

Julian Parkhill

List of Publications by Year in descending order

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Version: 2024-02-01

678
papers

122,834
citations

186

151
h-index

162

323
g-index

754
all docs

754
docs citations

754
times ranked

84308
citing authors

#	ARTICLE	IF	CITATIONS
1	Conservation of vaccine antigen sequences encoded by sequenced strains of <i>Streptococcus equi</i> subsp. <i>equi</i> . <i>Equine Veterinary Journal</i> , 2023, 55, 92-101.	1.7	3
2	Genomic Insights Into the Mechanism of Carbapenem Resistance Dissemination in Enterobacterales From a Tertiary Public Health Setting in South Asia. <i>Clinical Infectious Diseases</i> , 2023, 76, 119-133.	5.8	6
3	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
4	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	27.8	138
5	Screening for Highly Transduced Genes in <i>Staphylococcus aureus</i> Revealed Both Lateral and Specialized Transduction. <i>Microbiology Spectrum</i> , 2022, 10, e0242321.	3.0	6
6	Bacterial genotypic and patient risk factors for adverse outcomes in <i>Escherichia coli</i> bloodstream infections: a prospective molecular epidemiological study. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1753-1761.	3.0	5
7	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	4.4	4
8	Gut microbiomes from Gambian infants reveal the development of a non-industrialized <i>Prevotella</i> -based trophic network. <i>Nature Microbiology</i> , 2022, 7, 132-144.	13.3	30
9	<i>Mycobacterium tuberculosis</i> Lineages Associated with Mutations and Drug Resistance in Isolates from India. <i>Microbiology Spectrum</i> , 2022, 10, e0159421.	3.0	10
10	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	12.4	22
11	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal <i>Salmonella</i> from animals and humans in Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
12	Antimicrobial Resistance Exchange Between Humans and Animals: Why We Need to Know More. <i>Engineering</i> , 2022, 15, 11-12.	6.7	7
13	Profiling gut microbiota and bile acid metabolism in critically ill children. <i>Scientific Reports</i> , 2022, 12, .	3.3	5
14	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	13.3	53
15	Identifying virulence determinants of multidrug-resistant <i>Klebsiella pneumoniae</i> in <i>Galleria mellonella</i> . <i>Pathogens and Disease</i> , 2021, 79, .	2.0	27
16	Kill and cure: genomic phylogeny and bioactivity of <i>Burkholderia gladioli</i> bacteria capable of pathogenic and beneficial lifestyles. <i>Microbial Genomics</i> , 2021, 7, .	2.0	24
17	Batch effects account for the main findings of an in utero human intestinal bacterial colonization study. <i>Microbiome</i> , 2021, 9, 6.	11.1	34
18	Pathogenomic analyses of <i>Mycobacterium microti</i> , an ESX-1-deleted member of the <i>Mycobacterium tuberculosis</i> complex causing disease in various hosts. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11

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19	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021, 7, .	2.0	71
20	Globetrotting strangles: the unbridled national and international transmission of <i>Streptococcus equi</i> between horses. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
21	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
22	Genome Sequencing of a Historic <i>Staphylococcus aureus</i> Collection Reveals New Enterotoxin Genes and Sheds Light on the Evolution and Genomic Organization of This Key Virulence Gene Family. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	8
23	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .	12.6	91
24	Population structure and transmission of <i>Mycobacterium bovis</i> in Ethiopia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
25	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. <i>Scientific Reports</i> , 2021, 11, 10590.	3.3	17
26	Genomic and temporal analyses of <i>Mycobacterium bovis</i> in southern Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
27	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002–17: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
28	Increased Virulence of Outer Membrane Porin Mutants of <i>Mycobacterium abscessus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 706207.	3.5	3
29	<i>Mycobacterium tuberculosis</i> complex lineage 5 exhibits high levels of within-lineage genomic diversity and differing gene content compared to the type strain H37Rv. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
30	Identification of Tse8 as a Type VI secretion system toxin from <i>Pseudomonas aeruginosa</i> that targets the bacterial transamidosome to inhibit protein synthesis in prey cells. <i>Nature Microbiology</i> , 2021, 6, 1199-1210.	13.3	30
31	A role for arthropods as vectors of multidrug-resistant Enterobacterales in surgical site infections from South Asia. <i>Nature Microbiology</i> , 2021, 6, 1259-1270.	13.3	16
32	Large-scale genomic analysis of antimicrobial resistance in the zoonotic pathogen <i>Streptococcus suis</i> . <i>BMC Biology</i> , 2021, 19, 191.	3.8	26
33	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.	7.3	39
34	Dissemination of <i>Mycobacterium abscessus</i> via global transmission networks. <i>Nature Microbiology</i> , 2021, 6, 1279-1288.	13.3	47
35	Inferring <i>Mycobacterium bovis</i> transmission between cattle and badgers using isolates from the Randomised Badger Culling Trial. <i>PLoS Pathogens</i> , 2021, 17, e1010075.	4.7	20
36	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.	5.8	46

