

# Timothy P Stinear

## List of Publications by Citations

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223  
papers

8,962  
citations

50  
h-index

88  
g-index

259  
ext. papers

11,068  
ext. citations

8.1  
avg, IF

5.89  
L-index

#	Paper	IF	Citations
223	Reduced vancomycin susceptibility in <i>Staphylococcus aureus</i> , including vancomycin-intermediate and heterogeneous vancomycin-intermediate strains: resistance mechanisms, laboratory detection, and clinical implications. <i>Clinical Microbiology Reviews</i> , <b>2010</b> , 23, 99-139	34	655
222	Insights from the complete genome sequence of <i>Mycobacterium marinum</i> on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Genome Research</i> , <b>2008</b> , 18, 729-41	9.7	389
221	Giant plasmid-encoded polyketide synthases produce the macrolide toxin of <i>Mycobacterium ulcerans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 1345-9 <sup>5</sup>	11.5	303
220	Reductive evolution and niche adaptation inferred from the genome of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <i>Genome Research</i> , <b>2007</b> , 17, 192-200	9.7	296
219	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , <b>2013</b> , 45, 172-9	36.3	215
218	Evolution of multidrug resistance during <i>Staphylococcus aureus</i> infection involves mutation of the essential two component regulator WalKR. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002359	7.6	213
217	<i>Mycobacterium ulcerans</i> in mosquitoes captured during outbreak of Buruli ulcer, southeastern Australia. <i>Emerging Infectious Diseases</i> , <b>2007</b> , 13, 1653-60	10.2	172
216	Isolates with low-level vancomycin resistance associated with persistent methicillin-resistant <i>Staphylococcus aureus</i> bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2006</b> , 50, 3039-47	5.9	172
215	Buruli ulcer ( <i>M. ulcerans</i> infection): new insights, new hope for disease control. <i>PLoS Medicine</i> , <b>2005</b> , 2, e108	11.6	171
214	Two novel point mutations in clinical <i>Staphylococcus aureus</i> reduce linezolid susceptibility and switch on the stringent response to promote persistent infection. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000944	7.6	155
213	Prospective Whole-Genome Sequencing Enhances National Surveillance of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 333-42	9.7	152
212	Development and application of two multiplex real-time PCR assays for the detection of <i>Mycobacterium ulcerans</i> in clinical and environmental samples. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 4733-40	4.8	151
211	Bacterial membrane vesicles transport their DNA cargo into host cells. <i>Scientific Reports</i> , <b>2017</b> , 7, 7072	4.9	145
210	Buruli ulcer: reductive evolution enhances pathogenicity of <i>Mycobacterium ulcerans</i> . <i>Nature Reviews Microbiology</i> , <b>2009</b> , 7, 50-60	22.2	145
209	A major role for mammals in the ecology of <i>Mycobacterium ulcerans</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e791	4.8	130
208	Comparative genetic analysis of <i>Mycobacterium ulcerans</i> and <i>Mycobacterium marinum</i> reveals evidence of recent divergence. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 6322-30	3.5	129
207	<i>Mycobacterium</i> toxin induces analgesia in buruli ulcer by targeting the angiotensin pathways. <i>Cell</i> , <b>2014</b> , 157, 1565-76	56.2	126

