

Matthew T G Holden

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191 papers	21,158 citations	69 h-index	144 g-index
232 ext. papers	26,183 ext. citations	10.2 avg, IF	6.05 L-index

#	Paper	IF	Citations
191	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015 , 31, 3691-3	7.2	1949
190	Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18. <i>Nature</i> , 2001 , 413, 848-52	50.4	1010
189	Genome sequence of Yersinia pestis, the causative agent of plague. <i>Nature</i> , 2001 , 413, 523-7	50.4	1003
188	Evolution of MRSA during hospital transmission and intercontinental spread. <i>Science</i> , 2010 , 327, 469-74	33.3	858
187	Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica. <i>Nature Genetics</i> , 2003 , 35, 32-40	36.3	787
186	Complete genomes of two clinical Staphylococcus aureus 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, 9786-91	11.5	717
185	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. <i>Nature Genetics</i> , 2006 , 38, 779-86	36.3	679
184	Meticillin-resistant Staphylococcus aureus with a novel mecA homologue in human and bovine populations in the UK and Denmark: a descriptive study. <i>Lancet Infectious Diseases, The</i> , 2011 , 11, 595-603	25.5	617
183	Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14240-5	11.5	569
182	Rapid whole-genome sequencing for investigation of a neonatal MRSA outbreak. <i>New England Journal of Medicine</i> , 2012 , 366, 2267-75	59.2	480
181	Quorum-sensing cross talk: isolation and chemical characterization of cyclic dipeptides from Pseudomonas aeruginosa and other gram-negative bacteria. <i>Molecular Microbiology</i> , 1999 , 33, 1254-66	4.1	421
180	Whole-genome sequencing for analysis of an outbreak of meticillin-resistant Staphylococcus aureus: a descriptive study. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 130-6	25.5	414
179	Routine use of microbial whole genome sequencing in diagnostic and public health microbiology. <i>PLoS Pathogens</i> , 2012 , 8, e1002824	7.6	358
178	Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11105-10	11.5	328
177	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant Staphylococcus aureus pandemic. <i>Genome Research</i> , 2013 , 23, 653-64	9.7	325
176	Comparisons of dN/dS are time dependent for closely related bacterial genomes. <i>Journal of Theoretical Biology</i> , 2006 , 239, 226-35	2.3	313
175	Staphylococcus aureus: superbug, super genome?. <i>Trends in Microbiology</i> , 2004 , 12, 378-85	12.4	304

174	The global posttranscriptional regulator RsmA modulates production of virulence determinants and N-acylhomoserine lactones in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2001 , 183, 6676-83	3.5	291
173	LuxS: its role in central metabolism and the in vitro synthesis of 4-hydroxy-5-methyl-3(2H)-furanone. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 909-922	2.9	276
172	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016 , 2, e000093	4.4	271
171	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	9.5	270
170	The genome of <i>Burkholderia cenocepacia</i> J2315, an epidemic pathogen of cystic fibrosis patients. <i>Journal of Bacteriology</i> , 2009 , 191, 261-77	3.5	270
169	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. <i>Nucleic Acids Research</i> , 2003 , 31, 6516-23	20.1	255
168	Complete sequence and organization of pBtoxis, the toxin-coding plasmid of <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> . <i>Applied and Environmental Microbiology</i> , 2002 , 68, 5082-95	4.8	240
167	Extensive DNA inversions in the <i>B. fragilis</i> genome control variable gene expression. <i>Science</i> , 2005 , 307, 1463-5	33.3	233
166	Complete genome sequence and lytic phase transcription profile of a Coccolithovirus. <i>Science</i> , 2005 , 309, 1090-2	33.3	229
165	Genome sequence of a proteolytic (Group I) <i>Clostridium botulinum</i> strain Hall A and comparative analysis of the clostridial genomes. <i>Genome Research</i> , 2007 , 17, 1082-92	9.7	205
164	The complete genome sequence and comparative genome analysis of the high pathogenicity <i>Yersinia enterocolitica</i> strain 8081. <i>PLoS Genetics</i> , 2006 , 2, e206	6	192
163	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012 , 40, D98-108	20.1	186
162	Rapid evolution of virulence and drug resistance in the emerging zoonotic pathogen <i>Streptococcus suis</i> . <i>PLoS ONE</i> , 2009 , 4, e6072	3.7	183
161	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, 509-15	12	166
160	Structure, activity and evolution of the group I thiolactone peptide quorum-sensing system of <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2001 , 41, 503-12	4.1	163
159	Genomic evidence for the evolution of <i>Streptococcus equi</i> : host restriction, increased virulence, and genetic exchange with human pathogens. <i>PLoS Pathogens</i> , 2009 , 5, e1000346	7.6	160
158	Re-annotation and re-analysis of the <i>Campylobacter jejuni</i> NCTC11168 genome sequence. <i>BMC Genomics</i> , 2007 , 8, 162	4.5	160
157	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	3.8	156

