

# Kat Holt

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/9071800/kat-holt-publications-by-year.pdf>  
**Version:** 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
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	Polypolish: Short-read polishing of long-read bacterial genome assemblies.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009802	5	13
216	Whole genome sequence analysis of Salmonella Typhi in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials.. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010306	4.8	1
215	Distinct increase in antimicrobial resistance genes among Escherichia coli during 50 years of antimicrobial use in livestock production in China. <i>Nature Food</i> , <b>2022</b> , 3, 197-205	14.4	3
214	Linear plasmids in and other .. <i>Microbial Genomics</i> , <b>2022</b> , 8,	4.4	1
213	Burden of enteric fever at three urban sites in Africa and Asia: a multicentre population-based study. <i>The Lancet Global Health</i> , <b>2021</b> , 9, e1688-e1696	13.6	3
212	Detection of plasmid contigs in draft genome assemblies using customized Kraken databases. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	1
211	Evolution and genomic insight into methicillin-resistant Staphylococcus aureus ST9 in China. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2021</b> , 76, 1703-1711	5.1	2
210	Direct Nanopore Sequencing of mRNA Reveals Landscape of Transcript Isoforms in Apicomplexan Parasites. <i>MSystems</i> , <b>2021</b> , 6,	7.6	8
209	Silent spread of mobile colistin resistance gene mcr-9.1 on IncHI2 Superplasmids in clinical carbapenem-resistant Enterobacterales. <i>Clinical Microbiology and Infection</i> , <b>2021</b> , 27, 1856.e7-1856.e13	9.5	8
208	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. <i>Nature Communications</i> , <b>2021</b> , 12, 2879	17.4	12
207	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, Shigella sonnei. <i>Nature Communications</i> , <b>2021</b> , 12, 2684	17.4	9
206	Klebsiella MALDI TypeR: a web-based tool for Klebsiella identification based on MALDI-TOF mass spectrometry. <i>Research in Microbiology</i> , <b>2021</b> , 172, 103835	4	3
205	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients. <i>BMC Infectious Diseases</i> , <b>2021</b> , 21, 683	4	4
204	Developmental patterns in the nasopharyngeal microbiome during infancy are associated with asthma risk. <i>Journal of Allergy and Clinical Immunology</i> , <b>2021</b> , 147, 1683-1691	11.5	19
203	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , <b>2021</b> , 15, 1810-1825	11.9	15
202	Rapid Genomic Characterization and Global Surveillance of Klebsiella Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, S325-S335	11.6	7
201	A genomic surveillance framework and genotyping tool for Klebsiella pneumoniae and its related species complex. <i>Nature Communications</i> , <b>2021</b> , 12, 4188	17.4	74

200	Genomic Diversity and Antimicrobial Resistance of Haemophilus Colonizing the Airways of Young Children with Cystic Fibrosis. <i>MSystems</i> , <b>2021</b> , e0017821	7.6	1
199	Five years of GenoTyphi: updates to the global Salmonella Typhi genotyping framework. <i>Journal of Infectious Diseases</i> , <b>2021</b> ,	7	5
198	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	9
197	Mel genome remains stable after 7 years in Australian field populations. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	1
196	Trycycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , <b>2021</b> , 22, 266	18.3	26
195	Novel strains of Klebsiella africana and Klebsiella pneumoniae in Australian fruit bats (Pteropus poliocephalus). <i>Research in Microbiology</i> , <b>2021</b> , 172, 103879	4	1
194	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , <b>2021</b> , 10,	8.9	4
193	Gastrointestinal carriage of Klebsiella pneumoniae in a general adult population: a cross-sectional study of risk factors and bacterial genomic diversity. <i>Gut Microbes</i> , <b>2021</b> , 13, 1939599	8.8	6
192	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	2
191	A nationwide genomic study of clinical Klebsiella pneumoniae in Norway 2001-15: introduction and spread of ESBLs facilitated by clonal groups CG15 and CG307.. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2021</b> ,	5.1	2
190	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,	4.8	8
189	Impact of insertion sequences on convergent evolution of Shigella species. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008931	11	11
188	Population structure and antimicrobial resistance patterns of Salmonella Typhi isolates in urban Dhaka, Bangladesh from 2004 to 2016. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008036	4.8	16
187	Population genomics of Klebsiella pneumoniae. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 344-359	22.2	166
186	Genomic surveillance for hypervirulence and multi-drug resistance in invasive Klebsiella pneumoniae from South and Southeast Asia. <i>Genome Medicine</i> , <b>2020</b> , 12, 11	14.4	74
185	Novel Subclone of Carbapenem-Resistant Klebsiella pneumoniae Sequence Type 11 with Enhanced Virulence and Transmissibility, China. <i>Emerging Infectious Diseases</i> , <b>2020</b> , 26, 289-297	10.2	52
184	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacteriales. <i>ISME Journal</i> , <b>2020</b> , 14, 1713-1730	11.9	10
183	Persistent circulation of a fluoroquinolone-resistant Salmonella enterica Typhi clone in the Indian subcontinent. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2020</b> , 75, 337-341	5.1	13

