

Samuel K Sheppard

List of Publications by Year in descending order

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118
papers

7,031
citations

57758

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docs citations

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times ranked

6620
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1005-1015. | 1.8 | 497 |
| 2 | <i>Campylobacter</i> Genotyping to Determine the Source of Human Infection. <i>Clinical Infectious Diseases</i> , 2009, 48, 1072-1078. | 5.8 | 358 |
| 3 | Genome-wide association study identifies vitamin B ₅ biosynthesis as a host specificity factor in <i>Campylobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11923-11927. | 7.1 | 267 |
| 4 | Convergence of <i>Campylobacter</i> Species: Implications for Bacterial Evolution. <i>Science</i> , 2008, 320, 237-239. | 12.6 | 231 |
| 5 | Population genomics of bacterial host adaptation. <i>Nature Reviews Genetics</i> , 2018, 19, 549-565. | 16.3 | 186 |
| 6 | Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280. | 3.5 | 177 |
| 7 | CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , 2016, 2, e000086. | 2.0 | 176 |
| 8 | <i>Campylobacter</i> genotypes from food animals, environmental sources and clinical disease in Scotland 2005/6. <i>International Journal of Food Microbiology</i> , 2009, 134, 96-103. | 4.7 | 158 |
| 9 | PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. <i>GigaScience</i> , 2019, 8, . | 6.4 | 152 |
| 10 | A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of <i>Campylobacter</i> . <i>Genes</i> , 2012, 3, 261-277. | 2.4 | 135 |
| 11 | Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451. | 3.9 | 131 |
| 12 | Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328. | 2.5 | 130 |
| 13 | Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064. | 3.9 | 128 |
| 14 | Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016, 10, 721-729. | 9.8 | 123 |
| 15 | A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic <i>Campylobacter</i> . <i>PLoS ONE</i> , 2014, 9, e92798. | 2.5 | 122 |
| 16 | The Evolution of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a018119. | 5.5 | 119 |
| 17 | Attribution of <i>Campylobacter</i> Infections in Northeast Scotland to Specific Sources by Use of Multilocus Sequence Typing. <i>Journal of Infectious Diseases</i> , 2009, 199, 1205-1208. | 4.0 | 117 |
| 18 | Host Association of <i>Campylobacter</i> Genotypes Transcends Geographic Variation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5269-5277. | 3.1 | 116 |

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|----|--|-------|-----------|
| 19 | Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034. | 12.8 | 115 |
| 20 | <i>Campylobacter</i> epidemiology: a descriptive study reviewing 1 million cases in England and Wales between 1989 and 2011. <i>BMJ Open</i> , 2012, 2, e001179. | 1.9 | 108 |
| 21 | Niche segregation and genetic structure of <i>Campylobacter jejuni</i> populations from wild and agricultural host species. <i>Molecular Ecology</i> , 2011, 20, 3484-3490. | 3.9 | 105 |
| 22 | The significance of facultative scavenging in generalist predator nutrition: detecting decayed prey in the guts of predators using PCR. <i>Molecular Ecology</i> , 2005, 14, 4147-4158. | 3.9 | 102 |
| 23 | Trends in fluoroquinolone resistance in <i>Campylobacter</i> . <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 100 |
| 24 | Environmental Factors Determining the Epidemiology and Population Genetic Structure of the <i>Bacillus cereus</i> Group in the Field. <i>PLoS Pathogens</i> , 2010, 6, e1000905. | 4.7 | 94 |
| 25 | <i>Campylobacter</i> infection of broiler chickens in a free-range environment. <i>Environmental Microbiology</i> , 2008, 10, 2042-2050. | 3.8 | 89 |
| 26 | Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , 2017, 19, 361-380. | 3.8 | 88 |
| 27 | Population-genomic insights into emergence, crop adaptation and dissemination of <i>Pseudomonas syringae</i> pathogens. <i>Microbial Genomics</i> , 2016, 2, e000089. | 2.0 | 88 |
| 28 | Genome-Wide Identification of Host-Segregating Epidemiological Markers for Source Attribution in <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 3.1 | 82 |
| 29 | <i>Campylobacter</i> Excreted into the Environment by Animal Sources: Prevalence, Concentration Shed, and Host Association. <i>Foodborne Pathogens and Disease</i> , 2009, 6, 1161-1170. | 1.8 | 81 |
| 30 | The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 121. | 3.5 | 80 |
| 31 | Enhanced biofilm formation and multi-host transmission evolve from divergent genetic backgrounds in <i>Campylobacter jejuni</i> . <i>Environmental Microbiology</i> , 2015, 17, 4779-4789. | 3.8 | 76 |
| 32 | Evolution of an Agriculture-Associated Disease Causing <i>Campylobacter coli</i> Clade: Evidence from National Surveillance Data in Scotland. <i>PLoS ONE</i> , 2010, 5, e15708. | 2.5 | 75 |
| 33 | Rapid evolution of distinct <i>Helicobacter pylori</i> subpopulations in the Americas. <i>PLoS Genetics</i> , 2017, 13, e1006546. | 3.5 | 73 |
| 34 | The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , 2016, 33, 456-471. | 8.9 | 72 |
| 35 | Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765. | 12.8 | 69 |
| 36 | <i>Campylobacter</i> populations in wild and domesticated Mallard ducks (<i>Anas platyrhynchos</i>). <i>PLoS ONE</i> , 2024, 19, e0318688. | 10.24 | 68 |

