# Timothy P Stinear

## List of Publications by Year
## in descending order

Source: https://exaly.com/author-pdf/7252602/publications.pdf

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223

papers

12,582

citations

28190

55

h-index

33814

99

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259

all docs

259

docs citations

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times ranked

11946

citing authors

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Reduced Vancomycin Susceptibility in<i>Staphylococcus aureus</i>, Including Vancomycin-Intermediate and Heterogeneous Vancomycin-Intermediate Strains: Resistance Mechanisms, Laboratory Detection, and Clinical Implications. Clinical Microbiology Reviews, 2010, 23, 99-139. | 5.7 | 804 |
| 2 | Insights from the complete genome sequence of <i>Mycobacterium marinum</i> on the evolution of <i>Mycobacterium tuberculosis</i>. Genome Research, 2008, 18, 729-741. | 2.4 | 471 |
| 3 | Giant plasmid-encoded polyketide synthases produce the macrolide toxin of Mycobacterium ulcerans. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1345-1349. | 3.3 | 345 |
| 4 | Reductive evolution and niche adaptation inferred from the genome of Mycobacterium ulcerans, the causative agent of Buruli ulcer. Genome Research, 2007, 17, 192-200. | 2.4 | 345 |
| 5 | Evolution of Multidrug Resistance during Staphylococcus aureus Infection Involves Mutation of the Essential Two Component Regulator WalKR. PLoS Pathogens, 2011, 7, e1002359. | 2.1 | 315 |
| 6 | Bacterial membrane vesicles transport their DNA cargo into host cells. Scientific Reports, 2017, 7, 7072. | 1.6 | 267 |
| 7 | Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of Mycobacterium tuberculosis. Nature Genetics, 2013, 45, 172-179. | 9.4 | 264 |
| 8 | Prospective Whole-Genome Sequencing Enhances National Surveillance of Listeria monocytogenes. Journal of Clinical Microbiology, 2016, 54, 333-342. | 1.8 | 239 |
| 9 | Global spread of three multidrug-resistant lineages of Staphylococcus epidermidis. Nature Microbiology, 2018, 3, 1175-1185. | 5.9 | 206 |
| 10 | Buruli Ulcer (M. ulcerans Infection): New Insights, New Hope for Disease Control. PLoS Medicine, 2005, 2, e108. | 3.9 | 205 |
| 11 | Human blood MAIT cell subsets defined using MR1 tetramers. Immunology and Cell Biology, 2018, 96, 507-525. | 1.0 | 205 |
| 12 | Isolates with Low-Level Vancomycin Resistance Associated with Persistent Methicillin-Resistant Staphylococcus aureus Bacteremia. Antimicrobial Agents and Chemotherapy, 2006, 50, 3039-3047. | 1.4 | 199 |
| 13 | <i>Mycobacterium ulcerans</i>in Mosquitoes Captured during Outbreak of Buruli Ulcer, Southeastern Australia. Emerging Infectious Diseases, 2007, 13, 1653-1660. | 2.0 | 199 |
| 14 | Two Novel Point Mutations in Clinical Staphylococcus aureus Reduce Linezolid Susceptibility and Switch on the Stringent Response to Promote Persistent Infection. PLoS Pathogens, 2010, 6, e1000944. | 2.1 | 191 |
| 15 | Development and Application of Two Multiplex Real-Time PCR Assays for the Detection of Mycobacterium ulcerans in Clinical and Environmental Samples. Applied and Environmental Microbiology, 2007, 73, 4733-4740. | 1.4 | 189 |
| 16 | Buruli ulcer: reductive evolution enhances pathogenicity of Mycobacterium ulcerans. Nature Reviews Microbiology, 2009, 7, 50-60. | 13.6 | 175 |
| 17 | Complete Bypass of Restriction Systems for Major Staphylococcus aureus Lineages. MBio, 2015, 6, e00308-15. | 1.8 | 168 |
| 18 | A Major Role for Mammals in the Ecology of Mycobacterium ulcerans. PLoS Neglected Tropical Diseases, 2010, 4, e791. | 1.3 | 166 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | Increasing tolerance of hospital <i>Enterococcus faecium</i> to handwash alcohols. Science Translational Medicine, 2018, 10, . | 5.8 | 165 |
| 20 | Mycobacterial Toxin Induces Analgesia in Buruli Ulcer by Targeting the Angiotensin Pathways. Cell, 2014, 157, 1565-1576. | 13.5 | 160 |
| 21 | Identification and Characterization of IS <i>2404</i> and IS <i>2606</i> : Two Distinct Repeated Sequences for Detection of <i>Mycobacterium ulcerans</i> by PCR. Journal of Clinical Microbiology, 1999, 37, 1018-1023. | 1.8 | 154 |
| 22 | Evolution of virulence in Enterococcus faecium, a hospital-adapted opportunistic pathogen. Current Opinion in Microbiology, 2018, 41, 76-82. | 2.3 | 153 |