182	The inflated mitochondrial genomes of siphonous green algae reflect processes driving expansion of noncoding DNA and proliferation of introns. <i>PeerJ</i> , <b>2020</b> , 8, e8273	3.1	12
181	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> , <b>2020</b> , 6,	4.4	41
180	Systems biology and big data in asthma and allergy: recent discoveries and emerging challenges. <i>European Respiratory Journal</i> , <b>2020</b> , 55,	13.6	11
179	<i>Shigella sonnei</i> . <i>Trends in Microbiology</i> , <b>2020</b> , 28, 696-697	12.4	4
178	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. <i>Nature Communications</i> , <b>2020</b> , 11, 3761	17.4	8
177	Investigation of sequential outbreaks of Burkholderia cepacia and multidrug-resistant extended spectrum $\beta$ -lactamase producing Klebsiella species in a West African tertiary hospital neonatal unit: a retrospective genomic analysis.. <i>Lancet Microbe</i> , <b>2020</b> , 1, e119-e129	22.2	11
176	Pathogen genomic surveillance of typhoidal infection in adults and children reveals no association between clinical outcomes and infecting genotypes. <i>Tropical Medicine and Health</i> , <b>2020</b> , 48, 58	3.4	
175	GeneMates: an R package for detecting horizontal gene co-transfer between bacteria using gene-gene associations controlled for population structure. <i>BMC Genomics</i> , <b>2020</b> , 21, 658	4.5	5
174	Protection conferred by typhoid fever against recurrent typhoid fever in urban Kolkata. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008530	4.8	1
173	Z/1 Hybrid Virulence Plasmids Carrying Antimicrobial Resistance genes in Typhimurium from Australian Food Animal Production. <i>Microorganisms</i> , <b>2019</b> , 7,	4.9	4
172	Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007620	4.8	29
171	FastSpar: rapid and scalable correlation estimation for compositional data. <i>Bioinformatics</i> , <b>2019</b> , 35, 1064-1066	4.1	68
170	Performance of neural network basecalling tools for Oxford Nanopore sequencing. <i>Genome Biology</i> , <b>2019</b> , 20, 129	18.3	490
169	Empirical ways to identify novel Bedaquiline resistance mutations in AtpE. <i>PLoS ONE</i> , <b>2019</b> , 14, e0217169	3.7	27
168	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of Klebsiella pneumoniae. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008114	6	115
167	hicap: Serotyping of the Haemophilus influenzae Capsule Locus. <i>Journal of Clinical Microbiology</i> , <b>2019</b> , 57,	9.7	16
166	Convergence of virulence and MDR in a single plasmid vector in MDR Klebsiella pneumoniae ST15. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2019</b> , 74, 1218-1222	5.1	59
165	Dissecting the molecular evolution of fluoroquinolone-resistant Shigella sonnei. <i>Nature Communications</i> , <b>2019</b> , 10, 4828	17.4	17