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|----|--|-----|-----------|
| 37 | Gene pool transmission of multidrug resistance among <i>Campylobacter</i> from livestock, sewage and human disease. <i>Environmental Microbiology</i> , 2019, 21, 4597-4613. | 3.8 | 68 |
| 38 | Efficient Inference of Recombination Hot Regions in Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1593-1605. | 8.9 | 62 |
| 39 | Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. <i>GigaScience</i> , 2018, 7, 1-11. | 6.4 | 59 |
| 40 | Variation in Siderophore Biosynthetic Gene Distribution and Production across Environmental and Faecal Populations of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0117906. | 2.5 | 58 |
| 41 | Widespread acquisition of antimicrobial resistance among <i>Campylobacter</i> isolates from UK retail poultry and evidence for clonal expansion of resistant lineages. <i>BMC Microbiology</i> , 2013, 13, 160. | 3.3 | 57 |
| 42 | Comparative Genomics Study of <i>Staphylococcus epidermidis</i> Isolates from Orthopedic-Device-Related Infections Correlated with Patient Outcome. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3089-3103. | 3.9 | 55 |
| 43 | A GWAS on <i>Helicobacter pylori</i> strains points to genetic variants associated with gastric cancer risk. <i>BMC Biology</i> , 2018, 16, 84. | 3.8 | 55 |
| 44 | Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260. | 2.9 | 51 |
| 45 | Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028. | 7.1 | 50 |
| 46 | Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016, 11, e0151240. | 2.5 | 49 |
| 47 | Introgression in the genus <i>Campylobacter</i> : generation and spread of mosaic alleles. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1066-1074. | 1.8 | 47 |
| 48 | Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842. | 2.5 | 46 |
| 49 | Prevalence and risk factors of <i>Campylobacter</i> infection in broiler flocks from southern Spain. <i>Preventive Veterinary Medicine</i> , 2014, 114, 106-113. | 1.9 | 43 |
| 50 | Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540. | 3.9 | 43 |
| 51 | Ruminant and chicken: important sources of campylobacteriosis in France despite a variation of source attribution in 2009 and 2015. <i>Scientific Reports</i> , 2018, 8, 9305. | 3.3 | 43 |
| 52 | Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. <i>Genome Biology</i> , 2018, 19, 94. | 8.8 | 43 |
| 53 | Molecular Evidence for the Thriving of <i>Campylobacter jejuni</i> ST-4526 in Japan. <i>PLoS ONE</i> , 2012, 7, e48394. | 2.5 | 42 |
| 54 | Elucidating the Aetiology of Human <i>Campylobacter coli</i> Infections. <i>PLoS ONE</i> , 2013, 8, e64504. | 2.5 | 40 |

