

Vaughn S Cooper

List of Publications by Year in descending order

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116
papers

5,397
citations

109137

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123241

61
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169
all docs

169
docs citations

169
times ranked

6175
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The population genetics of ecological specialization in evolving <i>Escherichia coli</i> populations. <i>Nature</i> , 2000, 407, 736-739. | 13.7 | 447 |
| 2 | Mechanisms Causing Rapid and Parallel Losses of Ribose Catabolism in Evolving Populations of <i>Escherichia coli</i> B. <i>Journal of Bacteriology</i> , 2001, 183, 2834-2841. | 1.0 | 260 |
| 3 | Ceftolozane-Tazobactam for the Treatment of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Infections: Clinical Effectiveness and Evolution of Resistance. <i>Clinical Infectious Diseases</i> , 2017, 65, 110-120. | 2.9 | 224 |
| 4 | Tangled bank of experimentally evolved <i>Burkholderia</i> biofilms reflects selection during chronic infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E250-9. | 3.3 | 183 |
| 5 | Ecological succession in long-term experimentally evolved biofilms produces synergistic communities. <i>ISME Journal</i> , 2011, 5, 369-378. | 4.4 | 151 |
| 6 | EVOLUTION OF THERMAL DEPENDENCE OF GROWTH RATE OF <i>ESCHERICHIA COLI</i> POPULATIONS DURING 20,000 GENERATIONS IN A CONSTANT ENVIRONMENT. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 889. | 1.1 | 144 |
| 7 | Phylogenomic Study of <i>Burkholderia glathei</i> -like Organisms, Proposal of 13 Novel <i>Burkholderia</i> Species and Emended Descriptions of <i>Burkholderia sordidicola</i> , <i>Burkholderia zhejiangensis</i> , and <i>Burkholderia grimmiae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 877. | 1.5 | 120 |
| 8 | TRADEOFF BETWEEN HORIZONTAL AND VERTICAL MODES OF TRANSMISSION IN BACTERIAL PLASMIDS. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 315-329. | 1.1 | 120 |
| 9 | Evolutionary pathways to antibiotic resistance are dependent upon environmental structure and bacterial lifestyle. <i>ELife</i> , 2019, 8, . | 2.8 | 115 |
| 10 | Role of bacterial motility in differential resistance mechanisms of silver nanoparticles and silver ions. <i>Nature Nanotechnology</i> , 2021, 16, 996-1003. | 15.6 | 112 |
| 11 | Why Genes Evolve Faster on Secondary Chromosomes in Bacteria. <i>PLoS Computational Biology</i> , 2010, 6, e1000732. | 1.5 | 97 |
| 12 | The Environment Affects Epistatic Interactions to Alter the Topology of an Empirical Fitness Landscape. <i>PLoS Genetics</i> , 2013, 9, e1003426. | 1.5 | 94 |
| 13 | Long-Term Evolution of <i>Burkholderia multivorans</i> during a Chronic Cystic Fibrosis Infection Reveals Shifting Forces of Selection. <i>MSystems</i> , 2016, 1, . | 1.7 | 93 |
| 14 | Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2583-2591. | 0.8 | 89 |
| 15 | Experimental Evolution as a High-Throughput Screen for Genetic Adaptations. <i>MSphere</i> , 2018, 3, . | 1.3 | 88 |
| 16 | Systematic detection of horizontal gene transfer across genera among multidrug-resistant bacteria in a single hospital. <i>ELife</i> , 2020, 9, . | 2.8 | 85 |
| 17 | Genome-Wide Biases in the Rate and Molecular Spectrum of Spontaneous Mutations in <i>Vibrio cholerae</i> and <i>Vibrio fischeri</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 93-109. | 3.5 | 81 |
| 18 | Synonymous mutations make dramatic contributions to fitness when growth is limited by a weak-link enzyme. <i>PLoS Genetics</i> , 2018, 14, e1007615. | 1.5 | 77 |