164	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , <b>2019</b> , 8, 2138	3.6	53
163	Genomic evolution and local epidemiology of from a major hospital in Beijing, China, over a 15 year period: dissemination of known and novel high-risk clones. <i>Microbial Genomics</i> , <b>2019</b> , 7,	4.4	1
162	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 ISAba1. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	16
161	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	12
160	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	33
159	Insights from the revised complete genome sequences of strains AB307-0294 and ACICU belonging to global clones 1 and 2. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	5
158	Complete Genome Sequence of A388, an Antibiotic-Resistant <i>Acinetobacter baumannii</i> Global Clone 1 Isolate from Greece. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	4
157	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2019</b> , 74, 577-581	5.1	75
156	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> , <b>2019</b> , 63,	5.9	18
155	Co-circulation of Multidrug-resistant <i>Shigella</i> Among Men Who Have Sex With Men in Australia. <i>Clinical Infectious Diseases</i> , <b>2019</b> , 69, 1535-1544	11.6	41
154	Comment on: CG258 <i>Klebsiella pneumoniae</i> isolates without $\beta$ -lactam resistance at the onset of the carbapenem-resistant Enterobacteriaceae epidemic in New York City. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2019</b> , 74, 831-833	5.1	1
153	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , <b>2019</b> , 8, 2138	3.6	48
152	Multidrug-resistant <i>Shigella sonnei</i> carrying the plasmid-mediated mcr-1 gene in China. <i>International Journal of Antimicrobial Agents</i> , <b>2018</b> , 52, 14-21	14.3	8
151	Kaptive Web: User-Friendly Capsule and Lipopolysaccharide Serotype Prediction for <i>Klebsiella</i> Genomes. <i>Journal of Clinical Microbiology</i> , <b>2018</b> , 56,	9.7	126
150	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> , <b>2018</b> , 67, 161-170	11.6	57
149	<i>Klebsiella pneumoniae</i> as a key trafficker of drug resistance genes from environmental to clinically important bacteria. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 45, 131-139	7.9	159
148	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , <b>2018</b> , 8, 9868	4.9	11
147	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , <b>2018</b> , 18, 95	3	13

146	Diversity-Generating Machines: Genetics of Bacterial Sugar-Coating. <i>Trends in Microbiology</i> , <b>2018</b> , 26, 1008-1021	12.4	42
145	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , <b>2018</b> , 9, 2703	17.4	104
144	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> , <b>2018</b> , 3, 1063-1073	26.6	40
143	Trajectories of childhood immune development and respiratory health relevant to asthma and allergy. <i>ELife</i> , <b>2018</b> , 7,	8.9	14
142	Evolution of carbapenem resistance in <i>Acinetobacter baumannii</i> during a prolonged infection. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	37
141	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	106
140	Deepbiner: Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006583	5	87
139	Complete Genome Sequence of WM99c, an Antibiotic-Resistant <i>Acinetobacter baumannii</i> Global Clone 2 (GC2) Strain Representing an Australian GC2 Lineage. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	2
138	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , <b>2018</b> , 9, 5094	17.4	53
137	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , <b>2018</b> , 10, 77	14.4	83
136	Global expansion of lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , <b>2018</b> , 4, eaat5869	14.3	71
135	Airway Microbiota Dynamics Uncover a Critical Window for Interplay of Pathogenic Bacteria and Allergy in Childhood Respiratory Disease. <i>Cell Host and Microbe</i> , <b>2018</b> , 24, 341-352.e5	23.4	80
134	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , <b>2018</b> , 360, 733-738	33.3	146
133	Frequent transmission of the <i>Mycobacterium tuberculosis</i> Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam. <i>Nature Genetics</i> , <b>2018</b> , 50, 849-856	36.3	94
132	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> , <b>2018</b> , 12, e0006408	4.8	47
131	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> , <b>2017</b> , 72, 1031-1039	5.1	28
130	Comparative genomics of Crohn's disease-associated adherent-invasive. <i>Gut</i> , <b>2017</b> , 66, 1382-1389	19.2	64
129	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , <b>2017</b> , 8, 15483	17.4	79