206	Aquatic plants stimulate the growth of and biofilm formation by <i>Mycobacterium ulcerans</i> in axenic culture and harbor these bacteria in the environment. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 1097-103	4.8	125
205	Identification and characterization of IS2404 and IS2606: two distinct repeated sequences for detection of <i>Mycobacterium ulcerans</i> by PCR. <i>Journal of Clinical Microbiology</i> , <b>1999</b> , 37, 1018-23	9.7	124
204	Genomic analysis reveals a point mutation in the two-component sensor gene <i>graS</i> that leads to intermediate vancomycin resistance in clinical <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2008</b> , 52, 3755-62	5.9	121
203	Global spread of three multidrug-resistant lineages of <i>Staphylococcus epidermidis</i> . <i>Nature Microbiology</i> , <b>2018</b> , 3, 1175-1185	26.6	120
202	Human blood MAIT cell subsets defined using MR1 tetramers. <i>Immunology and Cell Biology</i> , <b>2018</b> , 96, 507-525	5	115
201	Genomic insights to control the emergence of vancomycin-resistant enterococci. <i>MBio</i> , <b>2013</b> , 4,	7.8	112
200	On the origin of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <i>BMC Genomics</i> , <b>2012</b> , 13, 258	4.5	111
199	Complete Bypass of Restriction Systems for Major <i>Staphylococcus aureus</i> Lineages. <i>MBio</i> , <b>2015</b> , 6, e00307815	10.8	105
198	Increasing tolerance of hospital to handwash alcohols. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	102
197	Comparative analysis of the first complete <i>Enterococcus faecium</i> genome. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 2334-41	3.5	97
196	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , <b>2020</b> , 11, 4376	17.4	97
195	Emergence of a ribotype 244 strain of <i>Clostridium difficile</i> associated with severe disease and related to the epidemic ribotype 027 strain. <i>Clinical Infectious Diseases</i> , <b>2014</b> , 58, 1723-30	11.6	93
194	Different bacterial gene expression patterns and attenuated host immune responses are associated with the evolution of low-level vancomycin resistance during persistent methicillin-resistant <i>Staphylococcus aureus</i> bacteraemia. <i>BMC Microbiology</i> , <b>2008</b> , 8, 39	4.5	92
193	Enterococcal <i>vanB</i> resistance locus in anaerobic bacteria in human faeces. <i>Lancet, The</i> , <b>2001</b> , 357, 855-6	4.0	91
192	Evolution of virulence in <i>Enterococcus faecium</i> , a hospital-adapted opportunistic pathogen. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 41, 76-82	7.9	87
191	The evolution of vancomycin intermediate <i>Staphylococcus aureus</i> (VISA) and heterogenous-VISA. <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 21, 575-82	4.5	81
190	Identification of <i>Mycobacterium ulcerans</i> in the environment from regions in Southeast Australia in which it is endemic with sequence capture-PCR. <i>Applied and Environmental Microbiology</i> , <b>2000</b> , 66, 3206-13	4.8	80
189	Natural product diversity associated with the nematode symbionts <i>Photobacterium</i> and <i>Xenorhabdus</i> . <i>Nature Microbiology</i> , <b>2017</b> , 2, 1676-1685	26.6	78

188	A sustained hospital outbreak of vancomycin-resistant <i>Enterococcus faecium</i> bacteremia due to emergence of vanB E. faecium sequence type 203. <i>Journal of Infectious Diseases</i> , <b>2010</b> , 202, 1278-86	7	78
187	Sensitive and rapid detection of viable <i>Giardia</i> cysts and <i>Cryptosporidium parvum</i> oocysts in large-volume water samples with wound fiberglass cartridge filters and reverse transcription-PCR. <i>Applied and Environmental Microbiology</i> , <b>1998</b> , 64, 1743-9	4.8	75
186	Outbreak investigation using high-throughput genome sequencing within a diagnostic microbiology laboratory. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 1396-401	9.7	73
185	Common evolutionary origin for the unstable virulence plasmid pMUM found in geographically diverse strains of <i>Mycobacterium ulcerans</i> . <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 1668-76	3.5	71
184	Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9876-81	11.5	69
183	Mycolactones and <i>Mycobacterium ulcerans</i> disease. <i>Lancet, The</i> , <b>2003</b> , 362, 1062-4	4.0	69
182	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. <i>Molecular Microbiology</i> , <b>2014</b> , 93, 835-52	4.1	66
181	Functional analysis and annotation of the virulence plasmid pMUM001 from <i>Mycobacterium ulcerans</i> . <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 683-692	2.9	64
180	pks5-recombination-mediated surface remodelling in <i>Mycobacterium tuberculosis</i> emergence. <i>Nature Microbiology</i> , <b>2016</b> , 1, 15019	26.6	63
179	<i>Mycobacterium chimaera</i> Spread from Heating and Cooling Units in Heart Surgery. <i>New England Journal of Medicine</i> , <b>2017</b> , 376, 600-602	59.2	62
178	Analysis of the small RNA transcriptional response in multidrug-resistant <i>Staphylococcus aureus</i> after antimicrobial exposure. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2013</b> , 57, 3864-74	5.9	61
177	The RpoB H <sub>476</sub> rifampicin resistance mutation and an active stringent response reduce virulence and increase resistance to innate immune responses in <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , <b>2013</b> , 207, 929-39	7	60
176	The dominant Australian community-acquired methicillin-resistant <i>Staphylococcus aureus</i> clone ST93-IV [2B] is highly virulent and genetically distinct. <i>PLoS ONE</i> , <b>2011</b> , 6, e25887	3.7	56
175	Molecular epidemiology of enterococcal bacteremia in Australia. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 897-905	9.7	53
174	A simple PCR method for rapid genotype analysis of <i>Mycobacterium ulcerans</i> . <i>Journal of Clinical Microbiology</i> , <b>2000</b> , 38, 1482-7	9.7	53
173	Deciphering the genetic basis for polyketide variation among mycobacteria producing mycolactones. <i>BMC Genomics</i> , <b>2008</b> , 9, 462	4.5	48
172	Genomic epidemiology and antimicrobial resistance of <i>Neisseria gonorrhoeae</i> in New Zealand. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2018</b> , 73, 353-364	5.1	45
171	Convergent adaptation in the dominant global hospital clone ST239 of methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , <b>2015</b> , 6, e00080	7.8	44