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|----|---|-----|-----------|
| 19 | The Rate and Molecular Spectrum of Spontaneous Mutations in the GC-Rich Multichromosome Genome of <i>Burkholderia cenocepacia</i> . <i>Genetics</i> , 2015, 200, 935-946. | 1.2 | 75 |
| 20 | Genome-wide analysis of influenza viral RNA and nucleoprotein association. <i>Nucleic Acids Research</i> , 2017, 45, 8968-8977. | 6.5 | 75 |
| 21 | Evolution of Ecological Diversity in Biofilms of <i>Pseudomonas aeruginosa</i> by Altered Cyclic Diguanylate Signaling. <i>Journal of Bacteriology</i> , 2016, 198, 2608-2618. | 1.0 | 74 |
| 22 | RelA Mutant <i>Enterococcus faecium</i> with Multiantibiotic Tolerance Arising in an Immunocompromised Host. <i>MBio</i> , 2017, 8, . | 1.8 | 72 |
| 23 | Laboratory Evolution of Microbial Interactions in Bacterial Biofilms. <i>Journal of Bacteriology</i> , 2016, 198, 2564-2571. | 1.0 | 69 |
| 24 | Evolution of Outbreak-Causing Carbapenem-Resistant <i>Klebsiella pneumoniae</i> ST258 at a Tertiary Care Hospital over 8 Years. <i>MBio</i> , 2019, 10, . | 1.8 | 66 |
| 25 | Parallel genetic adaptation across environments differing in mode of growth or resource availability. <i>Evolution Letters</i> , 2018, 2, 355-367. | 1.6 | 62 |
| 26 | Genetic requirements for <i>Staphylococcus aureus</i> nitric oxide resistance and virulence. <i>PLoS Pathogens</i> , 2018, 14, e1006907. | 2.1 | 62 |
| 27 | Structural modification of LPS in colistin-resistant, KPC-producing <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 3035-3042. | 1.3 | 59 |
| 28 | Parallel Evolution of Tobramycin Resistance across Species and Environments. <i>MBio</i> , 2020, 11, . | 1.8 | 59 |
| 29 | Genomic and Chemical Diversity of <i>Bacillus subtilis</i> Secondary Metabolites against Plant Pathogenic Fungi. <i>MSystems</i> , 2021, 6, . | 1.7 | 55 |
| 30 | Mapping of Influenza Virus RNA-RNA Interactions Reveals a Flexible Network. <i>Cell Reports</i> , 2020, 31, 107823. | 2.9 | 50 |
| 31 | Glutathione-S-transferase FosA6 of <i>Klebsiella pneumoniae</i> origin conferring fosfomycin resistance in ESBL-producing <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2460-2465. | 1.3 | 49 |
| 32 | Rapid phenotypic change and diversification of a soil bacterium during 1000 generations of experimental evolution. <i>Microbiology (United Kingdom)</i> , 2001, 147, 995-1006. | 0.7 | 48 |
| 33 | Parallel evolution of small colony variants in <i>Burkholderia cenocepacia</i> biofilms. <i>Genomics</i> , 2014, 104, 447-452. | 1.3 | 47 |
| 34 | Timing of transmission and the evolution of virulence of an insect virus. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1161-1165. | 1.2 | 46 |
| 35 | Outbreak of Vancomycin-resistant <i>Enterococcus faecium</i> in Interventional Radiology: Detection Through Whole-genome Sequencing-based Surveillance. <i>Clinical Infectious Diseases</i> , 2020, 70, 2336-2343. | 2.9 | 43 |
| 36 | Whole-Genome Sequencing Surveillance and Machine Learning of the Electronic Health Record for Enhanced Healthcare Outbreak Detection. <i>Clinical Infectious Diseases</i> , 2022, 75, 476-482. | 2.9 | 42 |