128	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 65, 208-215	11.6	193
127	Completing bacterial genome assemblies with multiplex MinION sequencing. <i>Microbial Genomics</i> , <b>2017</b> , 3, e000132	4.4	268
126	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005595	5	2223
125	Whole Genome Sequence Analysis of <i>Salmonella</i> Typhi Isolated in Thailand before and after the Introduction of a National Immunization Program. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005274	4.8	14
124	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , <b>2017</b> , 358, 785-789	33.3	157
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> , <b>2017</b> , 7, e016283	3	33
122	Vitamin D over the first decade and susceptibility to childhood allergy and asthma. <i>Journal of Allergy and Clinical Immunology</i> , <b>2017</b> , 139, 472-481.e9	11.5	55
121	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> , <b>2017</b> , 72, 700-704	5.1	29
120	<i>Klebsiella pneumoniae</i> Population Genomics and Antimicrobial-Resistant Clones. <i>Trends in Microbiology</i> , <b>2016</b> , 24, 944-956	12.4	130
119	Microbial mercury methylation in Antarctic sea ice. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16127	26.6	92
118	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16027	26.6	47
117	Evolution of atypical enteropathogenic <i>E. coli</i> by repeated acquisition of LEE pathogenicity island variants. <i>Nature Microbiology</i> , <b>2016</b> , 1, 15010	26.6	48
116	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , <b>2016</b> , 7, 12827	17.4	88
115	Differential host susceptibility and bacterial virulence factors driving <i>Klebsiella</i> liver abscess in an ethnically diverse population. <i>Scientific Reports</i> , <b>2016</b> , 6, 29316	4.9	55
114	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> , <b>2016</b> , 71, 2314-7	5.1	67
113	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> , <b>2016</b> , 84-85, 11-9	3.3	27
112	A small <i>Acinetobacter</i> plasmid carrying the <i>tet39</i> tetracycline resistance determinant. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 269-71	5.1	13
111	The genomic signatures of <i>Shigella</i> evolution, adaptation and geographical spread. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 235-50	22.2	88



110	Repeated local emergence of carbapenem-resistant in a single hospital ward. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000050	4.4	36
109	Five decades of genome evolution in the globally distributed, extensively antibiotic-resistant global clone 1. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000052	4.4	68
108	The diversity of surface polysaccharides. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000073	4.4	101
107	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> , <b>2016</b> , 2, e000064	4.4	69
106	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000094	4.4	135
105	Identification of capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000102	4.4	216
104	A novel ciprofloxacin-resistant subclade of H58 Salmonella Typhi is associated with fluoroquinolone treatment failure. <i>ELife</i> , <b>2016</b> , 5, e14003	8.9	79
103	Are Pathotypes Still Relevant in the Era of Whole-Genome Sequencing?. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2016</b> , 6, 141	5.9	73
102	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , <b>2016</b> , 16, 115	3	12
101	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant Shigella sonnei: A Cross-Sectional Study. <i>PLoS Medicine</i> , <b>2016</b> , 13, e1002055	11.6	56
100	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , <b>2016</b> , 10, e0004781	4.8	27
99	The Molecular and Spatial Epidemiology of Typhoid Fever in Rural Cambodia. <i>PLoS Neglected Tropical Diseases</i> , <b>2016</b> , 10, e0004785	4.8	26
98	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , <b>2016</b> , 3, 71-82	10.6	28
97	The complete sequence of Salmonella genomic island SGI2. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 617-9	5.1	12
96	Genomic resistance island AGI1 carrying a complex class 1 integron in a multiply antibiotic-resistant ST25 Acinetobacter baumannii isolate. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 2519-23	5.1	38
95	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> , <b>2015</b> , 112, E3574-81	11.5	588
94	The infant nasopharyngeal microbiome impacts severity of lower respiratory infection and risk of asthma development. <i>Cell Host and Microbe</i> , <b>2015</b> , 17, 704-15	23.4	512
93	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , <b>2015</b> , 47, 632-9	36.3	305