170	Complete genome sequence of Staphylococcus aureus strain JKD6008, an ST239 clone of methicillin-resistant Staphylococcus aureus with intermediate-level vancomycin resistance. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5848-9	3.5	44
169	Single nucleotide polymorphism typing of Mycobacterium ulcerans reveals focal transmission of buruli ulcer in a highly endemic region of Ghana. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e751	4.8	44
168	The genome, evolution and diversity of Mycobacterium ulcerans. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 522-9	4.5	43
167	Mycobacterium ulcerans low infectious dose and mechanical transmission support insect bites and puncturing injuries in the spread of Buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005553	4.8	43
166	Decreased vancomycin susceptibility in Staphylococcus aureus caused by IS256 tempering of WalkR expression. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2013</b> , 57, 3240-9	5.9	42
165	Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant Enterococcus faecium. <i>BMC Genomics</i> , <b>2013</b> , 14, 595	4.5	41
164	Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. <i>Journal of Medical Microbiology</i> , <b>2020</b> , 69, 1169-1178	3.2	39
163	Evaluation of VNTR typing for the identification of Mycobacterium ulcerans in environmental samples from Victoria, Australia. <i>FEMS Microbiology Letters</i> , <b>2008</b> , 287, 250-5	2.9	38
162	Hyperexpression of Hemolysin explains enhanced virulence of sequence type 93 community-associated methicillin-resistant Staphylococcus aureus. <i>BMC Microbiology</i> , <b>2014</b> , 14, 31	4.5	37
161	Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. <i>BioEssays</i> , <b>2009</b> , 31, 378-88	4.1	37
160	Mycobacterium ulcerans and other mycolactone-producing mycobacteria should be considered a single species. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e663	4.8	36
159	Complete genome sequence of the frog pathogen Mycobacterium ulcerans ecovar Liflandii. <i>Journal of Bacteriology</i> , <b>2013</b> , 195, 556-64	3.5	35
158	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak. <i>PeerJ</i> , <b>2018</b> , 6, e4210	3.1	35
157	Rapid Emergence and Evolution of Staphylococcus aureus Clones Harboring fusC-Containing Staphylococcal Cassette Chromosome Elements. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 2359-65	5.8	34
156	Genomics-Driven Discovery of NO-Donating Diazeniumdiolate Siderophores in Diverse Plant-Associated Bacteria. <i>Angewandte Chemie - International Edition</i> , <b>2019</b> , 58, 13024-13029	16.4	34
155	Complete genome sequence of Staphylococcus aureus strain JKD6159, a unique Australian clone of ST93-IV community methicillin-resistant Staphylococcus aureus. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5556-7	3.7	32
154	Mycolactone gene expression is controlled by strong SigA-like promoters with utility in studies of Mycobacterium ulcerans and buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , <b>2009</b> , 3, e553	4.8	32
153	The molecular epidemiology of the highly virulent ST93 Australian community Staphylococcus aureus strain. <i>PLoS ONE</i> , <b>2012</b> , 7, e43037	3.7	32

