Sharon J Peacock

List of Publications by Year in Descending Order

438 papers	30,611 citations	78 h-index	161 g-index
466 ext. papers	37,925 ext. citations	9 avg, IF	7.39 L-index

#	Paper	IF	Citations
438	Emergence of methicillin resistance predates the clinical use of antibiotics.. *Nature*, **2022**,	50.4	33
437	A2B-COVID: A tool for rapidly evaluating potential SARS-CoV-2 transmission events.. *Molecular Biology and Evolution*, **2022**,	8.3	3
436	Multiple phylogenetically-diverse, differentially-virulent Burkholderia pseudomallei isolated from a single soil sample collected in Thailand.. *PLoS Neglected Tropical Diseases*, **2022**, 16, e0010172	4.8	
435	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. *Nature Communications*, **2022**, 13, 751	17.4	7
434	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. *Nature Communications*, **2022**, 13, 1012	17.4	2
433	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies.. *Communications Biology*, **2022**, 5, 266	6.7	0
432	Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. *Virus Evolution*, **2022**, 8, veac023	3.7	1
431	Mycobacterium tuberculosis Lineages Associated with Mutations and Drug Resistance in Isolates from India.. *Microbiology Spectrum*, **2022**, e0159421	8.9	0
430	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. *Science*, **2021**, 374, eabl9551	33.3	31
429	Genomic epidemiology of COVID-19 in care homes in the east of England. *ELife*, **2021**, 10,	8.9	8
428	SARS-CoV-2 variants, spike mutations and immune escape. *Nature Reviews Microbiology*, **2021**, 19, 409-424	24.2	873
427	Laboratory informatics capacity for effective antimicrobial resistance surveillance in resource-limited settings. *Lancet Infectious Diseases, The*, **2021**, 21, e170-e174	25.5	2
426	Horses for courses? Assessing the potential value of a surrogate, point-of-care test for SARS-CoV-2 epidemic control. *Influenza and Other Respiratory Viruses*, **2021**, 15, 3-6	5.6	6
425	Impact of low blood culture usage on rates of antimicrobial resistance. *Journal of Infection*, **2021**, 82, 355-362	18.9	2
424	Quantifying acquisition and transmission of Enterococcus faecium using genomic surveillance. *Nature Microbiology*, **2021**, 6, 103-111	26.6	15
423	A common protocol for the simultaneous processing of multiple clinically relevant bacterial species for whole genome sequencing. *Scientific Reports*, **2021**, 11, 193	4.9	1
422	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. *Lancet Infectious Diseases, The*, **2021**, 21, 916-917	25.5	7

421	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. *Clinical Microbiology and Infection*, **2021**,	9.5	7
420	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. *ELife*, **2021**, 10,	8.9	15
419	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. *Lancet Microbe, The*, **2021**,	22.2	2
418	Defining nosocomial transmission of and antimicrobial resistance genes: a genomic surveillance study. *Lancet Microbe, The*, **2021**, 2, e472-e480	22.2	7
417	T cell response to SARS-CoV-2 infection in humans: A systematic review. *PLoS ONE*, **2021**, 16, e0245532	3.7	43
416	Significant variability exists in the cytotoxicity of global methicillin-resistant lineages.. *Microbiology (United Kingdom)*, **2021**, 167,	2.9	1
415	The prevalence and implications of single nucleotide polymorphisms in genes encoding the RNA polymerase of clinical isolates of Staphylococcus aureus. *MicrobiologyOpen*, **2020**, 9, e1058	3.4	1
414	Fetal inheritance of chromosomally integrated human herpesvirus 6 predisposes the mother to pre-eclampsia. *Nature Microbiology*, **2020**, 5, 901-908	26.6	12
413	Setting priorities for patient-centered surveillance of drug-resistant infections. *International Journal of Infectious Diseases*, **2020**, 97, 60-65	10.5	2
412	Association between bacterial homoplastic variants and radiological pathology in tuberculosis. *Thorax*, **2020**, 75, 584-591	7.3	2
411	Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. *Genome Medicine*, **2020**, 12, 27	14.4	30
410	Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19): A Review. *JAMA - Journal of the American Medical Association*, **2020**, 324, 782-793	27.4	1978
409	The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. *Lancet Infectious Diseases, The*, **2020**, 20, e51-e60	25.5	77
408	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. *Journal of Antimicrobial Chemotherapy*, **2020**, 75, 1117-1122	5.1	3
407	Leapfrogging laboratories: the promise and pitfalls of high-tech solutions for antimicrobial resistance surveillance in low-income settings. *BMJ Global Health*, **2020**, 5,	6.6	12
406	Antibody response to SARS-CoV-2 infection in humans: A systematic review. *PLoS ONE*, **2020**, 15, e0244126	3.7	130
405	Antibody response to SARS-CoV-2 infection in humans: A systematic review **2020**, 15, e0244126		1
404	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	7.6	6