| 23 | Tracking the COVID-19 pandemic in Australia using genomics. Nature Communications, 2020, 11, 4376. | 5.8 | 152 |
| 24 | Comparative Genetic Analysis of Mycobacterium ulcerans and Mycobacterium marinum Reveals Evidence of Recent Divergence. Journal of Bacteriology, 2000, 182, 6322-6330. | 1.0 | 150 |
| 25 | On the origin of Mycobacterium ulcerans, the causative agent of Buruli ulcer. BMC Genomics, 2012, 13, 258. | 1.2 | 139 |
| 26 | 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>. Antimicrobial Agents and Chemotherapy, 2008, 52, 3755-3762. | 1.4 | 137 |
| 27 | Genomic Insights to Control the Emergence of Vancomycin-Resistant Enterococci. MBio, 2013, 4, . | 1.8 | 136 |
| 28 | Natural product diversity associated with the nematode symbionts Photorhabdus and Xenorhabdus. Nature Microbiology, 2017, 2, 1676-1685. | 5.9 | 136 |
| 29 | Aquatic Plants Stimulate the Growth of and Biofilm Formation by Mycobacterium ulcerans in Axenic Culture and Harbor These Bacteria in the Environment. Applied and Environmental Microbiology, 2004, 70, 1097-1103. | 1.4 | 135 |
| 30 | Comparative Analysis of the First Complete Enterococcus faecium Genome. Journal of Bacteriology, 2012, 194, 2334-2341. | 1.0 | 133 |
| 31 | The evolution of vancomycin intermediate Staphylococcus aureus (VISA) and heterogenous-VISA. Infection, Genetics and Evolution, 2014, 21, 575-582. | 1.0 | 115 |
| 32 | Emergence of a Ribotype 244 Strain of Clostridium difficile Associated With Severe Disease and Related to the Epidemic Ribotype 027 Strain. Clinical Infectious Diseases, 2014, 58, 1723-1730. | 2.9 | 111 |
| 33 | Enterococcal vanB resistance locus in anaerobic bacteria in human faeces. Lancet, The, 2001, 357, 855-856. | 6.3 | 107 |
| 34 | Different bacterial gene expression patterns and attenuated host immune responses are associated with the evolution of low-level vancomycin resistance during persistent methicillin-resistant Staphylococcus aureus bacteraemia. BMC Microbiology, 2008, 8, 39. | 1.3 | 106 |
| 35 | Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9876-9881. | 3.3 | 103 |
| 36 | A Sustained Hospital Outbreak of Vancomycinâ€Resistant<i>Enterococcus faecium</i>Bacteremia due to Emergence of<i>vanB E. faecium</i>Sequence Type 203. Journal of Infectious Diseases, 2010, 202, 1278-1286. | 1.9 | 98 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 37 | The RpoB H481Y Rifampicin Resistance Mutation and an Active Stringent Response Reduce Virulence and Increase Resistance to Innate Immune Responses in Staphylococcus aureus. Journal of Infectious Diseases, 2013, 207, 929-939. | 1.9 | 94 |
| 38 | 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. Applied and Environmental Microbiology, 1998, 64, 1743-1749. | 1.4 | 90 |
| 39 | Outbreak Investigation Using High-Throughput Genome Sequencing within a Diagnostic Microbiology Laboratory. Journal of Clinical Microbiology, 2013, 51, 1396-1401. | 1.8 | 86 |
| 40 | Identification of Mycobacterium ulcerans in the Environment from Regions in Southeast Australia in Which It Is Endemic with Sequence Capture-PCR. Applied and Environmental Microbiology, 2000, 66, 3206-3213. | 1.4 | 85 |
| 41 | Analysis of the Small RNA Transcriptional Response in Multidrug-Resistant Staphylococcus aureus after Antimicrobial Exposure. Antimicrobial Agents and Chemotherapy, 2013, 57, 3864-3874. | 1.4 | 84 |
| 42 | Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant Staphylococcus aureus. MBio, 2015, 6, e00080. | 1.8 | 81 |
| 43 | pks5-recombination-mediated surface remodelling in Mycobacterium tuberculosis emergence. Nature Microbiology, 2016, 1, 15019. | 5.9 | 81 |
| 44 | <i>Staphylococcus aureus</i> membrane vesicles contain immunostimulatory DNA, RNA and peptidoglycan that activate innate immune receptors and induce autophagy. Journal of Extracellular Vesicles, 2021, 10, e12080. | 5.5 | 80 |
| 45 | Mycolactones and Mycobacterium ulcerans disease. Lancet, The, 2003, 362, 1062-1064. | 6.3 | 78 |
| 46 | The Dominant Australian Community-Acquired Methicillin-Resistant Staphylococcus aureus Clone ST93-IV [2B] Is Highly Virulent and Genetically Distinct. PLoS ONE, 2011, 6, e25887. | 1.1 | 78 |
| 47 | A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 93, 835-852. | 1.2 | 76 |