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37	Engineering bacteriocin-mediated resistance against the plant pathogen <i>Pseudomonas syringae</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 1296-1306.	8.3	32
38	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 4918.	12.8	12
39	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
40	SpeS: A Novel Superantigen and Its Potential as a Vaccine Adjuvant against Strangles. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4467.	4.1	1
41	Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among <i>Klebsiella pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25043-25054.	7.1	97
42	Relative abundance of the <i>Prevotella</i> genus within the human gut microbiota of elderly volunteers determines the inter-individual responses to dietary supplementation with wheat bran arabinoxylan-oligosaccharides. <i>BMC Microbiology</i> , 2020, 20, 283.	3.3	41
43	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020, 5, .	3.8	67
44	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , 2020, 1, .	2.1	34
45	Genomic Assemblies of Members of <i>Burkholderia</i> and Related Genera as a Resource for Natural Product Discovery. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
46	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	7.1	50
47	Fetal inheritance of chromosomally integrated human herpesvirus 6 predisposes the mother to pre-eclampsia. <i>Nature Microbiology</i> , 2020, 5, 901-908.	13.3	29
48	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	16.3	228
49	A Novel Inducible Prophage from <i>Burkholderia vietnamiensis</i> G4 Is Widely Distributed across the Species and Has Lytic Activity against Pathogenic <i>Burkholderia</i> . <i>Viruses</i> , 2020, 12, 601.	3.3	8
50	A whole-genome screen identifies <i>Salmonella enterica</i> serovar Typhi genes involved in fluoroquinolone susceptibility. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2516-2525.	3.0	11
51	Association between bacterial homoplastic variants and radiological pathology in tuberculosis. <i>Thorax</i> , 2020, 75, 584-591.	5.6	8
52	Cell Surface Remodeling of <i>Mycobacterium abscessus</i> under Cystic Fibrosis Airway Growth Conditions. <i>ACS Infectious Diseases</i> , 2020, 6, 2143-2154.	3.8	11
53	Genomic Profiling Reveals Distinct Routes To Complement Resistance in <i>Klebsiella pneumoniae</i> . <i>Infection and Immunity</i> , 2020, 88, .	2.2	44
54	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	8.2	58

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55	Lung function and microbiota diversity in cystic fibrosis. <i>Microbiome</i> , 2020, 8, 45.	11.1	138
56	Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. <i>MBio</i> , 2020, 11, .	4.1	66
57	Increasing incidence of group B streptococcus neonatal infections in the Netherlands is associated with clonal expansion of CC17 and CC23. <i>Scientific Reports</i> , 2020, 10, 9539.	3.3	25
58	Mechanisms of β -lactam resistance of <i>Streptococcus uberis</i> isolated from bovine mastitis cases. <i>Veterinary Microbiology</i> , 2020, 242, 108592.	1.9	18
59	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1117-1122.	3.0	10
60	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. <i>Wellcome Open Research</i> , 2020, 5, 223.	1.8	43
61	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant <i>Staphylococcus aureus</i> : a genomic epidemiology analysis. <i>Lancet Microbe</i> , The, 2020, 1, e328-e335.	7.3	75
62	Genomic surveillance of <i>Escherichia coli</i> ST131 identifies local expansion and serial replacement of subclones. <i>Microbial Genomics</i> , 2020, 6, .	2.0	33
63	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. <i>Microbial Genomics</i> , 2020, 6, .	2.0	4
64	Leapfrogging laboratories: the promise and pitfalls of high-tech solutions for antimicrobial resistance surveillance in low-income settings. <i>BMJ Global Health</i> , 2020, 5, e003622.	4.7	30
65	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14.	1.8	13
66	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. <i>Wellcome Open Research</i> , 2020, 5, 223.	1.8	38
67	Fundamental differences in physiology of <i>Bordetella pertussis</i> dependent on the two-component system Bvg revealed by gene essentiality studies. <i>Microbial Genomics</i> , 2020, 6, .	2.0	8
68	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	28
69	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019, 4, 1941-1950.	13.3	91
70	Draft genome sequence of a multidrug-resistant caprine isolate of <i>Staphylococcus cohnii</i> subsp. <i>urealyticus</i> from Tanzania encoding <i>ermB</i> , <i>tet(K)</i> , <i>dfrG</i> , <i>fusF</i> and <i>fosD</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 163-165.	2.2	4
71	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in <i>Mycobacterium tuberculosis</i> in Southern India. <i>Scientific Reports</i> , 2019, 9, 10283.	3.3	32
72	Complete Whole-Genome Sequence of <i>Haemophilus haemolyticus</i> NCTC 10839. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1

