

# Matthew T G Holden

## List of Publications by Year in descending order

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202  
papers

29,053  
citations

10650

74  
h-index

6686

161  
g-index

232  
all docs

232  
docs citations

232  
times ranked

28235  
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	13.7	138
2	Presence of <i>optrA</i> -mediated linezolid resistance in multiple lineages and plasmids of <i>Enterococcus faecalis</i> revealed by long read sequencing. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	9
3	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	5.9	352
4	Comparative epidemiology and factors associated with major healthcare-associated methicillin-resistant <i>Staphylococcus aureus</i> clones among interconnected acute-, intermediate- and long-term healthcare facilities in Singapore. <i>Clinical Microbiology and Infection</i> , 2021, 27, 785.e9-785.e16.	2.8	4
5	Clinical perspectives in integrating whole-genome sequencing into the investigation of healthcare and public health outbreaks – hype or help?. <i>Journal of Hospital Infection</i> , 2021, 109, 1-9.	1.4	32
6	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	5.9	88
7	Ecosystem engineers drive differing microbial community composition in intertidal estuarine sediments. <i>PLoS ONE</i> , 2021, 16, e0240952.	1.1	12
8	Globetrotting strangles: the unbridled national and international transmission of <i>Streptococcus equi</i> between horses. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
9	Genomic surveillance of <i>Neisseria gonorrhoeae</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 17-25.	0.3	3
10	Protocol for an interdisciplinary cross-sectional study investigating the social, biological and community-level drivers of antimicrobial resistance (AMR): Holistic Approach to Unravel Antibacterial Resistance in East Africa (HATUA). <i>BMJ Open</i> , 2021, 11, e041418.	0.8	24
11	Genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 6-16.	0.3	5
12	Genomic surveillance of <i>Pseudomonas aeruginosa</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 4-18.	0.3	3
13	Investigation of two cases of <i>Mycobacterium chelonae</i> infection in haemato-oncology patients using whole-genome sequencing and a potential link to the hospital water supply. <i>Journal of Hospital Infection</i> , 2021, 114, 111-116.	1.4	6
14	Dispensing Antibiotics without Prescription at Community Pharmacies and Accredited Drug Dispensing Outlets in Tanzania: A Cross-Sectional Study. <i>Antibiotics</i> , 2021, 10, 1025.	1.5	32
15	Complete genome for <i>Actinobacillus pleuropneumoniae</i> serovar 8 reference strain 405: comparative analysis with draft genomes for different laboratory stock cultures indicates little genetic variation. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
16	Rationally designed mariner vectors for functional genomic analysis of <i>Actinobacillus pleuropneumoniae</i> and other Pasteurellaceae species by transposon-directed insertion-site sequencing (TraDIS). <i>Animal Diseases</i> , 2021, 1, 29.	0.6	1
17	Genomic Analysis of Global <i>Staphylococcus argenteus</i> Strains Reveals Distinct Lineages With Differing Virulence and Antibiotic Resistance Gene Content. <i>Frontiers in Microbiology</i> , 2021, 12, 795173.	1.5	10
18	Genomic surveillance of <i>Acinetobacter baumannii</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 46-60.	0.3	1

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19	Pan-Resistome Characterization of Uropathogenic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Strains Circulating in Uganda and Kenya, Isolated from 2017–2018. <i>Antibiotics</i> , 2021, 10, 1547.	1.5	11
20	Gene accordions cause genotypic and phenotypic heterogeneity in clonal populations of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2020, 11, 3526.	5.8	19
21	SpeS: A Novel Superantigen and Its Potential as a Vaccine Adjuvant against Strangles. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4467.	1.8	1
22	The molecular basis of thioalcohol production in human body odour. <i>Scientific Reports</i> , 2020, 10, 12500.	1.6	16
23	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	5.8	62
24	A highly conserved complete accessory <i>Escherichia coli</i> type III secretion system 2 is widespread in bloodstream isolates of the ST69 lineage. <i>Scientific Reports</i> , 2020, 10, 4135.	1.6	12
25	Draft Genome Sequences of the Type Strains of <i>Actinobacillus indolicus</i> (46K2C) and <i>Actinobacillus porcicus</i> (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
26	Origin, maintenance and spread of antibiotic resistance genes within plasmids and chromosomes of bloodstream isolates of <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
27	Chlorhexidine and octenidine use, carriage of <i>qac</i> genes, and reduced antiseptic susceptibility in methicillin-resistant <i>Staphylococcus aureus</i> isolates from a healthcare network. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1154.e1-1154.e7.	2.8	37
28	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	9.4	120
29	Genomic identification of cryptic susceptibility to penicillins and $\beta$ -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	5.9	47
30	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
31	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
32	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
33	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
34	Antimicrobial resistance in atopic dermatitis. <i>Annals of Allergy, Asthma and Immunology</i> , 2019, 122, 236-240.	0.5	11
35	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	2.8	39
36	Proposal of serovars 17 and 18 of <i>Actinobacillus pleuropneumoniae</i> based on serological and genotypic analysis. <i>Veterinary Microbiology</i> , 2018, 217, 1-6.	0.8	64

