

Sharon J Peacock

List of Publications by Year in descending order

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Version: 2024-02-01

428
papers

42,502
citations

3919

88
h-index

3312

184
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466
all docs

466
docs citations

466
times ranked

38801
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	2.8	21
2	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	3.4	25
3	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
4	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	13.7	138
5	A2B-COVID: A Tool for Rapidly Evaluating Potential SARS-CoV-2 Transmission Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	12
6	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	1.3	3
7	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	5.8	27
8	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
9	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	2.0	4
10	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. <i>Virus Evolution</i> , 2022, 8, veac023.	2.2	19
11	<i>Mycobacterium tuberculosis</i> Lineages Associated with Mutations and Drug Resistance in Isolates from India. <i>Microbiology Spectrum</i> , 2022, 10, e0159421.	1.2	10
12	Miniaturised broth microdilution for simplified antibiotic susceptibility testing of Gram negative clinical isolates using microcapillary devices. <i>Analyst</i> , The, 2022, 147, 3558-3569.	1.7	5
13	Horses for courses? Assessing the potential value of a surrogate, point-of-care test for SARS-CoV-2 epidemic control. <i>Influenza and Other Respiratory Viruses</i> , 2021, 15, 3-6.	1.5	8
14	Impact of low blood culture usage on rates of antimicrobial resistance. <i>Journal of Infection</i> , 2021, 82, 355-362.	1.7	12
15	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	5.9	53
16	A common protocol for the simultaneous processing of multiple clinically relevant bacterial species for whole genome sequencing. <i>Scientific Reports</i> , 2021, 11, 193.	1.6	3
17	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 2021, 10, .	2.8	20
18	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	13.6	2,650

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19	Laboratory informatics capacity for effective antimicrobial resistance surveillance in resource-limited settings. <i>Lancet Infectious Diseases</i> , The, 2021, 21, e170-e174.	4.6	13
20	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	3.8	53
21	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 916-917.	4.6	14
22	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. <i>ELife</i> , 2021, 10, .	2.8	34
23	Defining nosocomial transmission of <i>Escherichia coli</i> and antimicrobial resistance genes: a genomic surveillance study. <i>Lancet Microbe</i> , The, 2021, 2, e472-e480.	3.4	39
24	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021, 16, e0245532.	1.1	228
25	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	6.0	111
26	Significant variability exists in the cytotoxicity of global methicillin-resistant <i>Staphylococcus aureus</i> lineages. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	10
27	Genomic Surveillance of Methicillin-resistant <i>Staphylococcus aureus</i> : A Mathematical Early Modeling Study of Cost-effectiveness. <i>Clinical Infectious Diseases</i> , 2020, 70, 1613-1619.	2.9	27
28	A One Health Study of the Genetic Relatedness of <i>Klebsiella pneumoniae</i> and Their Mobile Elements in the East of England. <i>Clinical Infectious Diseases</i> , 2020, 70, 219-226.	2.9	46
29	A review of published spoligotype data indicates the diversity of <i>Mycobacterium tuberculosis</i> from India is under-represented in global databases. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104072.	1.0	6
30	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 785-786.	1.3	1
31	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1263-1271.	4.6	352
32	The prevalence and implications of single nucleotide polymorphisms in genes encoding the RNA polymerase of clinical isolates of <i>Staphylococcus aureus</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1058.	1.2	2
33	Fetal inheritance of chromosomally integrated human herpesvirus 6 predisposes the mother to pre-eclampsia. <i>Nature Microbiology</i> , 2020, 5, 901-908.	5.9	29
34	Setting priorities for patient-centered surveillance of drug-resistant infections. <i>International Journal of Infectious Diseases</i> , 2020, 97, 60-65.	1.5	4
35	Association between bacterial homoplasmic variants and radiological pathology in tuberculosis. <i>Thorax</i> , 2020, 75, 584-591.	2.7	8
36	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	3.6	58

