

Matthew T G Holden

List of Publications by Year in descending order

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202
papers

29,053
citations

9264

74
h-index

5829

161
g-index

232
all docs

232
docs citations

232
times ranked

25908
citing authors

#	ARTICLE	IF	CITATIONS
1	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015, 31, 3691-3693.	4.1	4,099
2	Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18. <i>Nature</i> , 2001, 413, 848-852.	27.8	1,192
3	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague. <i>Nature</i> , 2001, 413, 523-527.	27.8	1,144
4	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. <i>Science</i> , 2010, 327, 469-474.	12.6	1,054
5	Comparative analysis of the genome sequences of <i>Bordetella pertussis</i> , <i>Bordetella parapertussis</i> and <i>Bordetella bronchiseptica</i> . <i>Nature Genetics</i> , 2003, 35, 32-40.	21.4	898
6	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	7.1	830
7	The multidrug-resistant human pathogen <i>Clostridium difficile</i> has a highly mobile, mosaic genome. <i>Nature Genetics</i> , 2006, 38, 779-786.	21.4	821
8	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.	9.1	751
9	Genomic plasticity of the causative agent of melioidosis, <i>Burkholderia pseudomallei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14240-14245.	7.1	675
10	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. <i>New England Journal of Medicine</i> , 2012, 366, 2267-2275.	27.0	609
11	Whole-genome sequencing for analysis of an outbreak of meticillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 130-136.	9.1	531
12	Quorum sensing cross talk: isolation and chemical characterization of cyclic dipeptides from <i>Pseudomonas aeruginosa</i> and other Gram-negative bacteria. <i>Molecular Microbiology</i> , 1999, 33, 1254-1266.	2.5	516
13	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	2.0	470
14	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	4.7	450
15	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.	6.0	428
16	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.	5.5	412
17	Comparisons of dN/dS are time dependent for closely related bacterial genomes. <i>Journal of Theoretical Biology</i> , 2006, 239, 226-235.	1.7	400
18	Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11105-11110.	7.1	366

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19	Staphylococcus aureus : superbug, super genome?. Trends in Microbiology, 2004, 12, 378-385.	7.7	353
20	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. Nature Microbiology, 2022, 7, 1161-1179.	13.3	352
21	The Global Posttranscriptional Regulator RsmA Modulates Production of Virulence Determinants and <i>N</i> -Acylhomoserine Lactones in <i>Pseudomonas aeruginosa</i> . Journal of Bacteriology, 2001, 183, 6676-6683.	2.2	344
22	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. Journal of Bacteriology, 2009, 191, 261-277.	2.2	329
23	LuxS: its role in central metabolism and the in vitro synthesis of 4-hydroxy-5-methyl-3(2H)-furanone. Microbiology (United Kingdom), 2002, 148, 909-922.	1.8	314
24	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. Nucleic Acids Research, 2003, 31, 6516-6523.	14.5	285
25	Extensive DNA Inversions in the <i>B. fragilis</i> Genome Control Variable Gene Expression. Science, 2005, 307, 1463-1465.	12.6	275
26	Complete Sequence and Organization of pBtoxis, the Toxin-Coding Plasmid of <i>Bacillus thuringiensis</i> subsp. israelensis. Applied and Environmental Microbiology, 2002, 68, 5082-5095.	3.1	270
27	Complete Genome Sequence and Lytic Phase Transcription Profile of a <i>Coccolithovirus</i> . Science, 2005, 309, 1090-1092.	12.6	270
28	Genome sequence of a proteolytic (Group I) <i>Clostridium botulinum</i> strain Hall A and comparative analysis of the clostridial genomes. Genome Research, 2007, 17, 1082-1092.	5.5	228
29	The Complete Genome Sequence and Comparative Genome Analysis of the High Pathogenicity <i>Yersinia enterocolitica</i> Strain 8081. PLoS Genetics, 2006, 2, e206.	3.5	227
30	GeneDB--an annotation database for pathogens. Nucleic Acids Research, 2012, 40, D98-D108.	14.5	217
31	Rapid Evolution of Virulence and Drug Resistance in the Emerging Zoonotic Pathogen <i>Streptococcus suis</i> . PLoS ONE, 2009, 4, e6072.	2.5	214
32	Genome Sequence of a Recently Emerged, Highly Transmissible, Multi-Antibiotic- and Antiseptic-Resistant Variant of Methicillin-Resistant <i>Staphylococcus aureus</i> , Sequence Type 239 (TW). Journal of Bacteriology, 2010, 192, 888-892.	2.2	211
33	Predicting the virulence of MRSA from its genome sequence. Genome Research, 2014, 24, 839-849.	5.5	210
34	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. Nature Communications, 2014, 5, 4544.	12.8	208
35	<i>Chlamydia trachomatis</i> : Genome sequence analysis of lymphogranuloma venereum isolates. Genome Research, 2008, 18, 161-171.	5.5	207
36	Genomic Evidence for the Evolution of <i>Streptococcus equi</i> : Host Restriction, Increased Virulence, and Genetic Exchange with Human Pathogens. PLoS Pathogens, 2009, 5, e1000346.	4.7	197