156	Chlamydia trachomatis: genome sequence analysis of lymphogranuloma venereum isolates. <i>Genome Research</i> , 2008 , 18, 161-71	9.7	154
155	Rapid bacterial whole-genome sequencing to enhance diagnostic and public health microbiology. <i>JAMA Internal Medicine</i> , 2013 , 173, 1397-404	11.5	152
154	Genome sequence of a recently emerged, highly transmissible, multi-antibiotic- and antiseptic-resistant variant of methicillin-resistant Staphylococcus aureus, sequence type 239 (TW). <i>Journal of Bacteriology</i> , 2010 , 192, 888-92	3.5	150
153	Streptococcus agalactiae clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014 , 5, 4544	17.4	144
152	The Chlamydomonas abortus genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005 , 15, 629-40	9.7	144
151	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant Staphylococcus aureus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 9107-12	11.5	138
150	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe. <i>MBio</i> , 2016 , 7,	7.8	135
149	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014 , 24, 839-49	9.7	126
148	Methicillin-resistant Staphylococcus aureus emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017 , 18, 130	18.3	121
147	Molecular tracing of the emergence, diversification, and transmission of S. aureus 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, 6738-43	11.5	121
146	A very early-branching Staphylococcus aureus lineage lacking the carotenoid pigment staphyloxanthin. <i>Genome Biology and Evolution</i> , 2011 , 3, 881-95	3.9	119
145	Guidelines for reporting novel mecA gene homologues. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 4997-9	5.9	119
144	A single multilocus sequence typing (MLST) scheme for seven pathogenic Leptospira species. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e1954	4.8	118
143	Emergence of scarlet fever Streptococcus pyogenes emm12 clones in Hong Kong is associated with toxin acquisition and multidrug resistance. <i>Nature Genetics</i> , 2015 , 47, 84-7	36.3	103
142	Comparative genomics of vancomycin-resistant Staphylococcus aureus strains and their positions within the clade most commonly associated with Methicillin-resistant S. aureus hospital-acquired infection in the United States. <i>MBio</i> , 2012 , 3,	7.8	97
141	Emergence of a New Highly Successful Acapsular Group A Streptococcus Clade of Genotype emm89 in the United Kingdom. <i>MBio</i> , 2015 , 6, e00622	7.8	93
140	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. <i>Nature Communications</i> , 2015 , 6, 6740	17.4	89
139	Properties of a novel PBP2A protein homolog from Staphylococcus aureus strain LGA251 and its contribution to the β -lactam-resistant phenotype. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36854-63	5.4	89

138	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017 , 2, 16263	26.6	87
137	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, 2885-97	3.5	87
136	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015 , 6, 6560	17.4	83
135	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012 , 13, R126	18.3	82
134	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1468-1478	12.3	80
133	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	3.4	80
132	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	4.5	77
131	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
130	Evolutionary dynamics of methicillin-resistant <i>Staphylococcus aureus</i> within a healthcare system. <i>Genome Biology</i> , 2015 , 16, 81	18.3	76
129	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, 7504-14	4.8	76
128	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015 , 25, 111-8	9.7	75
127	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, 17165-70	11.5	73
126	Genome sequence of <i>Staphylococcus lugdunensis</i> N920143 allows identification of putative colonization and virulence factors. <i>FEMS Microbiology Letters</i> , 2011 , 322, 60-7	2.9	73
125	Evidence for niche adaptation in the genome of the bovine pathogen <i>Streptococcus uberis</i> . <i>BMC Genomics</i> , 2009 , 10, 54	4.5	73
124	The impact of recombination on dN/dS within recently emerged bacterial clones. <i>PLoS Pathogens</i> , 2011 , 7, e1002129	7.6	71
123	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	7.8	70
122	Nonrandom distribution of <i>Burkholderia pseudomallei</i> clones in relation to geographical location and virulence. <i>Journal of Clinical Microbiology</i> , 2006 , 44, 2553-7	9.7	68
121	The G5 domain: a potential N-acetylglucosamine recognition domain involved in biofilm formation. <i>Bioinformatics</i> , 2005 , 21, 1301-3	7.2	68