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37	<i>Pseudomonas aeruginosa</i> intensive care unit outbreak: winnowing of transmissions with molecular and genomic typing. <i>Journal of Hospital Infection</i> , 2018, 98, 282-288.	1.4	41
38	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.	0.3	46
39	Genetic analysis of invasive <i>Escherichia coli</i> in Scotland reveals determinants of healthcare-associated versus community-acquired infections. <i>Microbial Genomics</i> , 2018, 4, .	1.0	33
40	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects <i>Staphylococcus aureus</i> from Killing by Host Phagocytes. <i>MBio</i> , 2018, 9, .	1.8	33
41	Distinct evolutionary patterns of <i>Neisseria meningitidis</i> serogroup B disease outbreaks at two universities in the USA. <i>Microbial Genomics</i> , 2018, 4, .	1.0	4
42	An Outbreak of <i>Streptococcus pyogenes</i> in a Mental Health Facility: Advantage of Well-Timed Whole-Genome Sequencing Over emm Typing. <i>Infection Control and Hospital Epidemiology</i> , 2018, 39, 852-860.	1.0	13
43	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
44	Global Scale Dissemination of ST93: A Divergent <i>Staphylococcus aureus</i> Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1453.	1.5	29
45	The widespread use of topical antimicrobials enriches for resistance in <i>Staphylococcus aureus</i> isolated from patients with atopic dermatitis. <i>British Journal of Dermatology</i> , 2018, 179, 951-958.	1.4	33
46	Comparative sequence analysis of the capsular polysaccharide loci of <i>Actinobacillus pleuropneumoniae</i> serovars 18, and development of two multiplex PCRs for comprehensive capsule typing. <i>Veterinary Microbiology</i> , 2018, 220, 83-89.	0.8	49
47	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
48	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
49	2015 Epidemic of Severe <i>Streptococcus agalactiae</i> Sequence Type 283 Infections in Singapore Associated With the Consumption of Raw Freshwater Fish: A Detailed Analysis of Clinical, Epidemiological, and Bacterial Sequencing Data. <i>Clinical Infectious Diseases</i> , 2017, 64, S145-S152.	2.9	80
50	ST3268: a geographically widespread primate MRSA clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2401-2403.	1.3	12
51	Enhanced nasopharyngeal infection and shedding associated with an epidemic lineage of emm3 group A <i>Streptococcus</i> . <i>Virulence</i> , 2017, 8, 1390-1400.	1.8	17
52	Diversity of <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> strains isolated from the Spanish sheep and goat population and the identification, function and prevalence of a novel arbutin utilisation system. <i>Veterinary Microbiology</i> , 2017, 207, 231-238.	0.8	7
53	Genomic Dissection of an Icelandic Epidemic of Respiratory Disease in Horses and Associated Zoonotic Cases. <i>MBio</i> , 2017, 8, .	1.8	20
54	MRSA Transmission Dynamics Among Interconnected Acute, Intermediate-Term, and Long-Term Healthcare Facilities in Singapore. <i>Clinical Infectious Diseases</i> , 2017, 64, S76-S81.	2.9	33