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|----|--|-----|-----------|
| 55 | Effects of soil improvement treatments on bacterial community structure and soil processes in an upland grassland soil. <i>FEMS Microbiology Ecology</i> , 2003, 46, 11-22. | 2.7 | 38 |
| 56 | Genome Comparison of Erythromycin Resistant <i>Campylobacter</i> from Turkeys Identifies Hosts and Pathways for Horizontal Spread of <i>erm(B)</i> Genes. <i>Frontiers in Microbiology</i> , 2017, 8, 2240. | 3.5 | 38 |
| 57 | Temporal Variation and Host Association in the <i>Campylobacter</i> Population in a Longitudinal Ruminant Farm Study. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6579-6586. | 3.1 | 37 |
| 58 | Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017, 26, 4497-4508. | 3.9 | 36 |
| 59 | Molecular epidemiology and comparative genomics of <i>Campylobacter concisus</i> strains from saliva, faeces and gut mucosal biopsies in inflammatory bowel disease. <i>Scientific Reports</i> , 2018, 8, 1902. | 3.3 | 35 |
| 60 | Genomic structure and insertion sites of <i>Helicobacter pylori</i> prophages from various geographical origins. <i>Scientific Reports</i> , 2017, 7, 42471. | 3.3 | 34 |
| 61 | Genomic plasticity and rapid host switching can promote the evolution of generalism: a case study in the zoonotic pathogen <i>Campylobacter</i> . <i>Scientific Reports</i> , 2017, 7, 9650. | 3.3 | 34 |
| 62 | Spatiotemporal Homogeneity of <i>Campylobacter</i> Subtypes from Cattle and Sheep across Northeastern and Southwestern Scotland. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6275-6281. | 3.1 | 32 |
| 63 | Comparison of <i>Campylobacter</i> populations isolated from a free-range broiler flock before and after slaughter. <i>International Journal of Food Microbiology</i> , 2010, 137, 259-264. | 4.7 | 32 |
| 64 | Distinct Phenotypic and Genomic Signatures Underlie Contrasting Pathogenic Potential of <i>Staphylococcus epidermidis</i> Clonal Lineages. <i>Frontiers in Microbiology</i> , 2019, 10, 1971. | 3.5 | 32 |
| 65 | Source attribution of <i>Campylobacter jejuni</i> shows variable importance of chicken and ruminants reservoirs in non-invasive and invasive French clinical isolates. <i>Scientific Reports</i> , 2019, 9, 8098. | 3.3 | 31 |
| 66 | A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. <i>Genome Medicine</i> , 2014, 6, 101. | 8.2 | 30 |
| 67 | Next-generation microbiology: from comparative genomics to gene function. <i>Genome Biology</i> , 2021, 22, 123. | 8.8 | 29 |
| 68 | Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the <i>Campylobacter jejuni</i> Sequence Type 403 Clonal Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3641-3647. | 3.1 | 27 |
| 69 | A Proposal for a Genome Similarity-Based Taxonomy for Plant-Pathogenic Bacteria that Is Sufficiently Precise to Reflect Phylogeny, Host Range, and Outbreak Affiliation Applied to <i>Pseudomonas syringae sensu lato</i> as a Proof of Concept. <i>Phytopathology</i> , 2017, 107, 18-28. | 2.2 | 26 |
| 70 | Genome Reduction for Niche Association in <i>Campylobacter Hepaticus</i> , A Cause of Spotty Liver Disease in Poultry. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 354. | 3.9 | 26 |
| 71 | Prevalence of faecal carriage of extended-spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> in veterinary hospital staff and students. <i>Veterinary Record Open</i> , 2019, 6, e000307. | 1.0 | 26 |
| 72 | Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019, 5, . | 2.0 | 26 |