92	Convergent adaptation in the dominant global hospital clone ST239 of methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , <b>2015</b> , 6, e00080	7.8	44
91	Multiple Genetic Mutations Associated with Polymyxin Resistance in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 7899-902	5.9	16
90	The complete sequence of <i>Salmonella</i> genomic island SGI1-K. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 305-6	5.1	15
89	A platform for leveraging next generation sequencing for routine microbiology and public health use. <i>Health Information Science and Systems</i> , <b>2015</b> , 3, S7	5.1	5
88	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , <b>2015</b> , 16, 667	4.5	81
87	Genome Sequence of <i>Acinetobacter baumannii</i> Strain D36, an Antibiotic-Resistant Isolate from Lineage 2 of Global Clone 1. <i>Genome Announcements</i> , <b>2015</b> , 3,		12
86	Draft Genome Sequence of a Clinical Isolate of <i>Serratia marcescens</i> , Strain AH0650_Sm1. <i>Genome Announcements</i> , <b>2015</b> , 3,		5
85	Bandage: interactive visualization of de novo genome assemblies. <i>Bioinformatics</i> , <b>2015</b> , 31, 3350-2	7.2	794
84	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the <i>Klebsiella pneumoniae</i> Clonal Group 258. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1267-79	3.9	73
83	Genome Sequence of <i>Acinetobacter baumannii</i> Strain A1, an Early Example of Antibiotic-Resistant Global Clone 1. <i>Genome Announcements</i> , <b>2015</b> , 3,		22
82	Carbapenem and amikacin resistance on a large conjugative <i>Acinetobacter baumannii</i> plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 1259-61	5.1	23
81	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> , <b>2015</b> , 70, 1021-5	5.1	15
80	Introduction and establishment of fluoroquinolone-resistant into Bhutan. <i>Microbial Genomics</i> , <b>2015</b> , 1, e000042	4.4	8
79	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> , <b>2014</b> , 196, 3036-44	3.5	24
78	Identification of a marker for two lineages within the GC1 clone of <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2014</b> , 69, 557-8	5.1	15
77	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> , <b>2014</b> , 69, 955-8	5.1	49
76	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> , <b>2014</b> , 69, 2625-8	5.1	44
75	Insertions in the OCL1 locus of <i>Acinetobacter baumannii</i> lead to shortened lipooligosaccharides. <i>Research in Microbiology</i> , <b>2014</b> , 165, 472-5	4	20

74	Elucidation of pathways driving asthma pathogenesis: development of a systems-level analytic strategy. <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 447	8.4	13
73	WGS Analysis and Interpretation in Clinical and Public Health Microbiology Laboratories: What Are the Requirements and How Do Existing Tools Compare?. <i>Pathogens</i> , <b>2014</b> , 3, 437-58	4.5	42
72	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , <b>2014</b> , 6, 90	14.4	603
71	An outpatient, ambulant-design, controlled human infection model using escalating doses of Salmonella Typhi challenge delivered in sodium bicarbonate solution. <i>Clinical Infectious Diseases</i> , <b>2014</b> , 58, 1230-40	11.6	96
70	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> , <b>2014</b> , 6, 366-78	3.9	25
69	Beginner's guide to comparative bacterial genome analysis using next-generation sequence data. <i>Microbial Informatics and Experimentation</i> , <b>2013</b> , 3, 2		87
68	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , <b>2013</b> , 45, 1176-82	36.3	676
67	Evidence of microevolution of Salmonella Typhimurium during a series of egg-associated outbreaks linked to a single chicken farm. <i>BMC Genomics</i> , <b>2013</b> , 14, 800	4.5	52
66	Draft Genome Sequences for Ten Salmonella enterica Serovar Typhimurium Phage Type 135 Variants. <i>Genome Announcements</i> , <b>2013</b> , 1,		3
65	Identification of Salmonella enterica serovar Typhi genotypes by use of rapid multiplex ligation-dependent probe amplification. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 2950-8	9.7	8
64	Genomic insights to control the emergence of vancomycin-resistant enterococci. <i>MBio</i> , <b>2013</b> , 4,	7.8	112
63	Genome and transcriptome adaptation accompanying emergence of the definitive type 2 host-restricted Salmonella enterica serovar Typhimurium pathovar. <i>MBio</i> , <b>2013</b> , 4, e00565-13	7.8	47
62	Global phylogeny of Shigella sonnei 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> , <b>2013</b> , 51, 303-5	9.7	16
61	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> , <b>2013</b> , 110, 17522-7	11.5	89
60	Characterization of the yehUT two-component regulatory system of Salmonella enterica Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , <b>2013</b> , 8, e84567	3.7	7
59	Shigella sonnei genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , <b>2012</b> , 44, 1056-9	36.3	203
58	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , <b>2012</b> , 13, R103	18.3	39
57	On the origin of Mycobacterium ulcerans, the causative agent of Buruli ulcer. <i>BMC Genomics</i> , <b>2012</b> , 13, 258	4.5	111