152	Unstable chromosome rearrangements in cause phenotype switching associated with persistent infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 20135-20140	11.5	32
151	Emergence of endemic MLST non-typeable vancomycin-resistant <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 3367-3371	5.1	31
150	Mycobacterial Pathogenomics and Evolution. <i>Microbiology Spectrum</i> , <b>2014</b> , 2, MGM2-0025-2013	8.9	31
149	Rapid and sensitive detection of <i>Mycobacterium ulcerans</i> by use of a loop-mediated isothermal amplification test. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1737-41	9.7	31
148	Evolutionary origins of the emergent ST796 clone of vancomycin resistant. <i>PeerJ</i> , <b>2017</b> , 5, e2916	3.1	31
147	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , <b>2019</b> , 57,	9.7	30
146	Detection of pathogenic <i>Yersinia enterocolitica</i> in environmental waters by PCR. <i>Journal of Applied Bacteriology</i> , <b>1996</b> , 80, 327-32		30
145	In-vitro activity of avermectins against <i>Mycobacterium ulcerans</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003549	4.8	29
144	Multiple Introductions and Recent Spread of the Emerging Human Pathogen <i>Mycobacterium ulcerans</i> across Africa. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 414-426	3.9	29
143	Ongoing genome reduction in <i>Mycobacterium ulcerans</i> . <i>Emerging Infectious Diseases</i> , <b>2007</b> , 13, 1008-15	10.2	29
142	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant. <i>MSphere</i> , <b>2018</b> , 3,	5	28
141	Whole-genome sequencing reveals transmission of gonococcal antibiotic resistance among men who have sex with men: an observational study. <i>Sexually Transmitted Infections</i> , <b>2018</b> , 94, 151-157	2.8	27
140	Analysis of a Novel <i>pncA</i> Mutation for Susceptibility to Pyrazinamide Therapy. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2018</b> , 198, 541-544	10.2	26
139	Comprehensive proteome analysis of <i>Mycobacterium ulcerans</i> and quantitative comparison of mycolactone biosynthesis. <i>Proteomics</i> , <b>2008</b> , 8, 3124-38	4.8	26
138	Population genetics and the evolution of virulence in <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 21, 554-62	4.5	25
137	Adaptive change inferred from genomic population analysis of the ST93 epidemic clone of community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 366-78	3.9	25
136	Serological evaluation of <i>Mycobacterium ulcerans</i> antigens identified by comparative genomics. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e872	4.8	25
135	Genome comparisons provide insights into the role of secondary metabolites in the pathogenic phase of the <i>Photobacterium</i> life cycle. <i>BMC Genomics</i> , <b>2016</b> , 17, 537	4.5	25

134	Investigating the role of free-living amoebae as a reservoir for <i>Mycobacterium ulcerans</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e3148	4.8	24
133	membrane vesicles contain immunostimulatory DNA, RNA and peptidoglycan that activate innate immune receptors and induce autophagy. <i>Journal of Extracellular Vesicles</i> , <b>2021</b> , 10, e12080	16.4	23
132	Identification of the <i>Mycobacterium ulcerans</i> protein MUL_3720 as a promising target for the development of a diagnostic test for Buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003477	4.8	22
131	Comparative Genomics Shows That <i>Mycobacterium ulcerans</i> Migration and Expansion Preceded the Rise of Buruli Ulcer in Southeastern Australia. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	21
130	Analysis of the vaccine potential of plasmid DNA encoding nine mycolactone polyketide synthase domains in <i>Mycobacterium ulcerans</i> infected mice. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e2604	4.8	21
129	First case of <i>Mycobacterium ulcerans</i> disease (Bairnsdale or Buruli ulcer) acquired in New South Wales. <i>Medical Journal of Australia</i> , <b>2007</b> , 186, 62-3	4	21
128	Zinc-binding to the cytoplasmic PAS domain regulates the essential Walk histidine kinase of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , <b>2019</b> , 10, 3067	17.4	20
127	Bystander Activation of Pulmonary Trm Cells Attenuates the Severity of Bacterial Pneumonia by Enhancing Neutrophil Recruitment. <i>Cell Reports</i> , <b>2019</b> , 29, 4236-4244.e3	10.6	20
126	Exposure Risk for Infection and Lack of Human-to-Human Transmission of <i>Mycobacterium ulcerans</i> Disease, Australia. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 837-840	10.2	19
125	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent <i>Staphylococcus aureus</i> bacteraemia. <i>Genome Medicine</i> , <b>2018</b> , 10, 65	14.4	19
124	Regulation of mycolactone, the <i>Mycobacterium ulcerans</i> toxin, depends on nutrient source. <i>PLoS Neglected Tropical Diseases</i> , <b>2013</b> , 7, e2502	4.8	19
123	The lipoprotein LpqW is essential for the mannosylation of periplasmic glycolipids in <i>Corynebacteria</i> . <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 42726-38	5.4	19
122	Genomic Analysis of Multiresistant <i>Staphylococcus capitis</i> Associated with Neonatal Sepsis. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	19
121	The changing landscape of vancomycin-resistant <i>Enterococcus faecium</i> in Australia: a population-level genomic study. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2018</b> , 73, 3268-3278	5.1	19
120	Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). <i>Genome Medicine</i> , <b>2018</b> , 10, 63	14.4	19
119	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008287	7.6	18
118	Subtractive hybridization reveals a type I polyketide synthase locus specific to <i>Mycobacterium ulcerans</i> . <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 6870-82	3.5	18
117	Genomics of vancomycin-resistant <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	18

