

Timothy P Stinear

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.

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	Inhibition of the master regulator of <i>Listeria monocytogenes</i> virulence enables bacterial clearance from spacious replication vacuoles in infected macrophages.. <i>PLoS Pathogens</i> , 2022 , 18, e1010166	7.6	0
222	Optimising genomic approaches for identifying vancomycin-resistant <i>Enterococcus faecium</i> transmission in healthcare settings.. <i>Nature Communications</i> , 2022 , 13, 509	17.4	2
221	Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 Infection.. <i>Frontiers in Immunology</i> , 2022 , 13, 832223	8.4	0
220	Lab-in-a-van: Rapid SARS-CoV-2 testing response with a mobile laboratory.. <i>EBioMedicine</i> , 2022 , 79, 103983	8.3	0
219	Detection of Chimeric Cellular: HIV mRNAs Generated Through Aberrant Splicing in HIV-1 Latently Infected Resting CD4+ T Cells.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 855290	5.9	0
218	Antimicrobial tolerance and its role in the development of resistance: Lessons from enterococci. <i>Advances in Microbial Physiology</i> , 2022 ,	4.4	0
217	Daptomycin Resistance Occurs Predominantly in -Type Vancomycin-Resistant in Australasia and Is Associated With Heterogeneous and Novel Mutations. <i>Frontiers in Microbiology</i> , 2021 , 12, 749935	5.7	1
216	membrane vesicles contain immunostimulatory DNA, RNA and peptidoglycan that activate innate immune receptors and induce autophagy. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12080	16.4	23
215	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> , 2021 , 9, 100115	5	12
214	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . <i>Nature Communications</i> , 2021 , 12, 2491	17.4	5
213	Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. <i>Cell Reports</i> , 2021 , 35, 109108	10.6	9
212	Systematic review of <i>M. Bovis</i> BCG and other candidate vaccines for Buruli ulcer prophylaxis. <i>Vaccine</i> , 2021 , 39, 7238-7252	4.1	2
211	Intracellular <i>Staphylococcus aureus</i> and host cell death pathways. <i>Cellular Microbiology</i> , 2021 , 23, e13317	3.9	7
210	From cloning to mutant in 5 days: rapid allelic exchange in. <i>Access Microbiology</i> , 2021 , 3, 000193	1	5
209	Reducing mosquito-borne disease transmission to humans: A systematic review of cluster randomised controlled studies that assess interventions other than non-targeted insecticide. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009601	4.8	1
208	In vitro activity of SPR719 against <i>Mycobacterium ulcerans</i> , <i>Mycobacterium marinum</i> and <i>Mycobacterium chimaera</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009636	4.8	
207	Multi-Omic Analysis of Symbiotic Bacteria Associated With Breeding Sites. <i>Frontiers in Microbiology</i> , 2021 , 12, 703711	5.7	1

206	Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis.. <i>Lancet Microbe, The</i> , 2021 , 2, e575-e583	22.2	6
205	Accessible Platform for High-Throughput COVID-19 Molecular Diagnostics and Genome Sequencing Using a Repurposed 3D Printer for RNA Extraction. <i>ACS Biomaterials Science and Engineering</i> , 2021 , 7, 4669-4676	5.5	1
204	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health, The</i> , 2021 , 6, e547-e556	22.4	17
203	Understanding the transmission of Mycobacterium ulcerans: A step towards controlling Buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009678	4.8	6
202	Bacterial endosymbionts protect beneficial soil fungus from nematode attack. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
201	Low-Cost, Open-Source Device for High-Performance Fluorescence Detection of Isothermal Nucleic Acid Amplification Reactions. <i>ACS Biomaterials Science and Engineering</i> , 2021 , 7, 4982-4990	5.5	0
200	Tuberculosis in Australia's tropical north: a population-based genomic epidemiological study. <i>The Lancet Regional Health - Western Pacific</i> , 2021 , 15, 100229	5	1
199	Use of emerging testing technologies and approaches for SARS-CoV-2: review of literature and global experience in an Australian context. <i>Pathology</i> , 2021 , 53, 689-699	1.6	4
198	Significant variability exists in the cytotoxicity of global methicillin-resistant lineages.. <i>Microbiology (United Kingdom)</i> , 2021 , 167,	2.9	1
197	Considerations for the Analysis of Bacterial Membrane Vesicles: Methods of Vesicle Production and Quantification Can Influence Biological and Experimental Outcomes.. <i>Microbiology Spectrum</i> , 2021 , 9, e0127321	8.9	4
196	Comprehensive Genomic Investigation of Adaptive Mutations Driving the Low-Level Oxacillin Resistance Phenotype in Staphylococcus aureus. <i>MBio</i> , 2020 , 11,	7.8	8
195	Vaccine-Specific Immune Responses against Mycobacterium ulcerans Infection in a Low-Dose Murine Challenge Model. <i>Infection and Immunity</i> , 2020 , 88,	3.7	6
194	YycH and YycI Regulate Expression of Autolysins by Activation of WalRK Phosphorylation. <i>Microorganisms</i> , 2020 , 8,	4.9	8
193	Oak-Associated Negativicute Equipped with Ancestral Aromatic Polyketide Synthase Produces Antimycobacterial Dendrubins. <i>Chemistry - A European Journal</i> , 2020 , 26, 13147-13151	4.8	7
192	induces cell-surface expression of immune stimulatory NKG2D ligands on human monocytes. <i>Journal of Biological Chemistry</i> , 2020 , 295, 11803-11821	5.4	2
191	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. <i>PLoS Pathogens</i> , 2020 , 16, e1008287	7.6	18
190	Mining Symbionts of a Spider-Transmitted Fungus Illuminates Uncharted Biosynthetic Pathways to Cytotoxic Benzolactones. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 7766-7771	16.4	8
189	Mining Symbionts of a Spider-Transmitted Fungus Illuminates Uncharted Biosynthetic Pathways to Cytotoxic Benzolactones. <i>Angewandte Chemie</i> , 2020 , 132, 7840-7845	3.6	

