

Matthew T G Holden

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , 2022 ,	50.4	33
190	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
189	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
188	Globetrotting strangles: the unbridled national and international transmission of between horses. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
187	Genomic surveillance of in the Philippines, 2013-2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 17-25	1	0
186	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
185	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
184	Genomic surveillance of in the Philippines, 2013-2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 4-18	1	
183	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
182	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
181	Ecosystem engineers drive differing microbial community composition in intertidal estuarine sediments. <i>PLoS ONE</i> , 2021 , 16, e0240952	3.7	4
180	Investigation of two cases of Mycobacterium chelonae 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
179	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
178	Genomic surveillance of in the Philippines, 2013-2014.. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021 , 12, 1-15	1	1
177	Pan-Resistome Characterization of Uropathogenic and Strains Circulating in Uganda and Kenya, Isolated from 2017-2018.. <i>Antibiotics</i> , 2021 , 10,	4.9	2
176	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020 , 11, 2719	17.4	27
175	A highly conserved complete accessory Escherichia coli type III secretion system 2 is widespread in bloodstream isolates of the ST69 lineage. <i>Scientific Reports</i> , 2020 , 10, 4135	4.9	4

174	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
173	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
172	"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
171	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
170	The molecular basis of thioalcohol production in human body odour. <i>Scientific Reports</i> , 2020 , 10, 12500	4.9	5
169	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
168	Chlorhexidine and octenidine use, carriage of qac 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
167	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019 , 51, 1035-1043	36.3	67
166	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
165	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019 , 8,	8.9	11
164	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
163	Genetic variation associated with infection and the environment in the accidental pathogen. <i>Communications Biology</i> , 2019 , 2, 428	6.7	9
162	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
161	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
160	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
159	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
158	<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
157	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

156	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
155	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
154	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
153	Comparative sequence analysis of the capsular polysaccharide loci of <i>Actinobacillus pleuropneumoniae</i> serovars 1-18, and development of two multiplex PCRs for comprehensive capsule typing. <i>Veterinary Microbiology</i> , 2018 , 220, 83-89	3.3	28
152	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
151	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
150	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
149	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
148	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
147	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017 , 2, 16263	26.6	87
146	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
145	ST3268: a geographically widespread primate MRSA clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2401-2403	5.1	5
144	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
143	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017 , 18, 130	18.3	121
142	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
141	Genomic Dissection of an Icelandic Epidemic of Respiratory Disease in Horses and Associated Zoonotic Cases. <i>MBio</i> , 2017 , 8,	7.8	13
140	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
139	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

138	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in. <i>Frontiers in Microbiology</i> , 2017 , 8, 311	5.7	31
137	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
136	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
135	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
134	Functional analysis of the EsaB component of the Type VII secretion system. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1851-1863	2.9	15
133	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , 2016 , 4,		16
132	Pan-genomic perspective on the evolution of the USA300 epidemic. <i>Microbial Genomics</i> , 2016 , 2, e000058	4.4	21
131	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
130	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016 , 2, e000093	4.4	271
129	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
128	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
127	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
126	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
125	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,	7.8	135
124	Genomics of Natural Populations of <i>Staphylococcus aureus</i> . <i>Annual Review of Microbiology</i> , 2016 , 70, 459-78	17.5	23
123	Development of a Multilocus Sequence Typing Scheme for Molecular Typing of <i>Mycoplasma pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3195-203	9.7	28
122	Emergence of a New Highly Successful Acapsular Group A <i>Streptococcus</i> Clade of Genotype emm89 in the United Kingdom. <i>MBio</i> , 2015 , 6, e00622	7.8	93
121	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