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37	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017, 18, 130.	8.8	193
38	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.	6.9	192
39	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, .	4.1	192
40	Structure, activity and evolution of the group I thiolactone peptide quorum-sensing system of <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2001, 41, 503-512.	2.5	189
41	Re-annotation and re-analysis of the <i>Campylobacter jejuni</i> NCTC11168 genome sequence. <i>BMC Genomics</i> , 2007, 8, 162.	2.8	189
42	Understanding the rise of the superbug: investigation of the evolution and genomic variation of <i>Staphylococcus aureus</i> . <i>Functional and Integrative Genomics</i> , 2006, 6, 186-201.	3.5	181
43	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	5.1	181
44	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.	7.1	176
45	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.	7.1	174
46	The <i>Chlamydomonas reinhardtii</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005, 15, 629-640.	5.5	158
47	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
48	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e1954.	3.0	153
49	Guidelines for Reporting Novel <i>mecA</i> Gene Homologues. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4997-4999.	3.2	144
50	A Very Early-Branching <i>Staphylococcus aureus</i> Lineage Lacking the Carotenoid Pigment Staphyloxanthin. <i>Genome Biology and Evolution</i> , 2011, 3, 881-895.	2.5	142
51	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	27.8	138
52	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.	21.4	135
53	Evolutionary dynamics of methicillin-resistant <i>Staphylococcus aureus</i> within a healthcare system. <i>Genome Biology</i> , 2015, 16, 81.	8.8	129
54	Emergence of a New Highly Successful Acapsular Group A <i>Streptococcus</i> Clade of Genotype <i>emm</i> 89 in the United Kingdom. <i>MBio</i> , 2015, 6, e00622.	4.1	126

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55	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, .	4.1	125
56	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
57	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	13.3	124
58	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	5.6	120
59	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
60	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.	2.2	119
61	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012, 13, R126.	9.6	118
62	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.	5.5	111
63	Properties of a Novel PBP2A Protein Homolog from <i>Staphylococcus aureus</i> Strain LGA251 and Its Contribution to the β -Lactam-resistant Phenotype. <i>Journal of Biological Chemistry</i> , 2012, 287, 36854-36863.	3.4	110
64	Functional Analysis of <i>luxS</i> in <i>Staphylococcus aureus</i> Reveals a Role in Metabolism but Not Quorum Sensing. <i>Journal of Bacteriology</i> , 2006, 188, 2885-2897.	2.2	105
65	The Impact of Recombination on dN/dS within Recently Emerged Bacterial Clones. <i>PLoS Pathogens</i> , 2011, 7, e1002129.	4.7	105
66	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015, 6, 6560.	12.8	105
67	Evidence for niche adaptation in the genome of the bovine pathogen <i>Streptococcus uberis</i> . <i>BMC Genomics</i> , 2009, 10, 54.	2.8	101
68	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.	7.1	98
69	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.	4.1	95
70	The <i>Ess</i> /Type VII secretion system of <i>Staphylococcus aureus</i> shows unexpected genetic diversity. <i>BMC Genomics</i> , 2016, 17, 222.	2.8	95
71	The genome sequence of the fish pathogen <i>Aliivibrio salmonicida</i> strain LFI1238 shows extensive evidence of gene decay. <i>BMC Genomics</i> , 2008, 9, 616.	2.8	90
72	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.	1.8	90