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|----|---|------|-----------|
| 37 | Benefit of transferred mutations is better predicted by the fitness of recipients than by their ecological or genetic relatedness. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5047-5052. | 3.3 | 41 |
| 38 | Phylogenomics of colistin-susceptible and resistant XDR <i>Acinetobacter baumannii</i> . Journal of Antimicrobial Chemotherapy, 2018, 73, 2952-2959. | 1.3 | 41 |
| 39 | Genetic characterization of clinical and environmental <i>Vibrio parahaemolyticus</i> from the Northeast USA reveals emerging resident and non-indigenous pathogen lineages. Frontiers in Microbiology, 2015, 6, 272. | 1.5 | 40 |
| 40 | Host-selected mutations converging on a global regulator drive an adaptive leap towards symbiosis in bacteria. ELife, 2017, 6, . | 2.8 | 40 |
| 41 | Antibiotic resistance correlates with transmission in plasmid evolution. Evolution; International Journal of Organic Evolution, 2014, 68, 3368-3380. | 1.1 | 39 |
| 42 | Character displacement and the evolution of niche complementarity in a model biofilm community. Evolution; International Journal of Organic Evolution, 2015, 69, 283-293. | 1.1 | 39 |
| 43 | <i>Pseudomonas aeruginosa</i> Interstrain Dynamics and Selection of Hyperbiofilm Mutants during a Chronic Infection. MBio, 2019, 10, . | 1.8 | 39 |
| 44 | <span style="font-size=" font-size. Virulence, 2011, 2, 158-161. | 1.8 | 37 |
| 45 | Thrombospondin-1 protects against pathogen-induced lung injury by limiting extracellular matrix proteolysis. JCI Insight, 2018, 3, . | 2.3 | 36 |
| 46 | Ecology and Genetic Structure of a Northern Temperate <i>Vibrio cholerae</i> Population Related to Toxicogenic Isolates. Applied and Environmental Microbiology, 2011, 77, 7568-7575. | 1.4 | 32 |
| 47 | Frequency and Mechanisms of Spontaneous Fosfomycin Nonsusceptibility Observed upon Disk Diffusion Testing of <i>Escherichia coli</i> . Journal of Clinical Microbiology, 2018, 56, . | 1.8 | 32 |
| 48 | Influence of Seasonality on the Genetic Diversity of <i>Vibrio parahaemolyticus</i> in New Hampshire Shellfish Waters as Determined by Multilocus Sequence Analysis. Applied and Environmental Microbiology, 2012, 78, 3778-3782. | 1.4 | 31 |
| 49 | <i>In Vitro</i> Susceptibility of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> following Treatment-Emergent Resistance to Ceftolozane-Tazobactam. Antimicrobial Agents and Chemotherapy, 2021, 65, . | 1.4 | 31 |
| 50 | Emergence of an early SARS-CoV-2 epidemic in the United States. Cell, 2021, 184, 4939-4952.e15. | 13.5 | 31 |
| 51 | Environmental Conditions Associated with Elevated <i>Vibrio parahaemolyticus</i> Concentrations in Great Bay Estuary, New Hampshire. PLoS ONE, 2016, 11, e0155018. | 1.1 | 31 |
| 52 | Periodic Variation of Mutation Rates in Bacterial Genomes Associated with Replication Timing. MBio, 2018, 9, . | 1.8 | 30 |
| 53 | Long-term experimental evolution in <i>Escherichia coli</i> . X. Quantifying the fundamental and realized niche. BMC Evolutionary Biology, 2002, 2, 12. | 3.2 | 29 |
| 54 | Evolutionary Rates and Gene Dispensability Associate with Replication Timing in the Archaeon <i>Sulfolobus islandicus</i> . Genome Biology and Evolution, 2010, 2, 859-869. | 1.1 | 29 |