403	Definition of a genetic relatedness cutoff to exclude recent transmission of meticillin-resistant : a genomic epidemiology analysis. *Lancet Microbe, The*, **2020**, 1, e328-e335	22.2	14
402	Genomic surveillance of ST131 identifies local expansion and serial replacement of subclones. *Microbial Genomics*, **2020**, 6,	4.4	16
401	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. *Microbial Genomics*, **2020**, 6,	4.4	2
400	RAntibiotic footprintRas a communication tool to aid reduction of antibiotic consumption-authorsR response. *Journal of Antimicrobial Chemotherapy*, **2020**, 75, 785-786	5.1	1
399	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. *Lancet Infectious Diseases, The*, **2020**, 20, 1263-1272	25.5	200
398	Genomic Surveillance of Methicillin-resistant Staphylococcus aureus: A Mathematical Early Modeling Study of Cost-effectiveness. *Clinical Infectious Diseases*, **2020**, 70, 1613-1619	11.6	12
397	A One Health Study of the Genetic Relatedness of Klebsiella pneumoniae and Their Mobile Elements in the East of England. *Clinical Infectious Diseases*, **2020**, 70, 219-226	11.6	24
396	A review of published spoligotype data indicates the diversity of Mycobacterium tuberculosis from India is under-represented in global databases. *Infection, Genetics and Evolution*, **2020**, 78, 104072	4.5	3
395	Antibody response to SARS-CoV-2 infection in humans: A systematic review **2020**, 15, e0244126		
394	Antibody response to SARS-CoV-2 infection in humans: A systematic review **2020**, 15, e0244126		
393	Antibody response to SARS-CoV-2 infection in humans: A systematic review **2020**, 15, e0244126		
392	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,	9.7	6
391	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. *Genome Biology*, **2019**, 20, 184	18.3	12
390	RAntibiotic footprintRas a communication tool to aid reduction of antibiotic consumption-authorsR response. *Journal of Antimicrobial Chemotherapy*, **2019**, 74, 2823	5.1	2
389	RAntibiotic footprintRas a communication tool to aid reduction of antibiotic consumption-authorsR response. *Journal of Antimicrobial Chemotherapy*, **2019**, 74, 3406-3408	5.1	3
388	One Health Genomic Surveillance of Escherichia coli Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. *MBio*, **2019**, 10,	7.8	64
387	Harnessing alternative sources of antimicrobial resistance data to support surveillance in low-resource settings. *Journal of Antimicrobial Chemotherapy*, **2019**, 74, 541-546	5.1	11
386	Genomic identification of cryptic susceptibility to penicillins and β-lactamase inhibitors in methicillin-resistant Staphylococcus aureus. *Nature Microbiology*, **2019**, 4, 1680-1691	26.6	24