188	Comparative Transcriptomic and Functional Assessments of Linezolid-Responsive Small RNA Genes in <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020 , 5,	7.6	3
187	Neutrophils play an ongoing role in preventing bacterial pneumonia by blocking the dissemination of <i>Staphylococcus aureus</i> from the upper to the lower airways. <i>Immunology and Cell Biology</i> , 2020 , 98, 577-594	5	4
186	High antibody titres induced by protein subunit vaccines using antigens Hsp18 and MUL_3720 with a TLR-2 agonist fail to protect against Buruli ulcer in mice. <i>PeerJ</i> , 2020 , 8, e9659	3.1	5
185	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> , 2020 , 69, 1169-1178	3.2	39
184	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020 , 6,	4.4	3
183	Identification and Mobilization of a Cryptic Antibiotic Biosynthesis Gene Locus from a Human-Pathogenic Isolate. <i>ACS Chemical Biology</i> , 2020 , 15, 1161-1168	4.9	4
182	Genome Mining and Heterologous Expression Reveal Two Distinct Families of Lasso Peptides Highly Conserved in Endofungal Bacteria. <i>ACS Chemical Biology</i> , 2020 , 15, 1169-1176	4.9	9
181	Symbiosis, virulence and natural-product biosynthesis in entomopathogenic bacteria are regulated by a small RNA. <i>Nature Microbiology</i> , 2020 , 5, 1481-1489	26.6	3
180	Global analysis of adenylate-forming enzymes reveals lactone biosynthesis pathway in pathogenic. <i>Journal of Biological Chemistry</i> , 2020 , 295, 14826-14839	5.4	16
179	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020 , 11, 4376	17.4	97
178	Introduction of <i>Mycobacterium ulcerans</i> disease in the Bankim Health District of Cameroon follows damming of the Mapou River. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008501	4.8	4
177	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
176	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
175	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
174	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
173	Reconstruction of the Genomes of Drug-Resistant Pathogens for Outbreak Investigation through Metagenomic Sequencing. <i>MSphere</i> , 2019 , 4,	5	9
172	Biosynthesis and Ether-Bridge Formation in Nargenicin Macrolides. <i>Angewandte Chemie</i> , 2019 , 131, 4036-4041	3.4	2
171	Biosynthesis and Ether-Bridge Formation in Nargenicin Macrolides. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 3996-4001	16.4	8

