospital neonatal unit: a retrospective genomic analysis.. <i>Lancet Microbe, The</i> , 2020 , 1, e119-e129	22.2	11
72	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacteriales. <i>ISME Journal</i> , 2020 , 14, 1713-1730	11.9	10
71	ModuleFinder and CoReg: alternative tools for linking gene expression modules with promoter sequences motifs to uncover gene regulation mechanisms in plants. <i>Plant Methods</i> , 2006 , 2, 8	5.8	9
70	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, Shigella sonnei. <i>Nature Communications</i> , 2021 , 12, 2684	17.4	9
69	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021 , 7,	4.4	9
68	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	8
67	Multidrug-resistant Shigella sonnei carrying the plasmid-mediated mcr-1 gene in China. <i>International Journal of Antimicrobial Agents</i> , 2018 , 52, 14-21	14.3	8
66	Identification of Salmonella enterica serovar Typhi genotypes by use of rapid multiplex ligation-dependent probe amplification. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 2950-8	9.7	8
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64	Introduction and establishment of fluoroquinolone-resistant into Bhutan. <i>Microbial Genomics</i> , 2015 , 1, e000042	4.4	8
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28	Genomic adaptations to an endolithic lifestyle in the coral-associated alga Ostreobium		2
27	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients		2
26	Population structure and antimicrobial resistance patterns of Salmonella Typhi isolates in Bangladesh from 2004 to 2016		2
25	Neonatal genetics of gene expression reveal the origins of autoimmune and allergic disease risk		2
24	Identification of Acinetobacter baumannii loci for capsular polysaccharide (KL) and lipooligosaccharide outer core (OCL) synthesis in genome assemblies using curated reference databases compatible with Kaptive		2
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