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|----|--|-----|-----------|
| 55 | New Insights from Elucidating the Role of LMP1 in Nasopharyngeal Carcinoma. <i>Cancers</i> , 2018, 10, 86. | 1.7 | 29 |
| 56 | Evolutionary Effects of Translocations in Bacterial Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 1256-1262. | 1.1 | 28 |
| 57 | Diverse phenotypic and genetic responses to short-term selection in evolving <i>Escherichia coli</i> populations. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 586-599. | 1.1 | 28 |
| 58 | Environment changes epistasis to alter trade-offs along alternative evolutionary paths. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2094-2105. | 1.1 | 28 |
| 59 | Genome sequence and comparative analysis of a putative entomopathogenic <i>Serratia</i> isolated from <i>Caenorhabditis briggsae</i> . <i>BMC Genomics</i> , 2015, 16, 531. | 1.2 | 27 |
| 60 | Parallel Evolution of Two Clades of an Atlantic-Endemic Pathogenic Lineage of <i>Vibrio parahaemolyticus</i> by Independent Acquisition of Related Pathogenicity Islands. <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 1.4 | 27 |
| 61 | Carbapenem-Resistant <i>Acinetobacter baumannii</i> in U.S. Hospitals: Diversification of Circulating Lineages and Antimicrobial Resistance. <i>MBio</i> , 2022, 13, e0275921. | 1.8 | 27 |
| 62 | Experimental Adaptation of <i>Burkholderia cenocepacia</i> to Onion Medium Reduces Host Range. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2387-2396. | 1.4 | 26 |
| 63 | There and back again: consequences of biofilm specialization under selection for dispersal. <i>Frontiers in Genetics</i> , 2015, 6, 18. | 1.1 | 26 |
| 64 | Outbreak of <i>Pseudomonas aeruginosa</i> Infections from a Contaminated Gastroscope Detected by Whole Genome Sequencing Surveillance. <i>Clinical Infectious Diseases</i> , 2021, 73, e638-e642. | 2.9 | 26 |
| 65 | Non-Uniform and Non-Random Binding of Nucleoprotein to Influenza A and B Viral RNA. <i>Viruses</i> , 2018, 10, 522. | 1.5 | 25 |
| 66 | Susceptibility of <i>Caenorhabditis elegans</i> to <i>Burkholderia</i> Infection Depends on Prior Diet and Secreted Bacterial Attractants. <i>PLoS ONE</i> , 2009, 4, e7961. | 1.1 | 25 |
| 67 | Sequence Type 631 <i>Vibrio parahaemolyticus</i> , an Emerging Foodborne Pathogen in North America. <i>Journal of Clinical Microbiology</i> , 2017, 55, 645-648. | 1.8 | 23 |
| 68 | High-Level Fosfomycin Resistance in Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>Emerging Infectious Diseases</i> , 2017, 23, 1902-1904. | 2.0 | 23 |
| 69 | Structural basis of DSF recognition by its receptor RpfR and its regulatory interaction with the DSF synthase RpfF. <i>PLoS Biology</i> , 2019, 17, e3000123. | 2.6 | 23 |
| 70 | Hidden resources in the <i>Escherichia coli</i> genome restore PLP synthesis and robust growth after deletion of the essential gene <i>pdxB</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24164-24173. | 3.3 | 23 |
| 71 | The Origins of Specialization: Insights from Bacteria Held 25 Years in Captivity. <i>PLoS Biology</i> , 2014, 12, e1001790. | 2.6 | 22 |
| 72 | The Fitness Effects of Spontaneous Mutations Nearly Unseen by Selection in a Bacterium with Multiple Chromosomes. <i>Genetics</i> , 2016, 204, 1225-1238. | 1.2 | 22 |