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73	Complete Whole-Genome Sequences of Two <i>Raoultella terrigena</i> Strains, NCTC 13097 and NCTC 13098, Isolated from Human Cases. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
74	Human placenta has no microbiome but can contain potential pathogens. <i>Nature</i> , 2019, 572, 329-334.	27.8	513
75	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
76	Genetic variation regulates the activation and specificity of Restriction-Modification systems in <i>Neisseria gonorrhoeae</i> . <i>Scientific Reports</i> , 2019, 9, 14685.	3.3	14
77	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. <i>Microbiome</i> , 2019, 7, 137.	11.1	22
78	Pilot Evaluation of a Fully Automated Bioinformatics System for Analysis of Methicillin-Resistant <i>Staphylococcus aureus</i> Genomes and Detection of Outbreaks. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	9
79	The Genome Sequences of Three <i>Paraburkholderia</i> sp. Strains Isolated from Wood-Decay Fungi Reveal Them as Novel Species with Antimicrobial Biosynthetic Potential. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
80	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.	8.8	22
81	Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994.	12.8	33
82	Emergence of dominant toxigenic MIT1 <i>Streptococcus pyogenes</i> clone during increased scarlet fever activity in England: a population-based molecular epidemiological study. <i>Lancet Infectious Diseases</i> , 2019, 19, 1209-1218.	9.1	106
83	A novel Ancestral Beijing sublineage of <i>Mycobacterium tuberculosis</i> suggests the transition site to Modern Beijing sublineages. <i>Scientific Reports</i> , 2019, 9, 13718.	3.3	35
84	Genomic characterization of novel <i>Neisseria</i> species. <i>Scientific Reports</i> , 2019, 9, 13742.	3.3	29
85	Separating Bacteria by Capsule Amount Using a Discontinuous Density Gradient. <i>Journal of Visualized Experiments</i> , 2019, . .	0.3	6
86	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, .	4.1	130
87	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
88	'Candidatus <i>Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	2.0	16
89	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.	13.3	47
90	Complete Assembly of <i>Escherichia coli</i> Sequence Type 131 Genomes Using Long Reads Demonstrates Antibiotic Resistance Gene Variation within Diverse Plasmid and Chromosomal Contexts. <i>MSphere</i> , 2019, 4, .	2.9	27

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91	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
92	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	4.1	106
93	Rapid sequencing of MRSA direct from clinical plates in a routine microbiology laboratory. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2153-2156.	3.0	8
94	An unusual <i>Burkholderia gladioli</i> double chain-initiating nonribosomal peptide synthetase assembles β -lactam antibiotics. <i>Chemical Science</i> , 2019, 10, 5489-5494.	7.4	34
95	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, .	3.9	22
96	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.	5.5	40
97	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium <i>Burkholderia ambifaria</i> . <i>Nature Microbiology</i> , 2019, 4, 996-1005.	13.3	106
98	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019, 14, e0209395.	2.5	20
99	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> Reference Strain PAK. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	26
100	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	4.4	19
101	A dual transacylation mechanism for polyketide synthase chain release in enacyloxin antibiotic biosynthesis. <i>Nature Chemistry</i> , 2019, 11, 906-912.	13.6	29
102	Multi-Compartment Profiling of Bacterial and Host Metabolites Identifies Intestinal Dysbiosis and Its Functional Consequences in the Critically Ill Child. <i>Critical Care Medicine</i> , 2019, 47, e727-e734.	0.9	19
103	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, .	4.1	50
104	Whole-Genome Sequences of Five Strains of <i>Kocuria rosea</i> , NCTC2676, NCTC7514, NCTC7512, NCTC7528, and NCTC7511. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
105	O-Antigen-Dependent Colicin Insensitivity of Uropathogenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	24
106	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019, 58, 548-550.	1.9	8
107	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.	2.5	33
108	A <i>mecC</i> allotype, <i>mecC3</i> , in the CoNS <i>Staphylococcus caeli</i> , encoded within a variant <i>SCCmecC</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 547-552.	3.0	7