385	PAntibiotic footprintRas a communication tool to aid reduction of antibiotic consumption. *Journal of Antimicrobial Chemotherapy*, **2019**, 74, 2122-2127	5.1	23
384	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate and Members of the Mycobacterium tuberculosis Complex. *Antimicrobial Agents and Chemotherapy*, **2019**, 63,	5.9	12
383	Rapid sequencing of MRSA direct from clinical plates in a routine microbiology laboratory. *Journal of Antimicrobial Chemotherapy*, **2019**, 74, 2153-2156	5.1	7
382	Methodology for Whole-Genome Sequencing of Methicillin-Resistant Isolates in a Routine Hospital Microbiology Laboratory. *Journal of Clinical Microbiology*, **2019**, 57,	9.7	8
381	Detection of vancomycin-resistant hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. *Genome Research*, **2019**, 29, 626-634	9.7	21
380	Genome Sequencing of Polydrug-, Multidrug-, and Extensively Drug-Resistant Mycobacterium tuberculosis Strains from South India. *Microbiology Resource Announcements*, **2019**, 8,	1.3	3
379	Improving the estimation of the global burden of antimicrobial resistant infections. *Lancet Infectious Diseases, The*, **2019**, 19, e392-e398	25.5	41
378	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in Mycobacterium tuberculosis in Southern India. *Scientific Reports*, **2019**, 9, 10283	4.9	20
377	Human placenta has no microbiome but can contain potential pathogens. *Nature*, **2019**, 572, 329-334	50.4	323
376	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. *Microbiome*, **2019**, 7, 137	16.6	12
375	Whole-Genome Sequencing of a Strain Isolated from Cattle in Chennai, India. *Microbiology Resource Announcements*, **2019**, 8,	1.3	1
374	Prospective genomic surveillance of methicillin-resistant (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. *Eurosurveillance*, **2019**, 24,	19.8	14
373	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. *ELife*, **2019**, 8,	8.9	11
372	Genomic surveillance of Escherichia coli in municipal wastewater treatment plants as an indicator of clinically relevant pathogens and their resistance genes. *Microbial Genomics*, **2019**, 5,	4.4	10
371	Clinical Epidemiology of 7126 Melioidosis Patients in Thailand and the Implications for a National Notifiable Diseases Surveillance System. *Open Forum Infectious Diseases*, **2019**, 6, ofz498	1	13
370	The Emergence of Successful Streptococcus pyogenes Lineages through Convergent Pathways of Capsule Loss and Recombination Directing High Toxin Expression. *MBio*, **2019**, 10,	7.8	8
369	Predictive Validity of the qSOFA Score for Sepsis in Adults with Community-Onset Staphylococcal Infection in Thailand. *Journal of Clinical Medicine*, **2019**, 8,	5.1	1
368	Isolation and comparative genomics of Mycobacterium tuberculosis isolates from cattle and their attendants in South India. *Scientific Reports*, **2019**, 9, 17892	4.9	4

367	Genetic variation associated with infection and the environment in the accidental pathogen. *Communications Biology*, **2019**, 2, 428	6.7	9
366	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. *MBio*, **2019**, 10,	7.8	22
365	Nasal carriage of Staphylococcus pseudintermedius in patients with granulomatosis with polyangiitis. *Rheumatology*, **2019**, 58, 548-550	3.9	8
364	Molecular epidemiology and expression of capsular polysaccharides in Staphylococcus aureus clinical isolates in the United States. *PLoS ONE*, **2019**, 14, e0208356	3.7	17
363	Melioidosis. *Nature Reviews Disease Primers*, **2018**, 4, 17107	51.1	236
362	Genome-Based Analysis of Enterococcus faecium Bacteremia Associated with Recurrent and Mixed-Strain Infection. *Journal of Clinical Microbiology*, **2018**, 56,	9.7	10
361	Duration of exposure to multiple antibiotics is associated with increased risk of VRE bacteraemia: a nested case-control study. *Journal of Antimicrobial Chemotherapy*, **2018**, 73, 1692-1699	5.1	25
360	Analysis of mutations in pncA reveals non-overlapping patterns among various lineages of Mycobacterium tuberculosis. *Scientific Reports*, **2018**, 8, 4628	4.9	4
359	Gene exchange drives the ecological success of a multi-host bacterial pathogen. *Nature Ecology and Evolution*, **2018**, 2, 1468-1478	12.3	80
358	Reply to Dookie et al., "Whole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosis". *Antimicrobial Agents and Chemotherapy*, **2018**, 62,	5.9	
357	Recognizing the reagent microbiome. *Nature Microbiology*, **2018**, 3, 851-853	26.6	161
356	Effect of temperature on Burkholderia pseudomallei growth, proteomic changes, motility and resistance to stress environments. *Scientific Reports*, **2018**, 8, 9167	4.9	11
355	Genomic survey of Clostridium difficile reservoirs in the East of England implicates environmental contamination of wastewater treatment plants by clinical lineages. *Microbial Genomics*, **2018**, 4,	4.4	11
354	Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC): Supporting the transition from strategy to action. *Wellcome Open Research*, **2018**, 3, 59	4.8	4
353	Presence of B. thailandensis and B. thailandensis expressing B. pseudomallei-like capsular polysaccharide in Thailand, and their associations with serological response to B. pseudomallei. *PLoS Neglected Tropical Diseases*, **2018**, 12, e0006193	4.8	14
352	Streptococcus bovimastitidis sp. nov., isolated from a dairy cow with mastitis. *International Journal of Systematic and Evolutionary Microbiology*, **2018**, 68, 21-27	2.2	4
351	Are commercial providers a viable option for clinical bacterial sequencing?. *Microbial Genomics*, **2018**, 4,	4.4	4
350	Naturally occurring polymorphisms in the virulence regulator Rsp modulate Staphylococcus aureus survival in blood and antibiotic susceptibility. *Microbiology (United Kingdom)*, **2018**, 164, 1189-1195	2.9	3