120	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019 , 51, 1035-1043	36.3	67
119	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	4	67
118	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, 594-7	5.1	65
117	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 911-8	5.1	62
116	Complete genome of acute rheumatic fever-associated serotype M5 <i>Streptococcus pyogenes</i> strain manfredo. <i>Journal of Bacteriology</i> , 2007 , 189, 1473-7	3.5	61
115	A <i>Staphylococcus xylosus</i> isolate with a new <i>mecC</i> allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 1524-8	5.9	58
114	Innate immunity. A Spaetzle-like role for nerve growth factor in vertebrate immunity to <i>Staphylococcus aureus</i> . <i>Science</i> , 2014 , 346, 641-646	33.3	55
113	Evolutionary history of the Coccolithoviridae. <i>Molecular Biology and Evolution</i> , 2006 , 23, 86-92	8.3	54
112	<i>Burkholderia pseudomallei</i> genome plasticity associated with genomic island variation. <i>BMC Genomics</i> , 2008 , 9, 190	4.5	52
111	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	11.6	51
110	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, e010007-8	7.8	51
109	The Ess/Type VII secretion system of <i>Staphylococcus aureus</i> shows unexpected genetic diversity. <i>BMC Genomics</i> , 2016 , 17, 222	4.5	51
108	Comparative whole genome sequence analysis of the carcinogenic bacterial model pathogen <i>Helicobacter felis</i> . <i>Genome Biology and Evolution</i> , 2011 , 3, 302-8	3.9	48
107	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, 4817-27	3.7	46
106	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 (Pt 6), 1495-1508	2.9	46
105	Genome specialization and decay of the strangles pathogen, <i>Streptococcus equi</i> , is driven by persistent infection. <i>Genome Research</i> , 2015 , 25, 1360-71	9.7	45
104	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	3.3	45
103	A novel streptococcal integrative conjugative element involved in iron acquisition. <i>Molecular Microbiology</i> , 2008 , 70, 1274-92	4.1	45

102	New signal molecules on the quorum-sensing block. <i>Trends in Microbiology</i> , 2000 , 8, 101-4; discussion 103-4	12.4	44
101	Burkholderia pseudomallei sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015 , 25, 129-41	9.7	43
100	Rapid single-colony whole-genome sequencing of bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 1275-81	5.1	42
99	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016 , 26, 263-70	9.7	41
98	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021 , 6, 112-122	26.6	39
97	Whole-genome sequencing confirms that Burkholderia pseudomallei multilocus sequence types common to both Cambodia and Australia are due to homoplasy. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 323-6	9.7	37
96	High rates of homologous recombination in the mite endosymbiont and opportunistic human pathogen Orientia tsutsugamushi. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e752	4.8	37
95	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and methicillin-resistant Staphylococcus aureus. <i>International Journal of Antimicrobial Agents</i> , 2015 , 45, 477-84	14.3	34
94	Molecular analysis of an outbreak of lethal postpartum sepsis caused by Streptococcus pyogenes. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 2089-95	9.7	34
93	Whole-genome sequencing reveals clonal expansion of multiresistant Staphylococcus haemolyticus in European hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2920-7	5.1	33
92	Burkholderia Hep_Hag autotransporter (BuHA) proteins elicit a strong antibody response during experimental glanders but not human melioidosis. <i>BMC Microbiology</i> , 2007 , 7, 19	4.5	33
91	Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , 2022 ,	50.4	33
90	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in. <i>Frontiers in Microbiology</i> , 2017 , 8, 311	5.7	31
89	Multiplex PCR assay for unequivocal differentiation of Actinobacillus pleuropneumoniae serovars 1 to 3, 5 to 8, 10, and 12. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 2380-5	9.7	30
88	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. <i>BMC Genomics</i> , 2014 , 15, 1179	4.5	29
87	Development of a Multilocus Sequence Typing Scheme for Molecular Typing of Mycoplasma pneumoniae. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3195-203	9.7	28
86	T Cell Immunity to the Alkyl Hydroperoxide Reductase of Burkholderia pseudomallei: A Correlate of Disease Outcome in Acute Melioidosis. <i>Journal of Immunology</i> , 2015 , 194, 4814-24	5.3	28
85	Comparative sequence analysis of the capsular polysaccharide loci of Actinobacillus pleuropneumoniae serovars 1-18, and development of two multiplex PCRs for comprehensive capsule typing. <i>Veterinary Microbiology</i> , 2018 , 220, 83-89	3.3	28

