

Kelly L Wyres

List of Publications by Year in descending order

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130
papers

22,450
citations

30551

56
h-index

15253

130
g-index

166
all docs

166
docs citations

166
times ranked

23666
citing authors

#	ARTICLE	IF	CITATIONS
1	Regional differences in carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases</i> , The, 2022, 22, 309-310.	4.6	13
2	Oral fosfomycin activity against <i>Klebsiella pneumoniae</i> in a dynamic bladder infection <i>in vitro</i> model. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1324-1333.	1.3	6
3	Multidrug-resistant <i>Klebsiella pneumoniae</i> : a retrospective study in Manaus, Brazil. <i>Archives of Microbiology</i> , 2022, 204, 202.	1.0	15
4	A curated collection of <i>Klebsiella</i> metabolic models reveals variable substrate usage and gene essentiality. <i>Genome Research</i> , 2022, , .	2.4	10
5	Kaptive 2.0: updated capsule and lipopolysaccharide locus typing for the <i>Klebsiella pneumoniae</i> species complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	52
6	Whole genome sequence analysis of <i>Salmonella Typhi</i> in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010306.	1.3	6
7	A nationwide genomic study of clinical <i>Klebsiella pneumoniae</i> in Norway 2001–15: introduction and spread of ESBLs facilitated by clonal groups CG15 and CG307. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 665-674.	1.3	16
8	Linear plasmids in <i>Klebsiella</i> and other Enterobacteriaceae. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
9	Transmission of <i>Klebsiella</i> strains and plasmids within and between grey-headed flying fox colonies. <i>Environmental Microbiology</i> , 2022, 24, 4425-4436.	1.8	3
10	Genomic epidemiology and temperature dependency of hypermucoviscous <i>Klebsiella pneumoniae</i> in Japan. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
11	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	5.8	51
12	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.	1.5	61
13	Multicentre stepped-wedge cluster randomised controlled trial of an antimicrobial stewardship programme in residential aged care: protocol for the START trial. <i>BMJ Open</i> , 2021, 11, e046142.	0.8	2
14	Detection of plasmid contigs in draft genome assemblies using customized Kraken databases. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
15	Evolution and genomic insight into methicillin-resistant <i>Staphylococcus aureus</i> ST9 in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1703-1711.	1.3	11
16	Genomic adaptations to an endolithic lifestyle in the coral-associated alga <i>Ostreobium</i> . <i>Current Biology</i> , 2021, 31, 1393-1402.e5.	1.8	40
17	Collateral Sensitivity to β -Lactam Drugs in Drug-Resistant Tuberculosis Is Driven by the Transcriptional Wiring of <i>Blal</i> Operon Genes. <i>MSphere</i> , 2021, 6, e0024521.	1.3	2
18	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.	5.8	56

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19	Klebsiella MALDI TypeR: a web-based tool for Klebsiella identification based on MALDI-TOF mass spectrometry. <i>Research in Microbiology</i> , 2021, 172, 103835.	1.0	9
20	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients. <i>BMC Infectious Diseases</i> , 2021, 21, 683.	1.3	18
21	A genomic surveillance framework and genotyping tool for <i>Klebsiella pneumoniae</i> and its related species complex. <i>Nature Communications</i> , 2021, 12, 4188.	5.8	394
22	Five Years of GenoTyphi: Updates to the Global <i>Salmonella</i> Typhi Genotyping Framework. <i>Journal of Infectious Diseases</i> , 2021, 224, S775-S780.	1.9	36
23	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021, 7, .	1.0	44
24	A novel hypermucoviscous <i>Klebsiella pneumoniae</i> ST3994-K2 clone belonging to Clonal Group 86. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	2
25	Novel strains of <i>Klebsiella africana</i> and <i>Klebsiella pneumoniae</i> in Australian fruit bats (<i>Pteropus</i>) Tj ETQq1 1 0.784314rgBT /Oyerlock 10	1.0	8
26	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , 2021, 10, .	2.8	29
27	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.	4.3	34
28	Addressing parachute research and removing barriers for LMIC researchers in <i>Microbial Genomics</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
29	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.	2.9	42
30	Context-aware genomic surveillance reveals hidden transmission of a carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
31	Investigation of sequential outbreaks of <i>Burkholderia cepacia</i> and multidrug-resistant extended spectrum β -lactamase producing <i>Klebsiella</i> species in a West African tertiary hospital neonatal unit: a retrospective genomic analysis. <i>Lancet Microbe</i> , The, 2020, 1, e119-e129.	3.4	26
32	Population genomics of <i>Klebsiella pneumoniae</i> . <i>Nature Reviews Microbiology</i> , 2020, 18, 344-359.	13.6	510
33	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.	3.6	178
34	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.	2.0	126
35	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacteriales. <i>ISME Journal</i> , 2020, 14, 1713-1730.	4.4	40
36	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, .	1.0	118