56	Short read sequence typing (SRST): multi-locus sequence types from short reads. <i>BMC Genomics</i> , <b>2012</b> , 13, 338	4.5	67
55	A bioinformatic strategy for the detection, classification and analysis of bacterial autotransporters. <i>PLoS ONE</i> , <b>2012</b> , 7, e43245	3.7	55
54	Involvement of PatE, a prophage-encoded AraC-like regulator, in the transcriptional activation of acid resistance pathways of enterohemorrhagic Escherichia coli strain EDL933. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 5083-92	4.8	8
53	High-resolution genotyping of the endemic Salmonella Typhi population during a Vi (typhoid) vaccination trial in Kolkata. <i>PLoS Neglected Tropical Diseases</i> , <b>2012</b> , 6, e1490	4.8	18
52	Design of multiple sequence alignment algorithms on parallel, distributed memory supercomputers. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , <b>2011</b> , 2011, 924-7	0.9	6
51	Combined high-resolution genotyping and geospatial analysis reveals modes of endemic urban typhoid fever transmission. <i>Open Biology</i> , <b>2011</b> , 1, 110008	7	85
50	Emergence of a globally dominant IncHI1 plasmid type associated with multiple drug resistant typhoid. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1245	4.8	95
49	Temporal fluctuation of multidrug resistant salmonella typhi haplotypes in the mekong river delta region of Vietnam. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e929	4.8	38
48	A Salmonella Typhimurium-Typhi genomic chimera: a model to study Vi polysaccharide capsule function in vivo. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002131	7.6	38
47	The burden and characteristics of enteric fever at a healthcare facility in a densely populated area of Kathmandu. <i>PLoS ONE</i> , <b>2010</b> , 5, e13988	3.7	46
46	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> , <b>2010</b> , 107, 7527-32	11.5	291
45	Typhoid in Kenya is associated with a dominant multidrug-resistant Salmonella enterica serovar Typhi haplotype that is also widespread in Southeast Asia. <i>Journal of Clinical Microbiology</i> , <b>2010</b> , 48, 2171-6	9.7	104
44	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> , <b>2010</b> , 65, 1631-41	5.1	33
43	Navigating the future of bacterial molecular epidemiology. <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 640-5	7.9	49
42	The sensitivity of real-time PCR amplification targeting invasive Salmonella serovars in biological specimens. <i>BMC Infectious Diseases</i> , <b>2010</b> , 10, 125	4	68
41	High-throughput bacterial SNP typing identifies distinct clusters of Salmonella Typhi causing typhoid in Nepalese children. <i>BMC Infectious Diseases</i> , <b>2010</b> , 10, 144	4	61
40	Detecting SNPs and estimating allele frequencies in clonal bacterial populations by sequencing pooled DNA. <i>Bioinformatics</i> , <b>2009</b> , 25, 2074-5	7.2	34
39	Epidemic multiple drug resistant Salmonella Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype. <i>Genome Research</i> , <b>2009</b> , 19, 2279-87	9.7	374