349	Changing the paradigm for hospital outbreak detection by leading with genomic surveillance of nosocomial pathogens. *Microbiology (United Kingdom)*, **2018**, 164, 1213-1219	2.9	38
348	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. *Antimicrobial Agents and Chemotherapy*, **2018**, 62,	5.9	58
347	Genomic Surveillance of Enterococcus faecium Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. *MBio*, **2018**, 9,	7.8	37
346	Detecting eukaryotic microbiota with single-cell sensitivity in human tissue. *Microbiome*, **2018**, 6, 151	16.6	13
345	Global and regional dissemination and evolution of Burkholderia pseudomallei. *Nature Microbiology* , **2017**, 2, 16263	26.6	87
344	Some Synonymous and Nonsynonymous Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. *Antimicrobial Agents and Chemotherapy*, **2017**, 61,	5.9	18
343	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental Klebsiella pneumoniae. *Genome Medicine*, **2017**, 9, 6	14.4	35
342	Evolution and Epidemiology of Multidrug-Resistant in the United Kingdom and Ireland. *MBio*, **2017**, 8,	7.8	59
341	Patient Characteristics, Management, and Predictors of Outcome from Severe Community-Onset Staphylococcal Sepsis in Northeast Thailand: A Prospective Multicenter Study. *American Journal of Tropical Medicine and Hygiene*, **2017**, 96, 1042-1049	3.2	7
340	Multitarget Quantitative PCR Improves Detection and Predicts Cultivability of the Pathogen Burkholderia pseudomallei. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	11
339	Complex Routes of Nosocomial Vancomycin-Resistant Enterococcus faecium Transmission Revealed by Genome Sequencing. *Clinical Infectious Diseases*, **2017**, 64, 886-893	11.6	59
338	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. *Science Translational Medicine*, **2017**, 9,	17.5	70
337	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant Staphylococcus aureus Transmission in a Community Setting. *Clinical Infectious Diseases*, **2017**, 65, 2069-2077	11.6	8
336	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis d-Cycloserine Resistance. *Antimicrobial Agents and Chemotherapy*, **2017**, 61,	5.9	16
335	AMR Surveillance in low and middle-income settings - A roadmap for participation in the Global Antimicrobial Surveillance System (GLASS). *Wellcome Open Research*, **2017**, 2, 92	4.8	72
334	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the identification of Burkholderia pseudomallei from Asia and Australia and differentiation between Burkholderia species. *PLoS ONE*, **2017**, 12, e0175294	3.7	25
333	Longitudinal genomic surveillance of multidrug-resistant Escherichia coli carriage in a long-term care facility in the United Kingdom. *Genome Medicine*, **2017**, 9, 70	14.4	27
332	Within-host evolution of Enterococcus faecium during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. *Genome Medicine*, **2017**, 9, 119	14.4	18

331	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing Klebsiella pneumoniae in a UK Teaching Hospital. *Open Forum Infectious Diseases*, **2017**, 4, S43-S44	1	78
330	Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. *Microbial Genomics*, **2017**, 3, e000114	4.4	19
329	Community outbreaks of group A Streptococcus revealed by genome sequencing. *Scientific Reports*, **2017**, 7, 8554	4.9	17
328	Systematic longitudinal survey of invasive in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. *Genome Research*, **2017**,	9.7	122
327	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in the East of England. *Scientific Reports*, **2017**, 7, 7406	4.9	15
326	Whole genome sequencing of ESBL-producing Escherichia coli isolated from patients, farm waste and canals in Thailand. *Genome Medicine*, **2017**, 9, 81	14.4	48
325	Clonal differences in Staphylococcus aureus bacteraemia-associated mortality. *Nature Microbiology*, **2017**, 2, 1381-1388	26.6	64
324	Evolution of the ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. *MBio*, **2017**, 8,	7.8	32
323	Melioidosis **2017**, 1073-1077.e1		2
322	Population structure of multidrug resistant Klebsiella oxytoca within hospitals across the UK and Ireland identifies sharing of virulence and resistance genes with K. pneumoniae. *Genome Biology and Evolution*, **2017**, 9, 574-587	3.9	24
321	Gastrointestinal tract involvement in melioidosis. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, **2017**, 111, 185-187	2	4
320	Evolution of mobile genetic element composition in an epidemic methicillin-resistant Staphylococcus aureus: temporal changes correlated with frequent loss and gain events. *BMC Genomics*, **2017**, 18, 684	4.5	23
319	Increased Von Willebrand factor, decreased ADAMTS13 and thrombocytopenia in melioidosis. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005468	4.8	5
318	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. *PLoS ONE*, **2017**, 12, e0189838	3.7	14
317	Presence of in Soil and Paddy Rice Water in a Rice Field in Northeast Thailand, but Not in Air and Rainwater. *American Journal of Tropical Medicine and Hygiene*, **2017**, 97, 1702-1705	3.2	11
316	Population genetic structuring of methicillin-resistant clone EMRSA-15 within UK reflects patient referral patterns. *Microbial Genomics*, **2017**, 3, e000113	4.4	12
315	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. *Microbial Genomics*, **2017**, 3, e000117	4.4	8
314	Whole-genome sequencing of multidrug-resistant Mycobacterium tuberculosis isolates from Myanmar. *Journal of Global Antimicrobial Resistance*, **2016**, 6, 113-117	3.4	21