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55	The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee. <i>Clinical Microbiology and Infection</i> , 2017, 23, 2-22.	2.8	428
56	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 311.	1.5	42
57	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017, 18, 130.	3.8	193
58	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
59	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
60	Haem-iron plays a key role in the regulation of the Ess/type VII secretion system of <i>Staphylococcus aureus</i> RN6390. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1839-1850.	0.7	25
61	Functional analysis of the EsaB component of the <i>Staphylococcus aureus</i> Type VII secretion system. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1851-1863.	0.7	19
62	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	1.0	470
63	ICEAp1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 810.	1.5	20
64	The Ess/Type VII secretion system of <i>Staphylococcus aureus</i> shows unexpected genetic diversity. <i>BMC Genomics</i> , 2016, 17, 222.	1.2	95
65	Genomic insights into the emergence and spread of international clones of healthcare-, community- and livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> : Blurring of the traditional definitions. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 95-101.	0.9	119
66	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
67	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	1.8	192
68	Genomics of Natural Populations of <i>Staphylococcus aureus</i> . <i>Annual Review of Microbiology</i> , 2016, 70, 459-478.	2.9	38
69	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	26
70	Pan-genomic perspective on the evolution of the <i>Staphylococcus aureus</i> USA300 epidemic. <i>Microbial Genomics</i> , 2016, 2, e000058.	1.0	34
71	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. <i>Microbial Genomics</i> , 2016, 2, e000067.	1.0	23
72	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1191.	1.5	27

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73	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	2.6	120
74	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and methicillin-resistant <i>Staphylococcus aureus</i> . <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 477-484.	1.1	39
75	Evolutionary dynamics of methicillin-resistant <i>Staphylococcus aureus</i> within a healthcare system. <i>Genome Biology</i> , 2015, 16, 81.	3.8	129
76	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015, 31, 3691-3693.	1.8	4,099
77	Whole-Genome Sequencing Confirms that <i>Burkholderia pseudomallei</i> Multilocus Sequence Types Common to Both Cambodia and Australia Are Due to Homoplasy. <i>Journal of Clinical Microbiology</i> , 2015, 53, 323-326.	1.8	44
78	Turner et al. Reply to "Emergence of the Same Successful Clade among Distinct Populations of emm 89 <i>Streptococcus pyogenes</i> in Multiple Geographic Regions". <i>MBio</i> , 2015, 6, e01883-15.	1.8	3
79	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015, 25, 111-118.	2.4	111
80	Development of a Multilocus Sequence Typing Scheme for Molecular Typing of <i>Mycoplasma pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3195-3203.	1.8	41
81	Emergence of a New Highly Successful Acapsular Group A <i>Streptococcus</i> Clade of Genotype emm 89 in the United Kingdom. <i>MBio</i> , 2015, 6, e00622.	1.8	126
82	Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant <i>Staphylococcus aureus</i> . <i>BMC Genomics</i> , 2015, 16, 388.	1.2	24
83	Colony Morphology Variation of <i>Burkholderia pseudomallei</i> Is Associated with Antigenic Variation and O-Polysaccharide Modification. <i>Infection and Immunity</i> , 2015, 83, 2127-2138.	1.0	28
84	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates with <i>mecC</i> Are Susceptible to a Combination of Penicillin and Clavulanic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7396-7404.	1.4	32
85	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015, 178, 279-282.	0.8	34
86	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	5.8	124
87	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015, 6, 6560.	5.8	105
88	Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2217-2222.	1.3	30
89	Genome specialization and decay of the stranglers pathogen, <i>Streptococcus equi</i> , is driven by persistent infection. <i>Genome Research</i> , 2015, 25, 1360-1371.	2.4	60
90	T Cell Immunity to the Alkyl Hydroperoxide Reductase of <i>Burkholderia pseudomallei</i> : A Correlate of Disease Outcome in Acute Melioidosis. <i>Journal of Immunology</i> , 2015, 194, 4814-4824.	0.4	44

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91	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015, 25, 129-141.	2.4	61
92	Emergence of scarlet fever <i>Streptococcus pyogenes</i> emm12 clones in Hong Kong is associated with toxin acquisition and multidrug resistance. <i>Nature Genetics</i> , 2015, 47, 84-87.	9.4	135
93	PinR mediates the generation of reversible population diversity in <i>Streptococcus zooepidemicus</i> . <i>Microbiology (United Kingdom)</i> , 2015, 161, 1105-1112.	0.7	2
94	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6738-6743.	3.3	176
95	Novel Determinants of Antibiotic Resistance: Identification of Mutated Loci in Highly Methicillin-Resistant Subpopulations of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01000.	1.8	70
96	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	1.8	95
97	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , 2014, 15, 1179.	1.2	34
98	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2238-2245.	1.3	27
99	Rapid single-colony whole-genome sequencing of bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1275-1281.	1.3	49
100	In vivo evolution of antimicrobial resistance in a series of <i>Staphylococcus aureus</i> patient isolates: the entire picture or a cautionary tale?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 363-367.	1.3	17
101	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	5.8	208
102	A Spaetzle-like role for nerve growth factor $\hat{I}^2$ in vertebrate immunity to <i>Staphylococcus aureus</i> . <i>Science</i> , 2014, 346, 641-646.	6.0	68
103	Multiplex PCR Assay for Unequivocal Differentiation of <i>Actinobacillus pleuropneumoniae</i> Serovars 1 to 3, 5 to 8, 10, and 12. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2380-2385.	1.8	36
104	Whole-genome sequencing reveals clonal expansion of multiresistant <i>Staphylococcus haemolyticus</i> in European hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2920-2927.	1.3	48
105	Microevolution of <i>Burkholderia pseudomallei</i> during an Acute Infection. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3418-3421.	1.8	30
106	Novel mutations in penicillin-binding protein genes in clinical <i>Staphylococcus aureus</i> isolates that are methicillin resistant on susceptibility testing, but lack the <i>mec</i> gene. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 594-597.	1.3	80
107	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 911-918.	1.3	73
108	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	2.4	210