84	Characterization of pneumonia due to <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> in dogs. <i>Vaccine Journal</i> , 2010 , 17, 1790-6		28
83	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015 , 178, 279-82	3.3	27
82	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020 , 11, 2719	17.4	27
81	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, 7396-404	5.9	26
80	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	4.3	25
79	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	26.6	24
78	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2238-45	5.1	24
77	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, 2217-22	5.1	23
76	Genomics of Natural Populations of <i>Staphylococcus aureus</i> . <i>Annual Review of Microbiology</i> , 2016 , 70, 459-78	17.5	23
75	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects <i>Staphylococcus aureus</i> from Killing by Host Phagocytes. <i>MBio</i> , 2018 , 9,	7.8	23
74	<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	6.9	22
73	Molecular genetics of carbapenem antibiotic biosynthesis. <i>Antonie Van Leeuwenhoek</i> , 1999 , 75, 135-41	2.1	22
72	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019 , 10,	7.8	22
71	Colony morphology variation of <i>Burkholderia pseudomallei</i> is associated with antigenic variation and O-polysaccharide modification. <i>Infection and Immunity</i> , 2015 , 83, 2127-38	3.7	21
70	Genome-wide analysis reveals loci encoding anti-macrophage factors in the human pathogen <i>Burkholderia pseudomallei</i> K96243. <i>PLoS ONE</i> , 2010 , 5, e15693	3.7	21
69	Pan-genomic perspective on the evolution of the USA300 epidemic. <i>Microbial Genomics</i> , 2016 , 2, e000058	17.4	21
68	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	4	20
67	MRSA Transmission Dynamics Among Interconnected Acute, Intermediate-Term, and Long-Term Healthcare Facilities in Singapore. <i>Clinical Infectious Diseases</i> , 2017 , 64, S76-S81	11.6	20

66	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	4.4	20
65	Microevolution of <i>Burkholderia pseudomallei</i> during an acute infection. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3418-21	9.7	19
64	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015 , 6, 1191	5.7	18
63	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	9.5	17
62	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	3.7	17
61	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,	4.4	17
60	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , 2016 , 4,		16
59	Global Scale Dissemination of ST93: A Divergent Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018 , 9, 1453	5.7	16
58	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, 363-7	5.1	16
57	The <i>Streptococcus equi</i> prophage-encoded protein SEQ2045 is a hyaluronan-specific hyaluronate lyase that is produced during equine infection. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 443-449	2.9	16
56	ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016 , 7, 810	5.7	16
55	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	4.5	15
54	Functional analysis of the EsaB component of the Type VII secretion system. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1851-1863	2.9	15
53	Genomic Dissection of an Icelandic Epidemic of Respiratory Disease in Horses and Associated Zoonotic Cases. <i>MBio</i> , 2017 , 8,	7.8	13
52	Pathogenomics of non-pathogens. <i>Nature Reviews Microbiology</i> , 2004 , 2, 91	22.2	13
51	Population genetic structuring of methicillin-resistant clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017 , 3, e000113	4.4	12
50	Superantigenic activity of emm3 <i>Streptococcus pyogenes</i> is abrogated by a conserved, naturally occurring smeZ mutation. <i>PLoS ONE</i> , 2012 , 7, e46376	3.7	11
49	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019 , 8,	8.9	11

48	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	2.9	11
47	Enhanced nasopharyngeal infection and shedding associated with an epidemic lineage of emm3 group A <i>Streptococcus</i> . <i>Virulence</i> , 2017 , 8, 1390-1400	4.7	10
46	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, 1563-4	5.9	10
45	Genetic variation associated with infection and the environment in the accidental pathogen. <i>Communications Biology</i> , 2019 , 2, 428	6.7	9
44	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017 , 3, e000117	4.4	8
43	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,	7.8	8
42	Antimicrobial resistance in atopic dermatitis: Need for an urgent rethink. <i>Annals of Allergy, Asthma and Immunology</i> , 2019 , 122, 236-240	3.2	7
41	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	6.9	7
40	Fitting the niche by genomic adaptation. <i>Nature Reviews Microbiology</i> , 2003 , 1, 92-3	22.2	6
39	Origin, maintenance and spread of antibiotic resistance genes within plasmids and chromosomes of bloodstream isolates of. <i>Microbial Genomics</i> , 2020 , 6,	4.4	6
38	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	2	6
37	ST3268: a geographically widespread primate MRSA clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2401-2403	5.1	5
36	"Gene accordions" cause genotypic and phenotypic heterogeneity in clonal populations of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2020 , 11, 3526	17.4	5
35	The molecular basis of thioalcohol production in human body odour. <i>Scientific Reports</i> , 2020 , 10, 12500	4.9	5
34	Dispensing Antibiotics without Prescription at Community Pharmacies and Accredited Drug Dispensing Outlets in Tanzania: A Cross-Sectional Study. <i>Antibiotics</i> , 2021 , 10,	4.9	5
33	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	4.9	4
32	See and Sequence: Integrating Whole-Genome Sequencing Within the National Antimicrobial Resistance Surveillance Program in the Philippines		4
31	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	3	4