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37	Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19). JAMA - Journal of the American Medical Association, 2020, 324, 782.	3.8	3,597
38	The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. Lancet Infectious Diseases, The, 2020, 20, e51-e60.	4.6	161
39	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. Journal of Antimicrobial Chemotherapy, 2020, 75, 1117-1122.	1.3	10
40	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant Staphylococcus aureus: a genomic epidemiology analysis. Lancet Microbe, The, 2020, 1, e328-e335.	3.4	75
41	Genomic surveillance of Escherichia coli ST131 identifies local expansion and serial replacement of subclones. Microbial Genomics, 2020, 6, .	1.0	33
42	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. Microbial Genomics, 2020, 6, .	1.0	4
43	Leapfrogging laboratories: the promise and pitfalls of high-tech solutions for antimicrobial resistance surveillance in low-income settings. BMJ Global Health, 2020, 5, e003622.	2.0	30
44	Antibody response to SARS-CoV-2 infection in humans: A systematic review. PLoS ONE, 2020, 15, e0244126.	1.1	269
45	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		1
46	Automating the Generation of Antimicrobial Resistance Surveillance Reports: Proof-of-Concept Study Involving Seven Hospitals in Seven Countries. Journal of Medical Internet Research, 2020, 22, e19762.	2.1	14
47	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
48	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
49	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
50	Improving the estimation of the global burden of antimicrobial resistant infections. Lancet Infectious Diseases, The, 2019, 19, e392-e398.	4.6	68
51	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in Mycobacterium tuberculosis in Southern India. Scientific Reports, 2019, 9, 10283.	1.6	32
52	Human placenta has no microbiome but can contain potential pathogens. Nature, 2019, 572, 329-334.	18.7	513
53	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. Microbiome, 2019, 7, 137.	4.9	22
54	Pilot Evaluation of a Fully Automated Bioinformatics System for Analysis of Methicillin-Resistant Staphylococcus aureus Genomes and Detection of Outbreaks. Journal of Clinical Microbiology, 2019, 57, .	1.8	9

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55	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	3.8	22
56	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2823-2823.	1.3	2
57	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3406-3408.	1.3	3
58	One Health Genomic Surveillance of <i>Escherichia coli</i> Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. <i>MBio</i> , 2019, 10, .	1.8	130
59	Harnessing alternative sources of antimicrobial resistance data to support surveillance in low-resource settings. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 541-546.	1.3	18
60	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	5.9	47
61	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2122-2127.	1.3	35
62	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	20
63	Rapid sequencing of MRSA direct from clinical plates in a routine microbiology laboratory. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2153-2156.	1.3	8
64	Methodology for Whole-Genome Sequencing of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates in a Routine Hospital Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	22
65	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. <i>Genome Research</i> , 2019, 29, 626-634.	2.4	40
66	Genome Sequencing of Polydrug-, Multidrug-, and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Strains from South India. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
67	Clinical Epidemiology of 7,126 Melioidosis Patients in Thailand and the Implications for a National Notifiable Diseases Surveillance System. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz498.	0.4	38
68	The Emergence of Successful <i>Streptococcus pyogenes</i> Lineages through Convergent Pathways of Capsule Loss and Recombination Directing High Toxin Expression. <i>MBio</i> , 2019, 10, .	1.8	22
69	Predictive Validity of the qSOFA Score for Sepsis in Adults with Community-Onset Staphylococcal Infection in Thailand. <i>Journal of Clinical Medicine</i> , 2019, 8, 1908.	1.0	3
70	Isolation and comparative genomics of <i>Mycobacterium tuberculosis</i> isolates from cattle and their attendants in South India. <i>Scientific Reports</i> , 2019, 9, 17892.	1.6	14
71	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	2.0	19
72	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	1.8	50