170	Genomewide Profiling of the <i>Enterococcus faecalis</i> Transcriptional Response to Teixobactin Reveals CroRS as an Essential Regulator of Antimicrobial Tolerance. <i>MSphere</i> , 2019 , 4,	5	5
169	Dual Gene Expression Analysis Identifies Factors Associated with <i>Staphylococcus aureus</i> Virulence in Diabetic Mice. <i>Infection and Immunity</i> , 2019 , 87,	3.7	12
168	<i>Mycobacterium ulcerans</i> Population Genomics To Inform on the Spread of Buruli Ulcer across Central Africa. <i>MSphere</i> , 2019 , 4,	5	11
167	Remodeling of pSK1 Family Plasmids and Enhanced Chlorhexidine Tolerance in a Dominant Hospital Lineage of Methicillin-Resistant. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	8
166	Genomic investigation of <i>Staphylococcus aureus</i> recovered from Gambian women and newborns following an oral dose of intra-partum azithromycin. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 3170-3178	5.1	3
165	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	30
164	Genome Mining Reveals Endopyrroles from a Nonribosomal Peptide Assembly Line Triggered in Fungal-Bacterial Symbiosis. <i>ACS Chemical Biology</i> , 2019 , 14, 1811-1818	4.9	9
163	Zinc-binding to the cytoplasmic PAS domain regulates the essential Walk histidine kinase of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2019 , 10, 3067	17.4	20
162	Genomics-Driven Discovery of NO-Donating Diazeniumdiolate Siderophores in Diverse Plant-Associated Bacteria. <i>Angewandte Chemie</i> , 2019 , 131, 13158-13163	3.6	12
161	Genomics-Driven Discovery of NO-Donating Diazeniumdiolate Siderophores in Diverse Plant-Associated Bacteria. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 13024-13029	16.4	34
160	In Vivo Imaging of Bioluminescent : A Tool to Refine the Murine Buruli Ulcer Tail Model. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019 , 101, 1312-1321	3.2	5
159	Population Genomics and Molecular Epidemiology of <i>Mycobacterium ulcerans</i> 2019 , 107-115		2
158	Genomics of vancomycin-resistant <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , 2019 , 5,	4.4	18
157	Mining the Methylome Reveals Extensive Diversity in <i>Staphylococcus epidermidis</i> Restriction Modification. <i>MBio</i> , 2019 , 10,	7.8	8
156	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> , 2019 , 116, 20135-20140	11.5	32
155	Bystander Activation of Pulmonary Trm Cells Attenuates the Severity of Bacterial Pneumonia by Enhancing Neutrophil Recruitment. <i>Cell Reports</i> , 2019 , 29, 4236-4244.e3	10.6	20
154	Buruli ulcers in a Spanish aid worker after a stay in Peru. <i>International Journal of Infectious Diseases</i> , 2019 , 78, 99-102	10.5	1
153	1,2,4-Oxadiazole antimicrobials act synergistically with daptomycin and display rapid kill kinetics against MDR <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 1562-1569	5.1	10

152	Analysis of a Novel <i>pncA</i> Mutation for Susceptibility to Pyrazinamide Therapy. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 198, 541-544	10.2	26
151	Human blood MAIT cell subsets defined using MR1 tetramers. <i>Immunology and Cell Biology</i> , 2018 , 96, 507-525	5	115
150	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> , 2018 , 84,	4.8	21
149	Genomic epidemiology and antimicrobial resistance of <i>Neisseria gonorrhoeae</i> in New Zealand. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 353-364	5.1	45
148	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant. <i>MSphere</i> , 2018 , 3,	5	28
147	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> , 2018 , 62,	5.9	15
146	Whole-genome sequencing reveals transmission of gonococcal antibiotic resistance among men who have sex with men: an observational study. <i>Sexually Transmitted Infections</i> , 2018 , 94, 151-157	2.8	27
145	Increasing tolerance of hospital to handwash alcohols. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	102
144	Vancomycin-resistant sequence type 796 - rapid international dissemination of a new epidemic clone. <i>Antimicrobial Resistance and Infection Control</i> , 2018 , 7, 44	6.2	13
143	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent <i>Staphylococcus aureus</i> bacteraemia. <i>Genome Medicine</i> , 2018 , 10, 65	14.4	19
142	The First Isolation and Whole Genome Sequencing of Murray Valley Encephalitis Virus from Cerebrospinal Fluid of a Patient with Encephalitis. <i>Viruses</i> , 2018 , 10,	6.2	6
141	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> , 2018 , 6, e4210	3.1	35
140	The BT1 large serine recombinase catalyzes DNA integration at pseudo- sites in the genus. <i>PeerJ</i> , 2018 , 6, e4784	3.1	1
139	IFN- γ and IL-5 whole blood response directed against mycolactone polyketide synthase domains in patients with infection. <i>PeerJ</i> , 2018 , 6, e5294	3.1	5
138	Evolution of virulence in <i>Enterococcus faecium</i> , a hospital-adapted opportunistic pathogen. <i>Current Opinion in Microbiology</i> , 2018 , 41, 76-82	7.9	87
137	Low incidence of recurrent Buruli ulcers in treated Australian patients living in an endemic region. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006724	4.8	2
136	Genomic Analysis of Multiresistant <i>Staphylococcus capitis</i> Associated with Neonatal Sepsis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	19
135	<i>Burkholderia lata</i> Infections from Intrinsically Contaminated Chlorhexidine Mouthwash, Australia, 2016. <i>Emerging Infectious Diseases</i> , 2018 , 24, 2109-2111	10.2	8