120	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
119	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
118	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
117	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015 , 6, 6740	17.4	89
116	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
115	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
114	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
113	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, 4814-24	5.3	28
112	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015 , 25, 129-41	9.7	43
111	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, 84-7	36.3	103
110	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
109	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
108	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, 477-84	14.3	34
107	Evolutionary dynamics of methicillin-resistant <i>Staphylococcus aureus</i> within a healthcare system. <i>Genome Biology</i> , 2015 , 16, 81	18.3	76
106	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015 , 31, 3691-3	7.2	1949
105	Whole-genome sequencing confirms that <i>Burkholderia pseudomallei</i> multilocus sequence types common to both Cambodia and Australia are due to homoplasmy. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 323-6	9.7	37
104	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
103	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

102	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
101	Rapid single-colony whole-genome sequencing of bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 1275-81	5.1	42
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, 363-7	5.1	16
99	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014 , 5, 4544	17.4	144
98	Innate immunity. A Spaetzle-like role for nerve growth factor β in vertebrate immunity to <i>Staphylococcus aureus</i> . <i>Science</i> , 2014 , 346, 641-646	33.3	55
97	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, 2380-5	9.7	30
96	Whole-genome sequencing reveals clonal expansion of multiresistant <i>Staphylococcus haemolyticus</i> in European hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2920-7	5.1	33
95	Microevolution of <i>Burkholderia pseudomallei</i> during an acute infection. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3418-21	9.7	19
94	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
93	A novel hybrid <i>SCCmec-mecC</i> region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 911-8	5.1	62
92	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014 , 24, 839-49	9.7	126
91	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, 6738-43	11.5	121
90	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	7.8	51
89	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
88	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	4.5	29
87	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2238-45	5.1	24
86	Rapid bacterial whole-genome sequencing to enhance diagnostic and public health microbiology. <i>JAMA Internal Medicine</i> , 2013 , 173, 1397-404	11.5	152
85	Whole-genome sequencing for analysis of an outbreak of methicillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. <i>Lancet Infectious Diseases</i> , 2013 , 13, 130-6	25.5	414

84	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, 653-64	9.7	325
83	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
82	Molecular analysis of an outbreak of lethal postpartum sepsis caused by <i>Streptococcus pyogenes</i> . <i>Journal of Clinical Microbiology</i> , 2013 , 51, 2089-95	9.7	34
81	A single multilocus sequence typing (MLST) scheme for seven pathogenic <i>Leptospira</i> species. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e1954	4.8	118
80	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
79	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
78	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, 9107-12	11.5	138
77	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
76	Superantigenic activity of <i>emm3</i> <i>Streptococcus pyogenes</i> is abrogated by a conserved, naturally occurring <i>smeZ</i> mutation. <i>PLoS ONE</i> , 2012 , 7, e46376	3.7	11
75	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
74	Routine use of microbial whole genome sequencing in diagnostic and public health microbiology. <i>PLoS Pathogens</i> , 2012 , 8, e1002824	7.6	358
73	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012 , 40, D98-108	20.1	186
72	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,	7.8	97
71	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, 36854-63	5.4	89
70	Guidelines for reporting novel <i>mecA</i> gene homologues. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 4997-9	5.9	119
69	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
68	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> , 2011 , 11, 595-603	25.5	617
67	A very early-branching <i>Staphylococcus aureus</i> lineage lacking the carotenoid pigment staphyloxanthin. <i>Genome Biology and Evolution</i> , 2011 , 3, 881-95	3.9	119

66	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
65	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
64	The impact of recombination on dN/dS within recently emerged bacterial clones. <i>PLoS Pathogens</i> , 2011 , 7, e1002129	7.6	71
63	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
62	Characterization of pneumonia due to <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> in dogs. <i>Vaccine Journal</i> , 2010 , 17, 1790-6		28
61	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
60	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	4.8	37
59	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). <i>Journal of Bacteriology</i> , 2010 , 192, 888-92	3.5	150
58	Evolution of MRSA during hospital transmission and intercontinental spread. <i>Science</i> , 2010 , 327, 469-74	33.3	858
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	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
55	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
54	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
53	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
52	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
51	A novel streptococcal integrative conjugative element involved in iron acquisition. <i>Molecular Microbiology</i> , 2008 , 70, 1274-92	4.1	45
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