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73	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019, 58, 548-550.	0.9	8
74	Molecular epidemiology and expression of capsular polysaccharides in <i>Staphylococcus aureus</i> clinical isolates in the United States. <i>PLoS ONE</i> , 2019, 14, e0208356.	1.1	33
75	Genomic surveillance of <i>Escherichia coli</i> in municipal wastewater treatment plants as an indicator of clinically relevant pathogens and their resistance genes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	29
76	Whole-Genome Sequencing of a <i>Mycobacterium orygis</i> Strain Isolated from Cattle in Chennai, India. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	12
77	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	3.9	19
78	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	2.8	39
79	Melioidosis. <i>Nature Reviews Disease Primers</i> , 2018, 4, 17107.	18.1	430
80	Genome-Based Analysis of <i>Enterococcus faecium</i> Bacteremia Associated with Recurrent and Mixed-Strain Infection. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	14
81	Duration of exposure to multiple antibiotics is associated with increased risk of VRE bacteraemia: a nested case-control study. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1692-1699.	1.3	40
82	Analysis of mutations in <i>pncA</i> reveals non-overlapping patterns among various lineages of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2018, 8, 4628.	1.6	5
83	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	83
84	Genomic Surveillance of <i>Enterococcus faecium</i> Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. <i>MBio</i> , 2018, 9, .	1.8	63
85	Detecting eukaryotic microbiota with single-cell sensitivity in human tissue. <i>Microbiome</i> , 2018, 6, 151.	4.9	21
86	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
87	Reply to Dookie et al., "Whole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosis". <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	1
88	Recognizing the reagent microbiome. <i>Nature Microbiology</i> , 2018, 3, 851-853.	5.9	255
89	Effect of temperature on <i>Burkholderia pseudomallei</i> growth, proteomic changes, motility and resistance to stress environments. <i>Scientific Reports</i> , 2018, 8, 9167.	1.6	18
90	Genomic survey of <i>Clostridium difficile</i> reservoirs in the East of England implicates environmental contamination of wastewater treatment plants by clinical lineages. <i>Microbial Genomics</i> , 2018, 4, .	1.0	19

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91	<i>Streptococcus bovimastitidis</i> sp. nov., isolated from a dairy cow with mastitis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 21-27.	0.8	12
92	Are commercial providers a viable option for clinical bacterial sequencing?. <i>Microbial Genomics</i> , 2018, 4, .	1.0	5
93	Naturally occurring polymorphisms in the virulence regulator Rsp modulate <i>Staphylococcus aureus</i> survival in blood and antibiotic susceptibility. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1189-1195.	0.7	6
94	Changing the paradigm for hospital outbreak detection by leading with genomic surveillance of nosocomial pathogens. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1213-1219.	0.7	61
95	Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC): Supporting the transition from strategy to action. <i>Wellcome Open Research</i> , 2018, 3, 59.	0.9	5
96	Presence of <i>B. thailandensis</i> and <i>B. thailandensis</i> expressing <i>B. pseudomallei</i> -like capsular polysaccharide in Thailand, and their associations with serological response to <i>B. pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006193.	1.3	22
97	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
98	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR <i>sls</i> Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	29
99	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2017, 9, 6.	3.6	61
100	Evolution and Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> in the United Kingdom and Ireland. <i>MBio</i> , 2017, 8, .	1.8	97
101	Patient Characteristics, Management, and Predictors of Outcome from Severe Community-Onset Staphylococcal Sepsis in Northeast Thailand: A Prospective Multicenter Study. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 16-0606.	0.6	7
102	Multitarget Quantitative PCR Improves Detection and Predicts Cultivability of the Pathogen <i>Burkholderia pseudomallei</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	20
103	Complex Routes of Nosocomial Vancomycin-Resistant <i>Enterococcus faecium</i> Transmission Revealed by Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 64, 886-893.	2.9	93
104	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	103
105	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , 2017, 65, 2069-2077.	2.9	11
106	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> <i>scpD</i> -Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	24
107	Community outbreaks of group A <i>Streptococcus</i> revealed by genome sequencing. <i>Scientific Reports</i> , 2017, 7, 8554.	1.6	26
108	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <i>Genome Research</i> , 2017, 27, 1437-1449.	2.4	231