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73	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
74	Gene expression changes linked to antimicrobial resistance, oxidative stress, iron depletion and retained motility are observed when <i>Burkholderia cenocepacia</i> grows in cystic fibrosis sputum. <i>BMC Infectious Diseases</i> , 2008, 8, 121.	2.9	85
75	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.	3.0	80
76	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.	5.8	80
77	The G5 domain: a potential N-acetylglucosamine recognition domain involved in biofilm formation. <i>Bioinformatics</i> , 2005, 21, 1301-1303.	4.1	78
78	Design, Validation, and Application of a Seven-Strain <i>Staphylococcus aureus</i> PCR Product Microarray for Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7504-7514.	3.1	77
79	Nonrandom Distribution of <i>Burkholderia pseudomallei</i> Clones in Relation to Geographical Location and Virulence. <i>Journal of Clinical Microbiology</i> , 2006, 44, 2553-2557.	3.9	73
80	Complete Genome of Acute Rheumatic Fever-Associated Serotype M5 <i>Streptococcus pyogenes</i> Strain Manfredo. <i>Journal of Bacteriology</i> , 2007, 189, 1473-1477.	2.2	73
81	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 911-918.	3.0	73
82	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.	4.1	70
83	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.	12.6	68
84	A <i>Staphylococcus xylosus</i> Isolate with a New <i>mecC</i> Allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1524-1528.	3.2	67
85	<i>Burkholderia pseudomallei</i> genome plasticity associated with genomic island variation. <i>BMC Genomics</i> , 2008, 9, 190.	2.8	66
86	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.	1.9	64
87	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.	5.5	63
88	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	12.8	62
89	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015, 25, 129-141.	5.5	61
90	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.	5.5	60

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91	Evolutionary History of the Coccolithoviridae. <i>Molecular Biology and Evolution</i> , 2006, 23, 86-92.	8.9	57
92	Identification of Three Novel Superantigen-Encoding Genes in <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> , <i>szef</i> , <i>szen</i> , and <i>szep</i> . <i>Infection and Immunity</i> , 2010, 78, 4817-4827.	2.2	56
93	A novel streptococcal integrative conjugative element involved in iron acquisition. <i>Molecular Microbiology</i> , 2008, 70, 1274-1292.	2.5	55
94	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.	2.5	55
95	High Rates of Homologous Recombination in the Mite Endosymbiont and Opportunistic Human Pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e752.	3.0	50
96	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
97	Rapid single-colony whole-genome sequencing of bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1275-1281.	3.0	49
98	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.	1.9	49
99	New signal molecules on the quorum-sensing block. <i>Trends in Microbiology</i> , 2000, 8, 101-103.	7.7	48
100	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.	3.0	48
101	Cryptic carbapenem antibiotic production genes are widespread in <i>Erwinia carotovora</i> : facile trans activation by the <i>carR</i> transcriptional regulator. <i>Microbiology (United Kingdom)</i> , 1998, 144, 1495-1508.	1.8	47
102	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
103	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
104	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.	3.9	44
105	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.	3.9	44
106	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.	0.8	44
107	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 311.	3.5	42
108	<i>Burkholderia</i> Hep_Hag autotransporter (BuHA) proteins elicit a strong antibody response during experimental glanders but not human melioidosis. <i>BMC Microbiology</i> , 2007, 7, 19.	3.3	41

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109	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.	3.9	41
110	<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.	2.9	41
111	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.	2.5	39
112	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	6.0	39
113	Genomics of Natural Populations of <i>Staphylococcus aureus</i> . <i>Annual Review of Microbiology</i> , 2016, 70, 459-478.	7.3	38
114	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.	6.0	37
115	Characterization of Pneumonia Due to <i>Streptococcus equi</i> subsp. <i>zooeconomicus</i> in Dogs. <i>Vaccine Journal</i> , 2010, 17, 1790-1796.	3.1	36
116	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.	3.9	36
117	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.	2.8	34
118	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015, 178, 279-282.	1.9	34
119	Pan-genomic perspective on the evolution of the <i>Staphylococcus aureus</i> USA300 epidemic. <i>Microbial Genomics</i> , 2016, 2, e000058.	2.0	34
120	MRSA Transmission Dynamics Among Interconnected Acute, Intermediate-Term, and Long-Term Healthcare Facilities in Singapore. <i>Clinical Infectious Diseases</i> , 2017, 64, S76-S81.	5.8	33
121	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, .	2.0	33
122	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects <i>Staphylococcus aureus</i> from Killing by Host Phagocytes. <i>MBio</i> , 2018, 9, .	4.1	33
123	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.	1.5	33
124	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
125	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.	3.2	32
126	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.	2.9	32

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127	Dispensing Antibiotics without Prescription at Community Pharmacies and Accredited Drug Dispensing Outlets in Tanzania: A Cross-Sectional Study. <i>Antibiotics</i> , 2021, 10, 1025.	3.7	32
128	Microevolution of <i>Burkholderia pseudomallei</i> during an Acute Infection. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3418-3421.	3.9	30
129	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.	3.0	30
130	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.	3.5	29
131	Molecular genetics of carbapenem antibiotic biosynthesis. <i>Antonie Van Leeuwenhoek</i> , 1999, 75, 135-141.	1.7	28
132	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.	2.2	28
133	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2238-2245.	3.0	27
134	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1191.	3.5	27
135	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
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