116	Whole genome comparisons suggest random distribution of <i>Mycobacterium ulcerans</i> genotypes in a Buruli ulcer endemic region of Ghana. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003681	4.8	17
115	Genomic Insights into a Sustained National Outbreak of <i>Yersinia pseudotuberculosis</i> . <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 3806-3814	3.9	17
114	multi-antigen sequence typing for. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000076	4.4	17
113	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health, The</i> , <b>2021</b> , 6, e547-e556	22.4	17
112	Emergence of multidrug resistance in locally-acquired human infections with <i>Salmonella</i> Typhimurium in Australia owing to a new clade harbouring bla. <i>International Journal of Antimicrobial Agents</i> , <b>2017</b> , 50, 101-105	14.3	16
111	Regulation of the 18 kDa heat shock protein in <i>Mycobacterium ulcerans</i> : an alpha-crystallin orthologue that promotes biofilm formation. <i>Molecular Microbiology</i> , <b>2010</b> , 78, 1216-31	4.1	16
110	Global analysis of adenylate-forming enzymes reveals $\epsilon$ -lactone biosynthesis pathway in pathogenic. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 14826-14839	5.4	16
109	Possible healthcare-associated transmission as a cause of secondary infection and population structure of <i>Staphylococcus aureus</i> isolates from two wound treatment centres in Ghana. <i>New Microbes and New Infections</i> , <b>2016</b> , 13, 92-101	4.1	16
108	Vancomycin-intermediate <i>Staphylococcus aureus</i> isolates are attenuated for virulence when compared with susceptible progenitors. <i>Clinical Microbiology and Infection</i> , <b>2017</b> , 23, 767-773	9.5	15
107	Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	15
106	Correspondence: Spontaneous secondary mutations confound analysis of the essential two-component system WalkR in <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , <b>2017</b> , 8, 14403	17.4	14
105	The cell wall-associated mycolactone polyketide synthases are necessary but not sufficient for mycolactone biosynthesis. <i>PLoS ONE</i> , <b>2013</b> , 8, e70520	3.7	14
104	Genomic analysis of ST88 community-acquired methicillin resistant in Ghana. <i>PeerJ</i> , <b>2017</b> , 5, e3047	3.1	14
103	A phylogenomic framework for assessing the global emergence and evolution of clonal complex 398 methicillin-resistant. <i>Microbial Genomics</i> , <b>2017</b> , 3, e000105	4.4	14
102	Vancomycin-resistant sequence type 796 - rapid international dissemination of a new epidemic clone. <i>Antimicrobial Resistance and Infection Control</i> , <b>2018</b> , 7, 44	6.2	13
101	Target-Specific Assay for Rapid and Quantitative Detection of <i>Mycobacterium chimaera</i> DNA. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 1847-1856	9.7	12
100	Dual Gene Expression Analysis Identifies Factors Associated with <i>Staphylococcus aureus</i> Virulence in Diabetic Mice. <i>Infection and Immunity</i> , <b>2019</b> , 87,	3.7	12
99	Sharing Is Caring: International Sharing of Data Enhances Genomic Surveillance of <i>Listeria</i> monocytogenes. <i>Clinical Infectious Diseases</i> , <b>2016</b> , 63, 846-8	11.6	12



98	Genomics-Driven Discovery of NO-Donating Diazeniumdiolate Siderophores in Diverse Plant-Associated Bacteria. <i>Angewandte Chemie</i> , <b>2019</b> , 131, 13158-13163	3.6	12
97	Genome sequence comparisons of serial multi-drug-resistant isolates over 21 years of infection in a single patient. <i>Microbial Genomics</i> , <b>2015</b> , 1, e000037	4.4	12
96	Genomic analysis of teicoplanin resistance emerging during treatment of vanB vancomycin-resistant <i>Enterococcus faecium</i> infections in solid organ transplant recipients including donor-derived cases. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 2134-9	5.1	12
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94	Multi-site assessment of rapid, point-of-care antigen testing for the diagnosis of SARS-CoV-2 infection in a low-prevalence setting: A validation and implementation study. <i>The Lancet Regional Health - Western Pacific</i> , <b>2021</b> , 9, 100115	5	12
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