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109	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	2.6	181
110	Whole-genome sequencing for analysis of an outbreak of methicillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 130-136.	4.6	531
111	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	2.4	412
112	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . <i>EMBO Molecular Medicine</i> , 2013, 5, 509-515.	3.3	192
113	Molecular Analysis of an Outbreak of Lethal Postpartum Sepsis Caused by <i>Streptococcus pyogenes</i> . <i>Journal of Clinical Microbiology</i> , 2013, 51, 2089-2095.	1.8	44
114	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e1954.	1.3	153
115	Arginine Catabolic Mobile Element in Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Clonal Group ST239-MRSA-III Isolates in Singapore: Implications for PCR-Based Screening Tests. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1563-1564.	1.4	13
116	A <i>Staphylococcus xylosum</i> Isolate with a New <i>mecC</i> Allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1524-1528.	1.4	67
117	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	2.1	450
118	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	6.5	217
119	Comparative Genomics of Vancomycin-Resistant <i>Staphylococcus aureus</i> Strains and Their Positions within the Clade Most Commonly Associated with Methicillin-Resistant <i>S. aureus</i> Hospital-Acquired Infection in the United States. <i>MBio</i> , 2012, 3, .	1.8	125
120	Properties of a Novel PBP2A Protein Homolog from <i>Staphylococcus aureus</i> Strain LGA251 and Its Contribution to the $\beta$ -Lactam-resistant Phenotype. <i>Journal of Biological Chemistry</i> , 2012, 287, 36854-36863.	1.6	110
121	Guidelines for Reporting Novel <i>mecA</i> Gene Homologues. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4997-4999.	1.4	144
122	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	3.3	174
123	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012, 13, R126.	13.9	118
124	Superantigenic Activity of emm3 <i>Streptococcus pyogenes</i> Is Abrogated by a Conserved, Naturally Occurring smeZ Mutation. <i>PLoS ONE</i> , 2012, 7, e46376.	1.1	11
125	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. <i>New England Journal of Medicine</i> , 2012, 366, 2267-2275.	13.9	609
126	Antimicrobial resistance to ceftazidime involving loss of penicillin-binding protein 3 in <i>Burkholderia pseudomallei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17165-17170.	3.3	98



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127	Meticillin-resistant <i>Staphylococcus aureus</i> with a novel <i>mecA</i> homologue in human and bovine populations in the UK and Denmark: a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 595-603.	4.6	751
128	A Very Early-Branching <i>Staphylococcus aureus</i> Lineage Lacking the Carotenoid Pigment Staphyloxanthin. <i>Genome Biology and Evolution</i> , 2011, 3, 881-895.	1.1	142
129	Comparative Whole Genome Sequence Analysis of the Carcinogenic Bacterial Model Pathogen <i>Helicobacter felis</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 302-308.	1.1	55
130	Genome sequence of <i>Staphylococcus lugdunensis</i> N920143 allows identification of putative colonization and virulence factors. <i>FEMS Microbiology Letters</i> , 2011, 322, 60-67.	0.7	90
131	The Impact of Recombination on dN/dS within Recently Emerged Bacterial Clones. <i>PLoS Pathogens</i> , 2011, 7, e1002129.	2.1	105
132	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. <i>Science</i> , 2010, 327, 469-474.	6.0	1,054
133	Cooking with GAS. <i>Nature Reviews Microbiology</i> , 2010, 8, 249-249.	13.6	0
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