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109	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	1.6	25
110	Whole genome sequencing of ESBL-producing <i>Escherichia coli</i> isolated from patients, farm waste and canals in Thailand. <i>Genome Medicine</i> , 2017, 9, 81.	3.6	73
111	Clonal differences in <i>Staphylococcus aureus</i> bacteraemia-associated mortality. <i>Nature Microbiology</i> , 2017, 2, 1381-1388.	5.9	118
112	Evolution of the <i>Staphylococcus argenteus</i> ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. <i>MBio</i> , 2017, 8, .	1.8	44
113	Melioidosis. , 2017, , 1073-1077.e1.		2
114	Population Structure of Multidrug-Resistant <i>Klebsiella oxytoca</i> within Hospitals across the United Kingdom and Ireland Identifies Sharing of Virulence and Resistance Genes with <i>K. pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 574-584.	1.1	35
115	Gastrointestinal tract involvement in melioidosis. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2017, 111, 185-187.	0.7	10
116	Evolution of mobile genetic element composition in an epidemic methicillin-resistant <i>Staphylococcus aureus</i> : temporal changes correlated with frequent loss and gain events. <i>BMC Genomics</i> , 2017, 18, 684.	1.2	43
117	AMR Surveillance in low and middle-income settings - A roadmap for participation in the Global Antimicrobial Surveillance System (GLASS). <i>Wellcome Open Research</i> , 2017, 2, 92.	0.9	114
118	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the identification of <i>Burkholderia pseudomallei</i> from Asia and Australia and differentiation between <i>Burkholderia</i> species. <i>PLoS ONE</i> , 2017, 12, e0175294.	1.1	36
119	Longitudinal genomic surveillance of multidrug-resistant <i>Escherichia coli</i> carriage in a long-term care facility in the United Kingdom. <i>Genome Medicine</i> , 2017, 9, 70.	3.6	44
120	Within-host evolution of <i>Enterococcus faecium</i> during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. <i>Genome Medicine</i> , 2017, 9, 119.	3.6	26
121	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in a UK Teaching Hospital. <i>Open Forum Infectious Diseases</i> , 2017, 4, S43-S44.	0.4	3
122	Sharing of carbapenemase-encoding plasmids between <i>Enterobacteriaceae</i> in UK sewage uncovered by MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000114.	1.0	33
123	Population genetic structuring of methicillin-resistant <i>Staphylococcus aureus</i> clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017, 3, e000113.	1.0	19
124	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017, 3, e000117.	1.0	10
125	Increased Von Willebrand factor, decreased ADAMTS13 and thrombocytopenia in melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005468.	1.3	7
126	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.	1.1	19

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127	Presence of <i>Burkholderia pseudomallei</i> in Soil and Paddy Rice Water in a Rice Field in Northeast Thailand, but Not in Air and Rainwater. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 1702-1705.	0.6	14
128	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011–2013. <i>Emerging Infectious Diseases</i> , 2016, 22, 1658-1659.	2.0	4
129	Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. <i>ELife</i> , 2016, 5, .	2.8	207
130	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	1.3	253
131	Barriers and Recommended Interventions to Prevent Melioidosis in Northeast Thailand: A Focus Group Study Using the Behaviour Change Wheel. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004823.	1.3	34
132	The Dynamics of <i>Staphylococcus aureus</i> carriage and Comparisons by Age in Two Studies of an Investigational <i>S aureus</i> 4-Antigen Vaccine (SA4Ag). <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.4	0
133	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. <i>Annals of Applied Statistics</i> , 2016, 10, 395-417.	0.5	52
134	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	2.4	63
135	<i>dhfrA thyA</i> Double Deletion in <i>para</i> -Aminosalicylic Acid-Resistant <i>Mycobacterium tuberculosis</i> Beijing Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3864-3867.	1.4	20
136	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1101-1109.	2.4	74
137	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	3.6	30
138	Soil Nutrient Depletion Is Associated with the Presence of <i>Burkholderia pseudomallei</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 7086-7092.	1.4	37
139	Whole-genome sequencing of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Myanmar. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 113-117.	0.9	28
140	The dissemination of multidrug-resistant <i>Enterobacter cloacae</i> throughout the UK and Ireland. <i>Nature Microbiology</i> , 2016, 1, 16173.	5.9	24
141	Genome-based characterization of hospital-adapted <i>Enterococcus faecalis</i> lineages. <i>Nature Microbiology</i> , 2016, 1, .	5.9	65
142	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1388-1396.	2.4	96
143	Predicted global distribution of <i>Burkholderia pseudomallei</i> and burden of melioidosis. <i>Nature Microbiology</i> , 2016, 1, .	5.9	704
144	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	1.9	45

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145	Wild-Type and Non-Wild-Type Mycobacterium tuberculosis MIC Distributions for the Novel Fluoroquinolone Antofloxacin Compared with Those for Ofloxacin, Levofloxacin, and Moxifloxacin. Antimicrobial Agents and Chemotherapy, 2016, 60, 5232-5237.	1.4	15
146	Comparison of two chromogenic media for the detection of vancomycin-resistant enterococcal carriage by nursing home residents. Diagnostic Microbiology and Infectious Disease, 2016, 85, 409-412.	0.8	7
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