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|----|--|-----|-----------|
| 73 | Forecasting Seasonal <i>Vibrio parahaemolyticus</i> Concentrations in New England Shellfish. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 4341. | 1.2 | 22 |
| 74 | Use of Whole-Genome Phylogeny and Comparisons for Development of a Multiplex PCR Assay To Identify Sequence Type 36 <i>Vibrio parahaemolyticus</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 1864-1872. | 1.8 | 21 |
| 75 | Outbreak of <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>Citrobacter freundii</i> at a Tertiary Acute Care Facility in Miami, Florida. <i>Infection Control and Hospital Epidemiology</i> , 2017, 38, 320-326. | 1.0 | 21 |
| 76 | NADH Dehydrogenases in <i>Pseudomonas aeruginosa</i> Growth and Virulence. <i>Frontiers in Microbiology</i> , 2019, 10, 75. | 1.5 | 20 |
| 77 | Polygenic Adaptation and Clonal Interference Enable Sustained Diversity in Experimental <i>Pseudomonas aeruginosa</i> Populations. <i>Molecular Biology and Evolution</i> , 2021, 38, 5359-5375. | 3.5 | 20 |
| 78 | The roles of history, chance, and natural selection in the evolution of antibiotic resistance. <i>ELife</i> , 2021, 10, . | 2.8 | 20 |
| 79 | Breaking the language barrier: experimental evolution of non-native <i>Vibrio fischeri</i> in squid tailors luminescence to the host. <i>Symbiosis</i> , 2010, 51, 85-96. | 1.2 | 19 |
| 80 | Structure of O-Antigen and Hybrid Biosynthetic Locus in <i>Burkholderia cenocepacia</i> Clonal Variants Recovered from a Cystic Fibrosis Patient. <i>Frontiers in Microbiology</i> , 2017, 8, 1027. | 1.5 | 19 |
| 81 | Adaptation and genomic erosion in fragmented <i>Pseudomonas aeruginosa</i> populations in the sinuses of people with cystic fibrosis. <i>Cell Reports</i> , 2021, 37, 109829. | 2.9 | 19 |
| 82 | One gene, multiple ecological strategies: A biofilm regulator is a capacitor for sustainable diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21647-21657. | 3.3 | 18 |
| 83 | Experimental Evolution <i>In Vivo</i> To Identify Selective Pressures during Pneumococcal Colonization. <i>MSystems</i> , 2020, 5, . | 1.7 | 18 |
| 84 | Quorum sensing provides a molecular mechanism for evolution to tune and maintain investment in cooperation. <i>ISME Journal</i> , 2021, 15, 1236-1247. | 4.4 | 18 |
| 85 | Use of online tools for antimicrobial resistance prediction by whole-genome sequencing in methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) and vancomycin-resistant enterococci (VRE). <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 136-143. | 0.9 | 17 |
| 86 | Comparative genomics of <i>Burkholderia multivorans</i> , a ubiquitous pathogen with a highly conserved genomic structure. <i>PLoS ONE</i> , 2017, 12, e0176191. | 1.1 | 17 |
| 87 | Mutations that improve efficiency of a weak-link enzyme are rare compared to adaptive mutations elsewhere in the genome. <i>ELife</i> , 2019, 8, . | 2.8 | 17 |
| 88 | Immunosuppression broadens evolutionary pathways to drug resistance and treatment failure during <i>Acinetobacter baumannii</i> pneumonia in mice. <i>Nature Microbiology</i> , 2022, 7, 796-809. | 5.9 | 17 |
| 89 | Expression of myeloid Src-family kinases is associated with poor prognosis in AML and influences Flt3-ITD kinase inhibitor acquired resistance. <i>PLoS ONE</i> , 2019, 14, e0225887. | 1.1 | 16 |
| 90 | The OmpR Regulator of <i>Burkholderia multivorans</i> Controls Mucoicid-to-Nonmucoicid Transition and Other Cell Envelope Properties Associated with Persistence in the Cystic Fibrosis Lung. <i>Journal of Bacteriology</i> , 2018, 200, . | 1.0 | 15 |