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|----|---|-----|-----------|
| 73 | Evidence of land-to-sea transfer of the zoonotic pathogen <i>Campylobacter</i> to a wildlife marine sentinel species. <i>Molecular Ecology</i> , 2015, 24, 208-221. | 3.9 | 25 |
| 74 | Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , 2016, 6, 38303. | 3.3 | 25 |
| 75 | Comparative Genomics of <i>Campylobacter fetus</i> from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2006-2019. | 2.5 | 25 |
| 76 | Genetic features of livestock-associated <i>Staphylococcus aureus</i> ST9 isolates from Chinese pigs that carry the <i>lsa(E)</i> gene for quinupristin/dalfopristin resistance. <i>International Journal of Medical Microbiology</i> , 2016, 306, 722-729. | 3.6 | 25 |
| 77 | Evidence for Phenotypic Plasticity among Multihost <i>Campylobacter jejuni</i> and <i>C. coli</i> Lineages, Obtained Using Ribosomal Multilocus Sequence Typing and Raman Spectroscopy. <i>Applied and Environmental Microbiology</i> , 2013, 79, 965-973. | 3.1 | 24 |
| 78 | <i>Campylobacter jejuni</i> genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021, 4, 1015. | 4.4 | 24 |
| 79 | A 500-year tale of co-evolution, adaptation, and virulence: <i>Helicobacter pylori</i> in the Americas. <i>ISME Journal</i> , 2021, 15, 78-92. | 9.8 | 23 |
| 80 | Genetic Diversity of Composite Enterotoxigenic <i>Staphylococcus epidermidis</i> Pathogenicity Islands. <i>Genome Biology and Evolution</i> , 2019, 11, 3498-3509. | 2.5 | 21 |
| 81 | Machine learning to predict the source of campylobacteriosis using whole genome data. <i>PLoS Genetics</i> , 2021, 17, e1009436. | 3.5 | 21 |
| 82 | From Escherich to the <i>Escherichia coli</i> genome. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 634-636. | 9.1 | 20 |
| 83 | Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533. | 3.0 | 20 |
| 84 | Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075. | 2.0 | 19 |
| 85 | The Potential of Isolation Source to Predict Colonization in Avian Hosts: A Case Study in <i>Campylobacter jejuni</i> Strains From Three Bird Species. <i>Frontiers in Microbiology</i> , 2018, 9, 591. | 3.5 | 18 |
| 86 | Operationalising Factors That Explain the Emergence of Infectious Diseases: A Case Study of the Human Campylobacteriosis Epidemic. <i>PLoS ONE</i> , 2013, 8, e79331. | 2.5 | 17 |
| 87 | Phasomelt: an omics™ approach to cataloguing the potential breadth of phase variation in the genus <i>Campylobacter</i> . <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 17 |
| 88 | Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, . | 6.0 | 17 |
| 89 | Stress resistance associated with multi-host transmission and enhanced biofilm formation at 42°C among hyper-aerotolerant generalist <i>Campylobacter jejuni</i> . <i>Food Microbiology</i> , 2021, 95, 103706. | 4.2 | 16 |
| 90 | Phylogenomic approaches to determine the zoonotic potential of Shiga toxin-producing <i>Escherichia coli</i> (STEC) isolated from Zambian dairy cattle. <i>Scientific Reports</i> , 2016, 6, 26589. | 3.3 | 15 |