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109	Limited contribution of non-intensive chicken farming to ESBL-producing <i>Escherichia coli</i> colonization in humans in Vietnam: an epidemiological and genomic analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 561-570.	3.0	35
110	Mutations in the MAB_2299c TetR Regulator Confer Cross-Resistance to Clofazimine and Bedaquiline in <i>Mycobacterium abscessus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	55
111	<i>Staphylococcus caeli</i> sp. nov., isolated from air sampling in an industrial rabbit holding. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 82-86.	1.7	12
112	<i>Staphylococcus pseudoxylosus</i> sp. nov., isolated from bovine mastitis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2208-2213.	1.7	18
113	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	30
114	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, .	2.0	29
115	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019, 5, .	2.0	26
116	The speciation and hybridization history of the genus <i>Salmonella</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	13
117	Transient Silencing of Antibiotic Resistance by Mutation Represents a Significant Potential Source of Unanticipated Therapeutic Failure. <i>MBio</i> , 2019, 10, .	4.1	39
118	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, .	7.0	19
119	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	6.0	39
120	The Impact of NOD2 Variants on Fecal Microbiota in Crohn's Disease and Controls Without Gastrointestinal Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 583-592.	1.9	40
121	Limited Impact of Adolescent Meningococcal ACWY Vaccination on <i>Neisseria meningitidis</i> Serogroup W Carriage in University Students. <i>Journal of Infectious Diseases</i> , 2018, 217, 608-616.	4.0	22
122	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
123	Genome-Based Analysis of <i>Enterococcus faecium</i> Bacteremia Associated with Recurrent and Mixed-Strain Infection. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	14
124	Gut microbiota trajectory in early life may predict development of celiac disease. <i>Microbiome</i> , 2018, 6, 36.	11.1	107
125	Low genomic diversity of <i>Legionella pneumophila</i> within clinical specimens. <i>Clinical Microbiology and Infection</i> , 2018, 24, 1020.e1-1020.e4.	6.0	5
126	The Microevolution and Epidemiology of <i>Staphylococcus aureus</i> Colonization during Atopic Eczema Disease Flare. <i>Journal of Investigative Dermatology</i> , 2018, 138, 336-343.	0.7	46

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127	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, .	3.2	83
128	706: LOSS OF FECAL MICROBIAL DENSITY AND INTESTINAL FERMENTATION EFFICIENCY IN CRITICALLY ILL CHILDREN. <i>Critical Care Medicine</i> , 2018, 46, 339-339.	0.9	0
129	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, .	4.1	63
130	The Capsule Regulatory Network of <i>Klebsiella pneumoniae</i> Defined by density-TraDISort. <i>MBio</i> , 2018, 9, .	4.1	78
131	Whole Genome Sequencing for Determining the Source of <i>Mycobacterium bovis</i> Infections in Livestock Herds and Wildlife in New Zealand. <i>Frontiers in Veterinary Science</i> , 2018, 5, 272.	2.2	44
132	A highly conserved <i>mecC</i> -encoding SCC type XI in a bovine isolate of methicillin-resistant <i>Staphylococcus xylosus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3516-3518.	3.0	13
133	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	1.8	42
134	<i>Streptococcus suis</i> contains multiple phase-variable methyltransferases that show a discrete lineage distribution. <i>Nucleic Acids Research</i> , 2018, 46, 11466-11476.	14.5	31
135	Comparative genomics of Czech vaccine strains of <i>Bordetella pertussis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	2.0	7
136	New Variant of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. <i>MBio</i> , 2018, 9, .	4.1	53
137	Detecting eukaryotic microbiota with single-cell sensitivity in human tissue. <i>Microbiome</i> , 2018, 6, 151.	11.1	21
138	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	3.3	20
139	Loss of Genomic Diversity in a <i>Neisseria meningitidis</i> Clone Through a Colonization Bottleneck. <i>Genome Biology and Evolution</i> , 2018, 10, 2102-2109.	2.5	2
140	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	7.8	156
141	Comparative genomics of <i>Mycobacterium africanum</i> Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018, 8, 11269.	3.3	34
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