134	The changing landscape of vancomycin-resistant <i>Enterococcus faecium</i> in Australia: a population-level genomic study. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 3268-3278	5.1	19
133	Global spread of three multidrug-resistant lineages of <i>Staphylococcus epidermidis</i> . <i>Nature Microbiology</i> , 2018 , 3, 1175-1185	26.6	120
132	Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). <i>Genome Medicine</i> , 2018 , 10, 63	14.4	19
131	Correspondence: Spontaneous secondary mutations confound analysis of the essential two-component system WalKR in <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2017 , 8, 14403	17.4	14
130	<i>Mycobacterium chimaera</i> Spread from Heating and Cooling Units in Heart Surgery. <i>New England Journal of Medicine</i> , 2017 , 376, 600-602	59.2	62
129	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> , 2017 , 50, 101-105	14.3	16
128	Target-Specific Assay for Rapid and Quantitative Detection of <i>Mycobacterium chimaera</i> DNA. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1847-1856	9.7	12
127	Vancomycin-intermediate <i>Staphylococcus aureus</i> isolates are attenuated for virulence when compared with susceptible progenitors. <i>Clinical Microbiology and Infection</i> , 2017 , 23, 767-773	9.5	15
126	Structure and Biosynthesis of Isatropolones, Bioactive Amine-Scavenging Fluorescent Natural Products from <i>Streptomyces</i> G86. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 4945-4949	16.4	11
125	Comment on: Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 635-636	5.1	
124	Natural product diversity associated with the nematode symbionts <i>Photorhabdus</i> and <i>Xenorhabdus</i> . <i>Nature Microbiology</i> , 2017 , 2, 1676-1685	26.6	78
123	Multiple Introductions and Recent Spread of the Emerging Human Pathogen <i>Mycobacterium ulcerans</i> across Africa. <i>Genome Biology and Evolution</i> , 2017 , 9, 414-426	3.9	29
122	Exposure Risk for Infection and Lack of Human-to-Human Transmission of <i>Mycobacterium ulcerans</i> Disease, Australia. <i>Emerging Infectious Diseases</i> , 2017 , 23, 837-840	10.2	19
121	A Supervised Statistical Learning Approach for Accurate <i>Legionella pneumophila</i> Source Attribution during Outbreaks. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	4
120	Bacterial membrane vesicles transport their DNA cargo into host cells. <i>Scientific Reports</i> , 2017 , 7, 7072	4.9	145
119	Methicillin Resistant Transmission in a Ghanaian Burn Unit: The Importance of Active Surveillance in Resource-Limited Settings. <i>Frontiers in Microbiology</i> , 2017 , 8, 1906	5.7	8
118	<i>Mycobacterium ulcerans</i> low infectious dose and mechanical transmission support insect bites and puncturing injuries in the spread of Buruli ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005553	4.8	43
117	Evolutionary origins of the emergent ST796 clone of vancomycin resistant. <i>PeerJ</i> , 2017 , 5, e2916	3.1	31

116	Genomic analysis of ST88 community-acquired methicillin resistant in Ghana. <i>PeerJ</i> , 2017 , 5, e3047	3.1	14
115	A phylogenomic framework for assessing the global emergence and evolution of clonal complex 398 methicillin-resistant. <i>Microbial Genomics</i> , 2017 , 3, e000105	4.4	14
114	Genomic Insights into a Sustained National Outbreak of <i>Yersinia pseudotuberculosis</i> . <i>Genome Biology and Evolution</i> , 2016 , 8, 3806-3814	3.9	17
113	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> , 2016 , 113, 9876-81	11.5	69
112	Emergence of endemic MLST non-typeable vancomycin-resistant <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 3367-3371	5.1	31
111	Use of bacterial whole-genome sequencing to understand and improve the management of invasive <i>Staphylococcus aureus</i> infections. <i>Expert Review of Anti-Infective Therapy</i> , 2016 , 14, 1023-1036	5.5	9
110	Leprosy in red squirrels. <i>Science</i> , 2016 , 354, 702-703	33.3	4
109	pks5-recombination-mediated surface remodelling in <i>Mycobacterium tuberculosis</i> emergence. <i>Nature Microbiology</i> , 2016 , 1, 15019	26.6	63
108	Sharing Is Caring: International Sharing of Data Enhances Genomic Surveillance of <i>Listeria monocytogenes</i> . <i>Clinical Infectious Diseases</i> , 2016 , 63, 846-8	11.6	12
107	Rapid Emergence and Evolution of <i>Staphylococcus aureus</i> Clones Harboring fusC-Containing Staphylococcal Cassette Chromosome Elements. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 2359-2365	5.9	34
106	Prospective Whole-Genome Sequencing Enhances National Surveillance of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , 2016 , 54, 333-42	9.7	152
105	Snapshot fecal survey of domestic animals in rural Ghana for <i>Mycobacterium ulcerans</i> . <i>PeerJ</i> , 2016 , 4, e2065	3.1	8
104	multi-antigen sequence typing for. <i>Microbial Genomics</i> , 2016 , 2, e000076	4.4	17
103	Functional analysis of the first complete genome sequence of a multidrug resistant sequence type 2. <i>Microbial Genomics</i> , 2016 , 2, e000077	4.4	12
102	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> , 2016 , 17, 537	4.5	25
101	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> , 2016 , 13, 92-101	4.1	16
100	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> , 2015 , 9, e0003681	4.8	17
99	In-vitro activity of avermectins against <i>Mycobacterium ulcerans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003549	4.8	29