30	Ecosystem engineers drive differing microbial community composition in intertidal estuarine sediments. <i>PLoS ONE</i> , 2021 , 16, e0240952	3.7	4
29	Turner et al. Reply to "Emergence of the Same Successful Clade among Distinct Populations of emm89 <i>Streptococcus pyogenes</i> in Multiple Geographic Regions". <i>MBio</i> , 2015 , 6, e01883-15	7.8	3
28	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	2.9	3
27	Globetrotting strangles: the unbridled national and international transmission of between horses. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
26	Distinct evolutionary patterns of <i>Neisseria meningitidis</i> serogroup B disease outbreaks at two universities in the USA. <i>Microbial Genomics</i> , 2018 , 4,	4.4	3
25	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	6.9	3
24	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. <i>Journal of Bacteriology</i> , 2009 , 191, 2907-2907	3.5	2
23	The magnificent seven. <i>Trends in Microbiology</i> , 2003 , 11, 12-4	12.4	2
22	The Global Posttranscriptional Regulator RsmA Modulates Production of Virulence Determinants and N-Acylhomoserine Lactones in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002 , 184, 335-335	3.5	2
21	Genomic Analysis of Global Strains Reveals Distinct Lineages With Differing Virulence and Antibiotic Resistance Gene Content.. <i>Frontiers in Microbiology</i> , 2021 , 12, 795173	5.7	2
20	The SARS-CoV-2 Alpha variant causes increased clinical severity of disease		2
19	Pan-Resistome Characterization of Uropathogenic and Strains Circulating in Uganda and Kenya, Isolated from 2017-2018.. <i>Antibiotics</i> , 2021 , 10,	4.9	2
18	Draft Genome Sequences of the Type Strains of <i>Actinobacillus indolicus</i> (46K2C) and <i>Actinobacillus porcinus</i> (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
17	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	3.3	1
16	Shrinking genomics. <i>Nature Reviews Microbiology</i> , 2004 , 2, 11	22.2	1
15	The good, the bad and the ugly?. <i>Trends in Microbiology</i> , 2003 , 11, 204-5	12.4	1
14	Food for thought. <i>Nature Reviews Microbiology</i> , 2005 , 3, 912-3	22.2	1
13	Rationally designed vectors for functional genomic analysis of and other species by transposon-directed insertion-site sequencing (TraDIS). <i>Animal Diseases</i> , 2021 , 1, 29		1

12	Emergence of optrA-mediated linezolid resistance in multiple lineages and plasmids of <i>Enterococcus faecalis</i> revealed by long read sequencing		1
11	Pan-resistome characterization of uropathogenic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> strains circulating in Uganda and Kenya isolated from 2017-2018		1
10	Genomic Surveillance of Methicillin-Resistant <i>Staphylococcus aureus</i> in the Philippines from 2013-2014		1
9	The emergence of successful <i>Streptococcus pyogenes</i> lineages through convergent pathways of capsule loss and recombination directing high toxin expression		1
8	The Staphylococci: A Postgenomic View 120-140		1
7	SpeS: A Novel Superantigen and Its Potential as a Vaccine Adjuvant against Strangles. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	1
6	Genomic surveillance of methicillin-resistant in the Philippines, 2013-2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 6-16	1	1
5	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> , 2020 ,	9.5	1
4	Genomic surveillance of in the Philippines, 2013-2014.. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 1-15	1	1
3	PinR mediates the generation of reversible population diversity in <i>Streptococcus zooepidemicus</i> . <i>Microbiology (United Kingdom)</i> , 2015 , 161, 1105-1112	2.9	0
2	Genomic surveillance of in the Philippines, 2013-2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 17-25	1	0
1	Genomic surveillance of in the Philippines, 2013-2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 4-18	1	