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37	Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers. PLoS Neglected Tropical Diseases, 2019, 13, e0007620.	1.3	62
38	FastSpar: rapid and scalable correlation estimation for compositional data. Bioinformatics, 2019, 35, 1064-1066.	1.8	190
39	Performance of neural network basecalling tools for Oxford Nanopore sequencing. Genome Biology, 2019, 20, 129.	3.8	1,971
40	Empirical ways to identify novel Bedaquiline resistance mutations in AtpE. PLoS ONE, 2019, 14, e0217169.	1.1	50
41	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of Klebsiella pneumoniae. PLoS Genetics, 2019, 15, e1008114.	1.5	228
42	hicap: <i>In Silico</i> Serotyping of the Haemophilus influenzae Capsule Locus. Journal of Clinical Microbiology, 2019, 57, .	1.8	32
43	Convergence of virulence and MDR in a single plasmid vector in MDR Klebsiella pneumoniae ST15. Journal of Antimicrobial Chemotherapy, 2019, 74, 1218-1222.	1.3	93
44	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307. Journal of Antimicrobial Chemotherapy, 2019, 74, 577-581.	1.3	137
45	Small IncQ1 and Col-Like Plasmids Harboring <i>bla</i> _{KPC-2} and Non-Tn <i>4401</i> Elements (NTE <i>KPC</i> -IId) in High-Risk Lineages of <i>Klebsiella pneumoniae</i> CG258. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	27
46	Co-circulation of Multidrug-resistant Shigella Among Men Who Have Sex With Men in Australia. Clinical Infectious Diseases, 2019, 69, 1535-1544.	2.9	77
47	Comment on: CG258 <i>Klebsiella pneumoniae</i> isolates without β -lactam resistance at the onset of the carbapenem-resistant Enterobacteriaceae epidemic in New York City. Journal of Antimicrobial Chemotherapy, 2019, 74, 831-833.	1.3	1
48	Evolution of a clade of Acinetobacter baumannii global clone 1, lineage 1 via acquisition of carbapenem- and aminoglycoside-resistance genes and dispersion of ISAba1. Microbial Genomics, 2019, 5, .	1.0	49
49	Global phylogenomics of multidrug-resistant Salmonella enterica serotype Kentucky ST198. Microbial Genomics, 2019, 5, .	1.0	69
50	Insights from the revised complete genome sequences of Acinetobacter baumannii strains AB307-0294 and ACICU belonging to global clones 1 and 2. Microbial Genomics, 2019, 5, .	1.0	12
51	Genomic evolution and local epidemiology of Klebsiella pneumoniae from a major hospital in Beijing, China, over a 15 year period: dissemination of known and novel high-risk clones. Microbial Genomics, 2019, 7, .	1.0	5
52	Kaptive Web: User-Friendly Capsule and Lipopolysaccharide Serotype Prediction for Klebsiella Genomes. Journal of Clinical Microbiology, 2018, 56, .	1.8	239
53	Antimicrobial-Resistant Klebsiella pneumoniae Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. Clinical Infectious Diseases, 2018, 67, 161-170.	2.9	108
54	Klebsiella pneumoniae as a key trafficker of drug resistance genes from environmental to clinically important bacteria. Current Opinion in Microbiology, 2018, 45, 131-139.	2.3	337

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55	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018, 4, .	1.0	197
56	Deepbiner: Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006583.	1.5	171
57	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	5.8	98
58	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018, 10, 77.	3.6	153
59	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018, 4, eaat5869.	4.7	130
60	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.	5.1	146
61	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018, 360, 733-738.	6.0	254
62	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.	9.4	167
63	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.	1.3	70
64	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	1.6	20
65	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , 2018, 18, 95.	3.2	16
66	Diversity-Generating Machines: Genetics of Bacterial Sugar-Coating. <i>Trends in Microbiology</i> , 2018, 26, 1008-1021.	3.5	83
67	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.	5.8	205
68	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.	5.9	89
69	Evolution of carbapenem resistance in <i>Acinetobacter baumannii</i> during a prolonged infection. <i>Microbial Genomics</i> , 2018, 4, .	1.0	49
70	Trajectories of childhood immune development and respiratory health relevant to asthma and allergy. <i>ELife</i> , 2018, 7, .	2.8	22
71	Comparative genomics of Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> . <i>Gut</i> , 2017, 66, 1382-1389.	6.1	114
72	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , 2017, 8, 15483.	5.8	132