| 48 | Common Evolutionary Origin for the Unstable Virulence Plasmid pMUM Found in Geographically Diverse Strains of Mycobacterium ulcerans. Journal of Bacteriology, 2005, 187, 1668-1676. | 1.0 | 74 |
| 49 | Mycobacterium ulcerans low infectious dose and mechanical transmission support insect bites and puncturing injuries in the spread of Buruli ulcer. PLoS Neglected Tropical Diseases, 2017, 11, e0005553. | 1.3 | 73 |
| 50 | Complete Genome Sequence of <i>Staphylococcus aureus</i> Strain JKD6008, an ST239 Clone of Methicillin-Resistant <i>Staphylococcus aureus</i> with Intermediate-Level Vancomycin Resistance. Journal of Bacteriology, 2010, 192, 5848-5849. | 1.0 | 71 |
| 51 | Molecular Epidemiology of Enterococcal Bacteremia in Australia. Journal of Clinical Microbiology, 2014, 52, 897-905. | 1.8 | 70 |
| 52 | <i>Mycobacterium chimaera</i> Spread from Heating and Cooling Units in Heart Surgery. New England Journal of Medicine, 2017, 376, 600-602. | 13.9 | 70 |
| 53 | Unstable chromosome rearrangements in <i>Staphylococcus aureus</i> cause phenotype switching associated with persistent infections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20135-20140. | 3.3 | 69 |
| 54 | Functional analysis and annotation of the virulence plasmid pMUM001 from Mycobacterium ulcerans. Microbiology (United Kingdom), 2005, 151, 683-692. | 0.7 | 68 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 55 | Hyperexpression of Î±-hemolysin explains enhanced virulence of sequence type 93 community-associated methicillin-resistant Staphylococcus aureus. BMC Microbiology, 2014, 14, 31. | 1.3 | 68 |
| 56 | Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak. PeerJ, 2018, 6, e4210. | 0.9 | 66 |
| 57 | Decreased Vancomycin Susceptibility in Staphylococcus aureus Caused by IS <i>256</i> Tempering of WalKR Expression. Antimicrobial Agents and Chemotherapy, 2013, 57, 3240-3249. | 1.4 | 62 |
| 58 | Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. Journal of Medical Microbiology, 2020, 69, 1169-1178. | 0.7 | 61 |
| 59 | A Simple PCR Method for Rapid Genotype Analysis of <i>Mycobacterium ulcerans</i>. Journal of Clinical Microbiology, 2000, 38, 1482-1487. | 1.8 | 58 |
| 60 | Genomic epidemiology and antimicrobial resistance of Neisseria gonorrhoeae in New Zealand. Journal of Antimicrobial Chemotherapy, 2018, 73, 353-364. | 1.3 | 57 |
| 61 | Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacterales</i> in Victoria, Australia, 2012 to 2016. Journal of Clinical Microbiology, 2019, 57, . | 1.8 | 56 |
| 62 | Deciphering the genetic basis for polyketide variation among mycobacteria producing mycolactones. BMC Genomics, 2008, 9, 462. | 1.2 | 55 |
| 63 | Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant Staphylococcus aureus. MSphere, 2018, 3, . | 1.3 | 55 |
| 64 | Complete Genome Sequence of <i>Staphylococcus aureus</i> Strain JKD6159, a Unique Australian Clone of ST93-IV Community Methicillin-Resistant <i>Staphylococcus aureus</i>. Journal of Bacteriology, 2010, 192, 5556-5557. | 1.0 | 54 |
| 65 | The genome, evolution and diversity of Mycobacterium ulcerans. Infection, Genetics and Evolution, 2012, 12, 522-529. | 1.0 | 54 |
| 66 | Genomicsâ€Driven Discovery of NOâ€Donating Diazeniumdiolate Siderophores in Diverse Plantâ€Associated Bacteria. Angewandte Chemie - International Edition, 2019, 58, 13024-13029. | 7.2 | 53 |
| 67 | Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. Lancet Public Health, The, 2021, 6, e547-e556. | 4.7 | 53 |
| 68 | Single Nucleotide Polymorphism Typing of Mycobacterium ulcerans Reveals Focal Transmission of Buruli Ulcer in a Highly Endemic Region of Ghana. PLoS Neglected Tropical Diseases, 2010, 4, e751. | 1.3 | 51 |
| 69 | Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. PLoS Pathogens, 2020, 16, e1008287. | 2.1 | 51 |
| 70 | Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant Enterococcus faecium. BMC Genomics, 2013, 14, 595. | 1.2 | 50 |
| 71 | Mycobacterium ulcerans and Other Mycolactone-Producing Mycobacteria Should Be Considered a Single Species. PLoS Neglected Tropical Diseases, 2010, 4, e663. | 1.3 | 49 |
| 72 | Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent Staphylococcus aureus bacteraemia. Genome Medicine, 2018, 10, 65. | 3.6 | 49 |