38	Variation in <i>Salmonella enterica</i> serovar typhi IncHI1 plasmids during the global spread of resistant typhoid fever. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2009</b> , 53, 716-27	5.9	73
37	Pseudogene accumulation in the evolutionary histories of <i>Salmonella enterica</i> serovars Paratyphi A and Typhi. <i>BMC Genomics</i> , <b>2009</b> , 10, 36	4.5	120
36	Identifying adaptive differences could provide insight. <i>Nature</i> , <b>2009</b> , 458, 145	50.4	1
35	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. <i>Nature Genetics</i> , <b>2008</b> , 40, 987-93	36.3	398
34	Cord blood hemopoietic progenitor profiles predict acute respiratory symptoms in infancy. <i>Pediatric Allergy and Immunology</i> , <b>2008</b> , 19, 239-47	4.2	16
33	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> , <b>2008</b> , 46, 1741-6	9.7	52
32	A linear plasmid truncation induces unidirectional flagellar phase change in H:z66 positive <i>Salmonella</i> Typhi. <i>Molecular Microbiology</i> , <b>2007</b> , 66, 1207-18	4.1	21
31	Multidrug-resistant <i>Salmonella enterica</i> serovar paratyphi A harbors IncHI1 plasmids similar to those found in serovar typhi. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 4257-64	3.5	64
30	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> , <b>2006</b> , 2, 8	5.8	9
29	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 8, 2138	3.6	5
28	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 8, 2138	3.6	14
27	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307		1
26	Genome-scale rates of evolutionary change in bacteria		2
25	Genomic analysis of <i>Mycobacterium tuberculosis</i> reveals complex etiology of tuberculosis in Vietnam including frequent introduction and transmission of Beijing lineage and positive selection for EsxW Beijing variant		1
24	Unicycler: resolving bacterial genome assemblies from short and long sequencing reads		8
23	Completing bacterial genome assemblies with multiplex MinION sequencing		5
22	Direct nanopore sequencing of mRNA reveals landscape of transcript isoforms in apicomplexan parasites		2
21	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria		3

20	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella</i> Typhi at Pathogenwatch	2
19	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments	6
18	Genomic adaptations to an endolithic lifestyle in the coral-associated alga <i>Ostreobium</i>	2
17	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients	2
16	Genomic diversity and antimicrobial resistance of <i>Haemophilus</i> colonising the airways of young children with cystic fibrosis	1
15	Dynamics of the upper airway microbiome in the pathogenesis of asthma-associated persistent wheeze in preschool children	4
14	Laboratory and Molecular Surveillance of Paediatric Typhoidal <i>Salmonella</i> in Nepal: Antimicrobial Resistance and Implications for Vaccine Policy	1
13	Kaptive Web: user-friendly capsule and lipopolysaccharide serotype prediction for <i>Klebsiella</i> genomes	5
12	Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks	8
11	Performance of neural network basecalling tools for Oxford Nanopore sequencing	8
10	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from south and southeast Asia	3
9	Population structure and antimicrobial resistance patterns of <i>Salmonella</i> Typhi isolates in Bangladesh from 2004 to 2016	2
8	Neonatal genetics of gene expression reveal the origins of autoimmune and allergic disease risk	2
7	Correcting index databases improves metagenomic studies	14
6	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	2
5	Gastrointestinal carriage is a major reservoir of <i>K. pneumoniae</i> infection in intensive care patients	3
4	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya	1
3	Five years of GenoTyphi: updates to the global <i>Salmonella</i> Typhi genotyping framework	1

2	Klebsiella pneumoniae with capsule type K64 is overrepresented among invasive disease in Vietnam. <i>F1000Research</i> ,10, 454	3.6	0
1	Recovery of small plasmid sequences via Oxford Nanopore sequencing		1