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|-----|--|-----|-----------|
| 91 | Core genome sequence analysis to characterize <i>Salmonella enterica</i> serovar Rissen ST469 from a swine production chain. <i>International Journal of Food Microbiology</i> , 2019, 304, 68-74. | 4.7 | 15 |
| 92 | Genome-Wide Identification of Host-Segregating Single-Nucleotide Polymorphisms for Source Attribution of Clinical <i>Campylobacter coli</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2020, 86, . | 3.1 | 15 |
| 93 | Genomic epidemiology of clinical <i>Campylobacter</i> spp. at a single health trust site. <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 15 |
| 94 | High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 0, 5, 14. | 1.8 | 14 |
| 95 | Large Sequence Diversity within the Biosynthesis Locus and Common Biochemical Features of <i>Campylobacter coli</i> Lipooligosaccharides. <i>Journal of Bacteriology</i> , 2016, 198, 2829-2840. | 2.2 | 13 |
| 96 | The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62. | 1.7 | 13 |
| 97 | High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14. | 1.8 | 13 |
| 98 | Whole-genome characterisation of multidrug resistant monophasic variants of <i>Salmonella</i> Typhimurium from pig production in Thailand. <i>PeerJ</i> , 0, 8, e9700. | 2.0 | 13 |
| 99 | Identification and initial characterisation of a protein involved in <i>Campylobacter jejuni</i> cell shape. <i>Microbial Pathogenesis</i> , 2017, 104, 202-211. | 2.9 | 12 |
| 100 | Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774. | 2.5 | 12 |
| 101 | Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. <i>PLoS Genetics</i> , 2021, 17, e1009829. | 3.5 | 11 |
| 102 | Comparative genomic survey of <i>Bacillus cereus</i> sensu stricto isolates from the dairy production chain in Brazil. <i>FEMS Microbiology Letters</i> , 2018, 365, . | 1.8 | 10 |
| 103 | Where Does <i>Campylobacter</i> Come From? A Molecular Odyssey. <i>Advances in Experimental Medicine and Biology</i> , 2010, 659, 47-56. | 1.6 | 10 |
| 104 | Determining the prevalence, identity and possible origin of bacterial pathogens in soil. <i>Environmental Microbiology</i> , 2020, 22, 5327-5340. | 3.8 | 9 |
| 105 | Strain wars and the evolution of opportunistic pathogens. <i>Current Opinion in Microbiology</i> , 2022, 67, 102138. | 5.1 | 9 |
| 106 | Impacts of Antibiotic Residues in the Environment on Bacterial Resistance and Human Health in Eastern China: An Interdisciplinary Mixed-Methods Study Protocol. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8145. | 2.6 | 8 |
| 107 | Phage Predation Shapes the Population Structure of Shiga-Toxigenic <i>Escherichia coli</i> O157:H7 in the UK: An Evolutionary Perspective. <i>Frontiers in Genetics</i> , 2019, 10, 763. | 2.3 | 7 |
| 108 | The emergence of plasmid-borne cfr-mediated linezolid resistant-staphylococci in Vietnam. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 462-465. | 2.2 | 7 |

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|-----|--|------|-----------|
| 109 | Genome-wide association study of signature genetic alterations among pseudomonas aeruginosa cystic fibrosis isolates. PLoS Pathogens, 2021, 17, e1009681. | 4.7 | 7 |
| 110 | Characterisation of Salmonella enterica clones carrying mcr-1 plasmids in meat products and patients in Northern Thailand using long read sequencing. International Journal of Food Microbiology, 2021, 358, 109314. | 4.7 | 7 |
| 111 | Characterization of nasal methicillin-resistant Staphylococcus aureus isolated from international human and veterinary surgeons. Journal of Medical Microbiology, 2017, 66, 360-370. | 1.8 | 5 |
| 112 | Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria – A Novel Biochemical Workflow. Frontiers in Microbiology, 2021, 12, 562157. | 3.5 | 4 |
| 113 | Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among <i>Bacillus cereus</i> clades. Molecular Ecology, 2022, 31, 3584-3597. | 3.9 | 4 |
| 114 | Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. Water Research, 2022, 217, 118415. | 11.3 | 3 |
| 115 | Local accessory gene sharing among Egyptian Campylobacter potentially promotes the spread of antimicrobial resistance. Microbial Genomics, 2022, 8, . | 2.0 | 3 |
| 116 | Addressing parachute research and removing barriers for LMIC researchers in Microbial Genomics. Microbial Genomics, 2021, 7, . | 2.0 | 2 |
| 117 | Draft Genome Sequence of an Enterobacter Species Associated with Illnesses and Powdered Infant Formula. Genome Announcements, 2016, 4, . | 0.8 | 1 |
| 118 | High Resolution Whole Genome Multilocus Sequence Typing (wgMLST) Schemes for Salmonella enterica Weltevreden Epidemiologic Investigations. Microbiology and Biotechnology Letters, 2018, 46, 162-170. | 0.4 | 1 |