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|---|---|---|---|
| 73 | In-vitro Activity of Avermectins against Mycobacterium ulcerans. PLoS Neglected Tropical Diseases, 2015, 9, e0003549. | 1.3 | 46 |
| 74 | Evolutionary origins of the emergent ST796 clone of vancomycin resistant<i>Enterococcus faecium</i>. PeerJ, 2017, 5, e2916. | 0.9 | 46 |
| 75 | Evaluation of VNTR typing for the identification of<i>Mycobacterium ulcerans</i>in environmental samples from Victoria, Australia. FEMS Microbiology Letters, 2008, 287, 250-255. | 0.7 | 45 |
| 76 | Complete Genome Sequence of the Frog Pathogen Mycobacterium ulcerans Ecovar Liflandii. Journal of Bacteriology, 2013, 195, 556-564. | 1.0 | 44 |
| 77 | Emergence of endemic MLST non-typeable vancomycin-resistant <i>Enterococcus faecium</i>. Journal of Antimicrobial Chemotherapy, 2016, 71, 3367-3371. | 1.3 | 44 |
| 78 | Bystander Activation of Pulmonary Trm Cells Attenuates the Severity of Bacterial Pneumonia by Enhancing Neutrophil Recruitment. Cell Reports, 2019, 29, 4236-4244.e3. | 2.9 | 44 |
| 79 | Genomics of vancomycin-resistant Enterococcus faecium. Microbial Genomics, 2019, 5, . | 1.0 | 44 |
| 80 | Whole-genome sequencing reveals transmission of gonococcal antibiotic resistance among men who have sex with men: an observational study. Sexually Transmitted Infections, 2018, 94, 151-157. | 0.8 | 42 |
| 81 | Bacterial endosymbionts protect beneficial soil fungus from nematode attack. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 42 |
| 82 | The Molecular Epidemiology of the Highly Virulent ST93 Australian Community Staphylococcus aureus Strain. PLoS ONE, 2012, 7, e43037. | 1.1 | 42 |
| 83 | Global analysis of biosynthetic gene clusters reveals conserved and unique natural products in entomopathogenic nematode-symbiotic bacteria. Nature Chemistry, 2022, 14, 701-712. | 6.6 | 42 |
| 84 | Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. BioEssays, 2009, 31, 378-388. | 1.2 | 41 |
| 85 | Rapid Emergence and Evolution of Staphylococcus aureus Clones Harboring <i>fusC</i> -Containing Staphylococcal Cassette Chromosome Elements. Antimicrobial Agents and Chemotherapy, 2016, 60, 2359-2365. | 1.4 | 41 |
| 86 | Adaptive Change Inferred from Genomic Population Analysis of the ST93 Epidemic Clone of Community-Associated Methicillin-Resistant Staphylococcus aureus. Genome Biology and Evolution, 2014, 6, 366-378. | 1.1 | 40 |
| 87 | Zinc-binding to the cytoplasmic PAS domain regulates the essential WalK histidine kinase of Staphylococcus aureus. Nature Communications, 2019, 10, 3067. | 5.8 | 38 |
| 88 | Mycolactone Gene Expression Is Controlled by Strong SigA-Like Promoters with Utility in Studies of Mycobacterium ulcerans and Buruli Ulcer. PLoS Neglected Tropical Diseases, 2009, 3, e553. | 1.3 | 37 |
| 89 | Analysis of a Novel <i>pncA</i> Mutation for Susceptibility to Pyrazinamide Therapy. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 541-544. | 2.5 | 37 |
| 90 | Detection of pathogenic <i>Yersinia enterocolitica</i> in environmental waters by PCR. Journal of Applied Bacteriology, 1996, 80, 327-332. | 1.1 | 36 |