313	The dissemination of multidrug-resistant Enterobacter cloacae throughout the UK and Ireland. *Nature Microbiology*, **2016**, 1, 16173	26.6	16
312	Genome-based characterization of hospital-adapted lineages. *Nature Microbiology*, **2016**, 1,	26.6	49
311	A decade of genomic history for healthcare-associated Enterococcus faecium in the United Kingdom and Ireland. *Genome Research*, **2016**, 26, 1388-1396	9.7	62
310	Predicted global distribution of and burden of melioidosis. *Nature Microbiology*, **2016**, 1,	26.6	463
309	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant Staphylococcus aureus USA300 in the East of England. *Journal of Infectious Diseases*, **2016**, 214, 447-53	7	25
308	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, 5232-7	5.9	11
307	Comparison of two chromogenic media for the detection of vancomycin-resistant enterococcal carriage by nursing home residents. *Diagnostic Microbiology and Infectious Disease*, **2016**, 85, 409-12	2.9	5
306	PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK. *Journal of Antimicrobial Chemotherapy*, **2016**, 71, 268-9	5.1	16
305	Comparison of 2 chromogenic media for the detection of extended-spectrum β-lactamase producing Enterobacteriaceae stool carriage in nursing home residents. *Diagnostic Microbiology and Infectious Disease*, **2016**, 84, 181-3	2.9	7
304	Whole-genome sequencing reveals transmission of vancomycin-resistant Enterococcus faecium in a healthcare network. *Genome Medicine*, **2016**, 8, 4	14.4	46
303	Validation of self-administered nasal swabs and postage for the isolation of Staphylococcus aureus. *Journal of Medical Microbiology*, **2016**, 65, 1434-1437	3.2	2
302	Pan-genomic perspective on the evolution of the USA300 epidemic. *Microbial Genomics*, **2016**, 2, e000058	4.4	21
301	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. *Microbial Genomics*, **2016**, 2, e000067	4.4	20
300	Comparison of bacterial genome assembly software for MinION data and their applicability to medical microbiology. *Microbial Genomics*, **2016**, 2, e000085	4.4	29
299	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011-2013. *Emerging Infectious Diseases*, **2016**, 22, 1658-9	10.2	4
298	Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. *ELife*, **2016**, 5,	8.9	138
297	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004403	4.8	170
296	Barriers and Recommended Interventions to Prevent Melioidosis in Northeast Thailand: A Focus Group Study Using the Behaviour Change Wheel. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004823	4.8	22