98	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> , 2015 , 9, e0003477	4.8	22
97	Convergent adaptation in the dominant global hospital clone ST239 of methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015 , 6, e00080	7.8	44
96	Proteomic characterization of a natural host-pathogen interaction: repertoire of in vivo expressed bacterial and host surface-associated proteins. <i>Journal of Proteome Research</i> , 2015 , 14, 120-32	5.6	7
95	Complete Bypass of Restriction Systems for Major <i>Staphylococcus aureus</i> Lineages. <i>MBio</i> , 2015 , 6, e00308815	7.8	105
94	Metabolomic profiles delineate mycolactone signature in Buruli ulcer disease. <i>Scientific Reports</i> , 2015 , 5, 17693	4.9	5
93	Changes in protein abundance are observed in bacterial isolates from a natural host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015 , 5, 71	5.9	4
92	A Genomic Approach to Resolving Relapse versus Reinfection among Four Cases of Buruli Ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004158	4.8	11
91	Genome sequence comparisons of serial multi-drug-resistant isolates over 21 years of infection in a single patient. <i>Microbial Genomics</i> , 2015 , 1, e000037	4.4	12
90	Large tandem chromosome expansions facilitate niche adaptation during persistent infection with drug-resistant. <i>Microbial Genomics</i> , 2015 , 1, e000026	4.4	11
89	Hyperexpression of Ehemolysin explains enhanced virulence of sequence type 93 community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2014 , 14, 31	4.5	37
88	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> , 2014 , 58, 1723-30	11.6	93
87	Molecular epidemiology of enterococcal bacteremia in Australia. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 897-905	9.7	53
86	Mycobacterial toxin induces analgesia in buruli ulcer by targeting the angiotensin pathways. <i>Cell</i> , 2014 , 157, 1565-76	56.2	126
85	Population genetics and the evolution of virulence in <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , 2014 , 21, 554-62	4.5	25
84	Mycobacterial Pathogenomics and Evolution. <i>Microbiology Spectrum</i> , 2014 , 2, MGM2-0025-2013	8.9	31
83	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> , 2014 , 8, e2604	4.8	21
82	Investigating the role of free-living amoebae as a reservoir for <i>Mycobacterium ulcerans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3148	4.8	24
81	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. <i>Molecular Microbiology</i> , 2014 , 93, 835-52	4.1	66

80	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> , 2014 , 6, 366-78	3.9	25
79	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. <i>Molecular Microbiology</i> , 2014 , 94, 742-742	4.1	
78	The evolution of vancomycin intermediate <i>Staphylococcus aureus</i> (VISA) and heterogenous-VISA. <i>Infection, Genetics and Evolution</i> , 2014 , 21, 575-82	4.5	81
77	Australian Enterococcal Sepsis Outcome Programme, 2011. <i>Communicable Diseases Intelligence</i> , 2014 , 38, E247-52		3
76	Australian Enterococcal Sepsis Outcome Programme annual report, 2013. <i>Communicable Diseases Intelligence</i> , 2014 , 38, E320-6		5
75	Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2013 , 14, 595	4.5	41
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10	Increasing tolerance of hospital <i>Enterococcus faecium</i> to hand-wash alcohols		3
9	High antibody titres induced by protein subunit vaccines against Buruli ulcer using <i>Mycobacterium ulcerans</i> antigens Hsp18 and MUL_3720		1

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