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|---|---|---|---|
| 91 | Rapid and Sensitive Detection of Mycobacterium ulcerans by Use of a Loop-Mediated Isothermal Amplification Test. Journal of Clinical Microbiology, 2012, 50, 1737-1741. | 1.8 | 36 |
| 92 | Mycobacterial Pathogenomics and Evolution. Microbiology Spectrum, 2014, 2, MGM2-0025-2013. | 1.2 | 36 |
| 93 | Genomic Analysis of Multiresistant Staphylococcus capitis Associated with Neonatal Sepsis. Antimicrobial Agents and Chemotherapy, 2018, 62, . | 1.4 | 34 |
| 94 | Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis. Lancet Microbe, The, 2021, 2, e575-e583. | 3.4 | 33 |
| 95 | Mycobacterium ulcerans â€" a mini-review. Journal of Medical Microbiology, 1999, 48, 511-513. | 0.7 | 33 |
| 96 | Ongoing Genome Reduction inMycobacterium ulcerans. Emerging Infectious Diseases, 2007, 13, 1008-1015. | 2.0 | 32 |
| 97 | Population genetics and the evolution of virulence in Staphylococcus aureus. Infection, Genetics and Evolution, 2014, 21, 554-562. | 1.0 | 32 |
| 98 | Multiple introductions and recent spread of the emerging human pathogen <i>Mycobacterium ulcerans</i> across Africa. Genome Biology and Evolution, 2017, 9, evx003. | 1.1 | 32 |
| 99 | Comparative Genomics Shows That Mycobacterium ulcerans Migration and Expansion Preceded the Rise of Buruli Ulcer in Southeastern Australia. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 32 |
| 100 | Genomic insights into a sustained national outbreak of <i>Yersinia pseudotuberculosis</i>. Genome Biology and Evolution, 2016, 8, evw285. | 1.1 | 31 |
| 101 | Intracellular<scp><i>Staphylococcus aureus</i></scp>and host cell death pathways. Cellular Microbiology, 2021, 23, e13317. | 1.1 | 31 |
| 102 | NGMASTER: in silico multi-antigen sequence typing for Neisseria gonorrhoeae. Microbial Genomics, 2016, 2, e000076. | 1.0 | 31 |
| 103 | Serological Evaluation of Mycobacterium ulcerans Antigens Identified by Comparative Genomics. PLoS Neglected Tropical Diseases, 2010, 4, e872. | 1.3 | 30 |
| 104 | Genome comparisons provide insights into the role of secondary metabolites in the pathogenic phase of the Photorhabdus life cycle. BMC Genomics, 2016, 17, 537. | 1.2 | 30 |
| 105 | Vancomycin-intermediate Staphylococcus aureus isolates are attenuated for virulence when compared with susceptible progenitors. Clinical Microbiology and Infection, 2017, 23, 767-773. | 2.8 | 30 |
| 106 | Vancomycin-resistant Enterococcus faecium sequence type 796 - rapid international dissemination of a new epidemic clone. Antimicrobial Resistance and Infection Control, 2018, 7, 44. | 1.5 | 30 |
| 107 | Considerations for the Analysis of Bacterial Membrane Vesicles: Methods of Vesicle Production and Quantification Can Influence Biological and Experimental Outcomes. Microbiology Spectrum, 2021, 9, e0127321. | 1.2 | 30 |
| 108 | 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. The Lancet Regional Health - Western Pacific, 2021, 9, 100115. | 1.3 | 29 |