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73	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , 2017, 65, 208-215.	2.9	381
74	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	6.0	255
75	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.	1.5	76
76	Completing bacterial genome assemblies with multiplex MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000132.	1.0	559
77	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. <i>PLoS Computational Biology</i> , 2017, 13, e1005595.	1.5	5,135
78	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	0.8	21
79	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	0.8	23
80	The diversity of <i>Klebsiella pneumoniae</i> surface polysaccharides. <i>Microbial Genomics</i> , 2016, 2, e000073.	1.0	185
81	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.	1.0	110
82	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016, 2, e000102.	1.0	372
83	A novel ciprofloxacin-resistant subclade of H58 <i>Salmonella</i> Typhi is associated with fluoroquinolone treatment failure. <i>ELife</i> , 2016, 5, e14003.	2.8	111
84	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
85	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	1.3	46
86	The Molecular and Spatial Epidemiology of Typhoid Fever in Rural Cambodia. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004785.	1.3	40
87	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , 2016, 3, 71-82.	2.9	48
88	<i>Klebsiella pneumoniae</i> Population Genomics and Antimicrobial-Resistant Clones. <i>Trends in Microbiology</i> , 2016, 24, 944-956.	3.5	217
89	Evolution of atypical enteropathogenic <i>E. coli</i> by repeated acquisition of LEE pathogenicity island variants. <i>Nature Microbiology</i> , 2016, 1, 15010.	5.9	60
90	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.	1.6	87

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91	Paradoxical Hypersusceptibility of Drug-resistant <i>Mycobacterium tuberculosis</i> to β -lactam Antibiotics. <i>EBioMedicine</i> , 2016, 9, 170-179.	2.7	39
92	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.	1.3	82
93	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.	0.4	39
94	A small <i>Acinetobacter</i> plasmid carrying the <i>tet39</i> tetracycline resistance determinant. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 269-271.	1.3	18
95	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	1.0	65
96	Carbapenem and amikacin resistance on a large conjugative <i>Acinetobacter baumannii</i> plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1259-1261.	1.3	42
97	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.	1.3	30
98	A platform for leveraging next generation sequencing for routine microbiology and public health use. <i>Health Information Science and Systems</i> , 2015, 3, S7.	3.4	7
99	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , 2015, 16, 667.	1.2	119
100	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
101	Draft Genome Sequence of a Clinical Isolate of <i>Serratia marcescens</i> , Strain AH0650_Sm1. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
102	Bandage: interactive visualization of <i>de novo</i> genome assemblies. <i>Bioinformatics</i> , 2015, 31, 3350-3352.	1.8	1,671
103	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.	1.1	99
104	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
105	The complete sequence of <i>Salmonella</i> genomic island SGI2. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 617-619.	1.3	16
106	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.	1.3	50
107	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , 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.	3.3	942
108	The Infant Nasopharyngeal Microbiome Impacts Severity of Lower Respiratory Infection and Risk of Asthma Development. <i>Cell Host and Microbe</i> , 2015, 17, 704-715.	5.1	721

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109	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	9.4	403
110	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant Staphylococcus aureus. <i>MBio</i> , 2015, 6, e00080.	1.8	81
111	The complete sequence of Salmonella genomic island SGI1-K. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 305-306.	1.3	19
112	Introduction and establishment of fluoroquinolone-resistant Shigella sonnei into Bhutan. <i>Microbial Genomics</i> , 2015, 1, e000042.	1.0	11
113	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.	1.2	50
114	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014, 6, 90.	3.6	953
115	Analysis of Salmonella enterica 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.	1.0	31
116	A conjugative plasmid carrying the carbapenem resistance gene blaOXA-23 in AbaR4 in an extensively resistant GC1 Acinetobacter baumannii isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2625-2628.	1.3	57
117	Insertions in the OCL1 locus of Acinetobacter baumannii lead to shortened lipooligosaccharides. <i>Research in Microbiology</i> , 2014, 165, 472-475.	1.0	33
118	Elucidation of Pathways Driving Asthma Pathogenesis: Development of a Systems-Level Analytic Strategy. <i>Frontiers in Immunology</i> , 2014, 5, 447.	2.2	16
119	Streptococcus pneumoniae Carriage Prevalence in Nepal: Evaluation of a Method for Delayed Transport of Samples from Remote Regions and Implications for Vaccine Implementation. <i>PLoS ONE</i> , 2014, 9, e98739.	1.1	21
120	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
121	Evidence of antimicrobial resistance-conferring genetic elements among pneumococci isolated prior to 1974. <i>BMC Genomics</i> , 2013, 14, 500.	1.2	40
122	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.	1.2	67
123	Pneumococcal Capsular Switching: A Historical Perspective. <i>Journal of Infectious Diseases</i> , 2013, 207, 439-449.	1.9	172
124	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.	3.3	124
125	Characterization of the yehUT Two-Component Regulatory System of Salmonella enterica Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , 2013, 8, e84567.	1.1	16
126	High-Resolution Genotyping of the Endemic Salmonella Typhi Population during a Vi (Typhoid) Vaccination Trial in Kolkata. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1490.	1.3	21

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127	Shigella sonnei genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012, 44, 1056-1059.	9.4	278
128	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012, 13, R103.	13.9	62
129	Short read sequence typing (SRST): multi-locus sequence types from short reads. <i>BMC Genomics</i> , 2012, 13, 338.	1.2	84
130	Environmental Factors Determining the Epidemiology and Population Genetic Structure of the <i>Bacillus cereus</i> Group in the Field. <i>PLoS Pathogens</i> , 2010, 6, e1000905.	2.1	94