295	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. *Annals of Applied Statistics*, **2016**, 10, 395-417	2.1	39
294	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. *Genome Research*, **2016**, 26, 263-70	9.7	41
293	dfrA thyA Double Deletion in para-Aminosalicylic Acid-Resistant Mycobacterium tuberculosis Beijing Strains. *Antimicrobial Agents and Chemotherapy*, **2016**, 60, 3864-7	5.9	13
292	Recent independent emergence of multiple multidrug-resistant Serratia marcescens clones within the United Kingdom and Ireland. *Genome Research*, **2016**, 26, 1101-9	9.7	47
291	Transmission of methicillin-resistant Staphylococcus aureus in long-term care facilities and their related healthcare networks. *Genome Medicine*, **2016**, 8, 102	14.4	28
290	Soil Nutrient Depletion Is Associated with the Presence of Burkholderia pseudomallei. *Applied and Environmental Microbiology*, **2016**, 82, 7086-7092	4.8	30
289	Trimethoprim/sulfamethoxazole resistance in clinical isolates of Burkholderia pseudomallei from Thailand. *International Journal of Antimicrobial Agents*, **2015**, 45, 557-9	14.3	19
288	Colony morphology variation of Burkholderia pseudomallei is associated with antigenic variation and O-polysaccharide modification. *Infection and Immunity*, **2015**, 83, 2127-38	3.7	21
287	Competition between Burkholderia pseudomallei and B. thailandensis. *BMC Microbiology*, **2015**, 15, 56	4.5	22
286	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant Staphylococcus aureus Isolates with mecC Are Susceptible to a Combination of Penicillin and Clavulanic Acid. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 7396-404	5.9	26
285	Clinical, environmental, and serologic surveillance studies of melioidosis in Gabon, 2012-2013. *Emerging Infectious Diseases*, **2015**, 21, 40-7	10.2	29
284	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. *Nature Communications*, **2015**, 6, 6560	17.4	83
283	Early insights into the potential of the Oxford Nanopore MinION for the detection of antimicrobial resistance genes. *Journal of Antimicrobial Chemotherapy*, **2015**, 70, 2775-8	5.1	75
282	Antimicrobial Disk Susceptibility Testing of Leptospira spp. Using Leptospira Vanaporn Wuthiekanun (LVW) Agar. *American Journal of Tropical Medicine and Hygiene*, **2015**, 93, 241-243	3.2	11
281	Characterization of plasmids in extensively drug-resistant acinetobacter strains isolated in India and Pakistan. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 923-9	5.9	31
280	Moving pathogen genomics out of the lab and into the clinic: what will it take?. *Genome Medicine*, **2015**, 7, 132	14.4	4
279	Consensus on the development of vaccines against naturally acquired melioidosis. *Emerging Infectious Diseases*, **2015**, 21,	10.2	39
278	Public awareness of melioidosis in Thailand and potential use of video clips as educational tools. *PLoS ONE*, **2015**, 10, e0121311	3.7	15

277	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. *PLoS Biology*, **2015**, 13, e1002229	9.7	76
276	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and meticillin-resistant Staphylococcus aureus. *International Journal of Antimicrobial Agents*, **2015**, 45, 477-84	14.3	34
275	Evolutionary dynamics of methicillin-resistant Staphylococcus aureus within a healthcare system. *Genome Biology*, **2015**, 16, 81	18.3	76
274	Mechanisms of Methicillin Resistance in Staphylococcus aureus. *Annual Review of Biochemistry*, **2015**, 84, 577-601	29.1	268
273	Cost-effectiveness analysis of parenteral antimicrobials for acute melioidosis in Thailand. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, **2015**, 109, 416-8	2	4
272	Whole-genome sequencing confirms that Burkholderia pseudomallei multilocus sequence types common to both Cambodia and Australia are due to homoplasy. *Journal of Clinical Microbiology*, **2015**, 53, 323-6	9.7	37
271	Drug-resistance mechanisms and tuberculosis drugs. *Lancet, The*, **2015**, 385, 305-7	40	19
270	Public perceptions of bacterial whole-genome sequencing for tuberculosis. *Trends in Genetics*, **2015**, 31, 58-60	8.5	3
269	Clinical and molecular epidemiology of Staphylococcus argenteus infections in Thailand. *Journal of Clinical Microbiology*, **2015**, 53, 1005-8	9.7	53
268	Genome sequencing defines phylogeny and spread of methicillin-resistant Staphylococcus aureus in a high transmission setting. *Genome Research*, **2015**, 25, 111-8	9.7	75
267	Rapid single-colony whole-genome sequencing of bacterial pathogens. *Journal of Antimicrobial Chemotherapy*, **2014**, 69, 1275-81	5.1	42
266	Innate immunity. A Spaetzle-like role for nerve growth factor β in vertebrate immunity to Staphylococcus aureus. *Science*, **2014**, 346, 641-646	33.3	55
265	Fatal melioidosis in goats in Bangkok, Thailand. *American Journal of Tropical Medicine and Hygiene*, **2014**, 91, 287-290	3.2	5
264	Microevolution of Burkholderia pseudomallei during an acute infection. *Journal of Clinical Microbiology*, **2014**, 52, 3418-21	9.7	19
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3	Comparison of bacterial genome assembly software for MinION data	1
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