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|---|---|---|---|
| 109 | Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2018, 62, . | 1.4 | 28 |
| 110 | Mining the Methylome Reveals Extensive Diversity in Staphylococcus epidermidis Restriction Modification. MBio, 2019, 10, . | 1.8 | 28 |
| 111 | Investigating the Role of Free-living Amoebae as a Reservoir for Mycobacterium ulcerans. PLoS Neglected Tropical Diseases, 2014, 8, e3148. | 1.3 | 27 |
| 112 | The changing landscape of vancomycin-resistant Enterococcus faecium in Australia: a population-level genomic study. Journal of Antimicrobial Chemotherapy, 2018, 73, 3268-3278. | 1.3 | 27 |
| 113 | Comprehensive Genomic Investigation of Adaptive Mutations Driving the Low-Level Oxacillin Resistance Phenotype in Staphylococcus aureus. MBio, 2020, 11, . | 1.8 | 27 |
| 114 | Comprehensive proteome analysis of <b><i>Mycobacterium ulcerans</i></b> and quantitative comparison of mycolactone biosynthesis. Proteomics, 2008, 8, 3124-3138. | 1.3 | 26 |
| 115 | Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). Genome Medicine, 2018, 10, 63. | 3.6 | 26 |
| 116 | Understanding the transmission of Mycobacterium ulcerans: A step towards controlling Buruli ulcer. PLoS Neglected Tropical Diseases, 2021, 15, e0009678. | 1.3 | 26 |
| 117 | The Lipoprotein LpqW Is Essential for the Mannosylation of Periplasmic Glycolipids in Corynebacteria. Journal of Biological Chemistry, 2012, 287, 42726-42738. | 1.6 | 25 |
| 118 | Analysis of the Vaccine Potential of Plasmid DNA Encoding Nine Mycolactone Polyketide Synthase Domains in Mycobacterium ulcerans Infected Mice. PLoS Neglected Tropical Diseases, 2014, 8, e2604. | 1.3 | 25 |
| 119 | Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. Cell Reports, 2021, 35, 109108. | 2.9 | 25 |
| 120 | Regulation of Mycolactone, the Mycobacterium ulcerans Toxin, Depends on Nutrient Source. PLoS Neglected Tropical Diseases, 2013, 7, e2502. | 1.3 | 24 |
| 121 | Identification of the Mycobacterium ulcerans Protein MUL_3720 as a Promising Target for the Development of a Diagnostic Test for Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0003477. | 1.3 | 24 |
| 122 | Exposure Risk for Infection and Lack of Human-to-Human Transmission of<i>Mycobacterium ulcerans</i>Disease, Australia. Emerging Infectious Diseases, 2017, 23, 837-840. | 2.0 | 24 |
| 123 | Genome Mining Reveals Endopyrroles from a Nonribosomal Peptide Assembly Line Triggered in Fungalâ€“Bacterial Symbiosis. ACS Chemical Biology, 2019, 14, 1811-1818. | 1.6 | 24 |
| 124 | Symbiosis, virulence and natural-product biosynthesis in entomopathogenic bacteria are regulated by a small RNA. Nature Microbiology, 2020, 5, 1481-1489. | 5.9 | 24 |
| 125 | A phylogenomic framework for assessing the global emergence and evolution of clonal complex 398 methicillin-resistant Staphylococcus aureus. Microbial Genomics, 2017, 3, e000105. | 1.0 | 24 |
| 126 | Whole Genome Comparisons Suggest Random Distribution of Mycobacterium ulcerans Genotypes in a Buruli Ulcer Endemic Region of Ghana. PLoS Neglected Tropical Diseases, 2015, 9, e0003681. | 1.3 | 23 |