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|-----|--|-----|-----------|
| 91 | Adaptation and Survival of <i>Burkholderia cepacia</i> and <i>B. contaminans</i> During Long-Term Incubation in Saline Solutions Containing Benzalkonium Chloride. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 630. | 2.0 | 14 |
| 92 | Rampant prophage movement among transient competitors drives rapid adaptation during infection. <i>Science Advances</i> , 2021, 7, . | 4.7 | 14 |
| 93 | <i>Clostridioides difficile</i> : a potential source of NpmA in the clinical environment. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 521-523. | 1.3 | 13 |
| 94 | Negative frequency-dependent selection maintains coexisting genotypes during fluctuating selection. <i>Molecular Ecology</i> , 2020, 29, 138-148. | 2.0 | 13 |
| 95 | Complete Genome Sequences of 13 <i>Bacillus subtilis</i> Soil Isolates for Studying Secondary Metabolite Diversity. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.3 | 13 |
| 96 | Characterization of a Novel IncHI2 Plasmid Carrying Tandem Copies of <i>bla</i> CTX-M-2 in a <i>fosA6</i> -Harboring <i>Escherichia coli</i> Sequence Type 410 Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6742-6747. | 1.4 | 12 |
| 97 | A method of processing nasopharyngeal swabs to enable multiple testing. <i>Pediatric Research</i> , 2019, 86, 651-654. | 1.1 | 12 |
| 98 | High-Level Carbapenem Resistance in OXA-232-Producing <i>Raoultella ornithinolytica</i> Triggered by Ertapenem Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 64, . | 1.4 | 11 |
| 99 | Genomic Diversity of Hospital-Acquired Infections Revealed through Prospective Whole-Genome Sequencing-Based Surveillance. <i>MSystems</i> , 2022, 7, . | 1.7 | 10 |
| 100 | EVOLUTION OF THERMAL DEPENDENCE OF GROWTH RATE OF <i>ESCHERICHIA COLI</i> POPULATIONS DURING 20,000 GENERATIONS IN A CONSTANT ENVIRONMENT. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 889-896. | 1.1 | 9 |
| 101 | Evolutionary Divergence of the Wsp Signal Transduction Systems in Beta- and Gammaproteobacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0130621. | 1.4 | 9 |
| 102 | The Nutritional Environment Is Sufficient To Select Coexisting Biofilm and Quorum Sensing Mutants of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2022, 204, JB0044421. | 1.0 | 8 |
| 103 | EvolvingSTEM: a microbial evolution-in-action curriculum that enhances learning of evolutionary biology and biotechnology. <i>Evolution: Education and Outreach</i> , 2019, 12, 12. | 0.3 | 7 |
| 104 | Comparative Evolutionary Patterns of <i>Burkholderia cenocepacia</i> and <i>B. multivorans</i> During Chronic Co-infection of a Cystic Fibrosis Patient Lung. <i>Frontiers in Microbiology</i> , 2020, 11, 574626. | 1.5 | 7 |
| 105 | <i>Staphylococcus aureus</i> genotype variation among and within periprosthetic joint infections. <i>Journal of Orthopaedic Research</i> , 2022, 40, 420-428. | 1.2 | 7 |
| 106 | Quantitative mapping of mRNA 3' ends in <i>Pseudomonas aeruginosa</i> reveals a pervasive role for premature 3' end formation in response to azithromycin. <i>PLoS Genetics</i> , 2021, 17, e1009634. | 1.5 | 7 |
| 107 | Improved Detection of Culprit Pathogens by Bacterial DNA Sequencing Affects Antibiotic Management Decisions in Severe Pneumonia. <i>American Journal of Case Reports</i> , 2018, 19, 1405-1409. | 0.3 | 5 |
| 108 | Use of a cohorting-unit and systematic surveillance cultures to control a <i>Klebsiella pneumoniae</i> carbapenemase (KPC)-producing Enterobacteriaceae outbreak. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 767-773. | 1.0 | 5 |

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|-----|---|-----|-----------|
| 109 | Evolved resistance to a novel cationic peptide antibiotic requires high mutation supply. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 266-276. | 1.1 | 5 |
| 110 | SprayNPray: user-friendly taxonomic profiling of genome and metagenome contigs. <i>BMC Genomics</i> , 2022, 23, 202. | 1.2 | 4 |
| 111 | Reduced ceftazidime and ertapenem susceptibility due to production of OXA-2 in <i>Klebsiella pneumoniae</i> ST258. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2203-2208. | 1.3 | 3 |
| 112 | Evolution towards Virulence in a <i>Burkholderia</i> Two-Component System. <i>MBio</i> , 2021, 12, e0182321. | 1.8 | 3 |
| 113 | The Study of Microbial Adaptation by Long-Term Experimental Evolution. , 0, , 55-81. | | 2 |
| 114 | Precise measurement of the fitness effects of spontaneous mutations by droplet digital PCR in <i>Burkholderia cenocepacia</i> . <i>Genetics</i> , 2021, 219, . | 1.2 | 1 |
| 115 | Experimental Evolution of Pathogens. , 0, , 215-224. | | 0 |
| 116 | Full characterization of plasmids from <i>Achromobacter ruhlandii</i> isolates recovered from a single patient with cystic fibrosis (CF). <i>Revista Argentina De Microbiologia</i> , 2021, , . | 0.4 | 0 |