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|---|---|---|---|
| 127 | Structure and Biosynthesis of Isatropolones, Bioactive Amineâ€Scavenging Fluorescent Natural Products from <i>Streptomyces</i>â€…GÃ¶66. Angewandte Chemie - International Edition, 2017, 56, 4945-4949. | 7.2 | 22 |
| 128 | Dual Gene Expression Analysis Identifies Factors Associated with Staphylococcus aureus Virulence in Diabetic Mice. Infection and Immunity, 2019, 87, . | 1.0 | 22 |
| 129 | Global analysis of adenylate-forming enzymes reveals Î²-lactone biosynthesis pathway in pathogenic Nocardia. Journal of Biological Chemistry, 2020, 295, 14826-14839. | 1.6 | 22 |
| 130 | Mining Symbionts of a Spiderâ€Transmitted Fungus Illuminates Uncharted Biosynthetic Pathways to Cytotoxic Benzolactones. Angewandte Chemie - International Edition, 2020, 59, 7766-7771. | 7.2 | 22 |
| 131 | First case of Mycobacterium ulcerans disease (Bairnsdale or Buruli ulcer) acquired in New South Wales. Medical Journal of Australia, 2007, 186, 62-63. | 0.8 | 21 |
| 132 | Regulation of the 18â€ƒkDa heat shock protein in <i>Mycobacterium ulcerans</i>: an alphaâ€crystallin orthologue that promotes biofilm formation. Molecular Microbiology, 2010, 78, 1216-1231. | 1.2 | 20 |
| 133 | Emergence of multidrug resistance in locally-acquired human infections with Salmonella Typhimurium in Australia owing to a new clade harbouring bla CTX-M-9. International Journal of Antimicrobial Agents, 2017, 50, 101-105. | 1.1 | 20 |
| 134 | Genome Mining and Heterologous Expression Reveal Two Distinct Families of Lasso Peptides Highly Conserved in Endofungal Bacteria. ACS Chemical Biology, 2020, 15, 1169-1176. | 1.6 | 20 |
| 135 | From cloning to mutant in 5 days: rapid allelic exchange in Staphylococcus aureus. Access Microbiology, 2020, 3, 000193. | 0.2 | 20 |
| 136 | Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen Mycobacterium kansasii. Nature Communications, 2021, 12, 2491. | 5.8 | 20 |
| 137 | Genomic analysis of ST88 community-acquired methicillin resistant<i>Staphylococcus aureus</i>in Ghana. PeerJ, 2017, 5, e3047. | 0.9 | 20 |
| 138 | Optimising genomic approaches for identifying vancomycin-resistant Enterococcus faecium transmission in healthcare settings. Nature Communications, 2022, 13, 509. | 5.8 | 20 |
| 139 | Subtractive Hybridization Reveals a Type I Polyketide Synthase Locus Specific to Mycobacterium ulcerans. Journal of Bacteriology, 2003, 185, 6870-6882. | 1.0 | 19 |
| 140 | Genomic analysis of teicoplanin resistance emerging during treatment of vanB vancomycin-resistant Enterococcus faecium infections in solid organ transplant recipients including donor-derived cases. Journal of Antimicrobial Chemotherapy, 2013, 68, 2134-2139. | 1.3 | 19 |
| 141 | Possible healthcare-associated transmission as a cause of secondary infection and population structure of Staphylococcus aureus isolates from two wound treatment centres in Ghana. New Microbes and New Infections, 2016, 13, 92-101. | 0.8 | 19 |
| 142 | YycH and YycI Regulate Expression of Staphylococcus aureus Autolysins by Activation of WalRK Phosphorylation. Microorganisms, 2020, 8, 870. | 1.6 | 19 |
| 143 | Correspondence: Spontaneous secondary mutations confound analysis of the essential two-component system WalKR in Staphylococcus aureus. Nature Communications, 2017, 8, 14403. | 5.8 | 18 |
| 144 | Remodeling of pSK1 Family Plasmids and Enhanced Chlorhexidine Tolerance in a Dominant Hospital Lineage of Methicillin-Resistant <i>Staphylococcus aureus</i>. Antimicrobial Agents and Chemotherapy, 2019, 63, . | 1.4 | 18 |

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|---|---|---|---|
| 145 | The Cell Wall-Associated Mycolactone Polyketide Synthases Are Necessary but Not Sufficient for Mycolactone Biosynthesis. PLoS ONE, 2013, 8, e70520. | 1.1 | 18 |
| 146 | Niche-specific genome degradation and convergent evolution shaping Staphylococcus aureus adaptation during severe infections. ELife, 0, 11, . | 2.8 | 18 |
| 147 | Target-Specific Assay for Rapid and Quantitative Detection of Mycobacterium chimaera DNA. Journal of Clinical Microbiology, 2017, 55, 1847-1856. | 1.8 | 17 |
| 148 | Functional analysis of the first complete genome sequence of a multidrug resistant sequence type 2 Staphylococcus epidermidis. Microbial Genomics, 2016, 2, e000077. | 1.0 | 17 |
| 149 | Use of bacterial whole-genome sequencing to understand and improve the management of invasive<i>Staphylococcus aureus</i>infections. Expert Review of Anti-Infective Therapy, 2016, 14, 1023-1036. | 2.0 | 16 |
| 150 | Burkholderia lata Infections from Intrinsically Contaminated Chlorhexidine Mouthwash, Australia, 2016. Emerging Infectious Diseases, 2018, 24, 2109-2111. | 2.0 | 16 |
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