

Vaughn S Cooper

List of Publications by Year in descending order

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126
papers

5,747
citations

85075

36
h-index

97596

63
g-index

202
all docs

202
docs citations

202
times ranked

6554
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.	35.3	451
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.	2.3	264
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.	5.6	234
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.	7.4	185
5	Ecological succession in long-term experimentally evolved biofilms produces synergistic communities. <i>ISME Journal</i> , 2011, 5, 369-378.	9.8	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.	2.2	144
7	Role of bacterial motility in differential resistance mechanisms of silver nanoparticles and silver ions. <i>Nature Nanotechnology</i> , 2021, 16, 996-1003.	29.6	132
8	Evolutionary pathways to antibiotic resistance are dependent upon environmental structure and bacterial lifestyle. <i>ELife</i> , 2019, 8, .	5.8	127
9	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.	3.5	123
10	TRADEOFF BETWEEN HORIZONTAL AND VERTICAL MODES OF TRANSMISSION IN BACTERIAL PLASMIDS. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 315-329.	2.2	123
11	Why Genes Evolve Faster on Secondary Chromosomes in Bacteria. <i>PLoS Computational Biology</i> , 2010, 6, e1000732.	3.0	98
12	The Environment Affects Epistatic Interactions to Alter the Topology of an Empirical Fitness Landscape. <i>PLoS Genetics</i> , 2013, 9, e1003426.	3.3	98
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, .	3.9	94
14	Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2583-2591.	1.9	94
15	Systematic detection of horizontal gene transfer across genera among multidrug-resistant bacteria in a single hospital. <i>ELife</i> , 2020, 9, .	5.8	93
16	Experimental Evolution as a High-Throughput Screen for Genetic Adaptations. <i>MSphere</i> , 2018, 3, .	3.1	92
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.	9.0	85
18	Synonymous mutations make dramatic contributions to fitness when growth is limited by a weak-link enzyme. <i>PLoS Genetics</i> , 2018, 14, e1007615.	3.3	83

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19	RelA Mutant <i>Enterococcus faecium</i> with Multiantibiotic Tolerance Arising in an Immunocompromised Host. <i>MBio</i> , 2017, 8, .	4.2	80
20	Genome-wide analysis of influenza viral RNA and nucleoprotein association. <i>Nucleic Acids Research</i> , 2017, 45, 8968-8977.	13.8	80
21	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.	2.9	78
22	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.	2.3	75
23	Laboratory Evolution of Microbial Interactions in Bacterial Biofilms. <i>Journal of Bacteriology</i> , 2016, 198, 2564-2571.	2.3	73
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, .	4.2	72
25	Genetic requirements for <i>Staphylococcus aureus</i> nitric oxide resistance and virulence. <i>PLoS Pathogens</i> , 2018, 14, e1006907.	4.0	68
26	Parallel Evolution of Tobramycin Resistance across Species and Environments. <i>MBio</i> , 2020, 11, .	4.2	67
27	Parallel genetic adaptation across environments differing in mode of growth or resource availability. <i>Evolution Letters</i> , 2018, 2, 355-367.	3.2	66
28	Genomic and Chemical Diversity of <i>Bacillus subtilis</i> Secondary Metabolites against Plant Pathogenic Fungi. <i>MSystems</i> , 2021, 6, .	3.9	66
29	Structural modification of LPS in colistin-resistant, KPC-producing <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 3035-3042.	3.1	63
30	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.	5.6	52
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.	3.1	51
32	Mapping of Influenza Virus RNA-RNA Interactions Reveals a Flexible Network. <i>Cell Reports</i> , 2020, 31, 107823.	6.2	51
33	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.	5.6	48
34	Rapid phenotypic change and diversification of a soil bacterium during 1000 generations of experimental evolution. <i>Microbiology (United Kingdom)</i> , 2001, 147, 995-1006.	1.7	48
35	Antibiotic resistance correlates with transmission in plasmid evolution. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3368-3380.	2.2	47
36	Parallel evolution of small colony variants in <i>Burkholderia cenocepacia</i> biofilms. <i>Genomics</i> , 2014, 104, 447-452.	2.9	47

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37	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.	2.7	46
38	Benefit of transferred mutations is better predicted by the fitness of recipients than by their ecological or genetic relatedness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5047-5052.	7.4	44
39	Phylogenomics of colistin-susceptible and resistant XDR <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2952-2959.	3.1	42
40	Genetic characterization of clinical and environmental <i>Vibrio parahaemolyticus</i> from the Northeast USA reveals emerging resident and non-indigenous pathogen lineages. <i>Frontiers in Microbiology</i> , 2015, 6, 272.	3.5	41
41	<i>Pseudomonas aeruginosa</i> Interstrain Dynamics and Selection of Hyperbiofilm Mutants during a Chronic Infection. <i>MBio</i> , 2019, 10, .	4.2	41
42	Character displacement and the evolution of niche complementarity in a model biofilm community. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 283-293.	2.2	40
43	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	27.3	39
44	Thrombospondin-1 protects against pathogen-induced lung injury by limiting extracellular matrix proteolysis. <i>Journal of Clinical Investigation</i> , 2018, 3, .	6.5	39
45	<i>In Vitro</i> Susceptibility of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> following Treatment-Emergent Resistance to Ceftolozane-Tazobactam. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.3	37
46	Carbapenem-Resistant <i>Acinetobacter baumannii</i> in U.S. Hospitals: Diversification of Circulating Lineages and Antimicrobial Resistance. <i>MBio</i> , 2022, 13, e0275921.	4.2	37
47	Environmental Conditions Associated with Elevated <i>Vibrio parahaemolyticus</i> Concentrations in Great Bay Estuary, New Hampshire. <i>PLoS ONE</i> , 2016, 11, e0155018.	2.5	35
48	Frequency and Mechanisms of Spontaneous Fosfomycin Nonsusceptibility Observed upon Disk Diffusion Testing of <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	4.3	34
49	Ecology and Genetic Structure of a Northern Temperate <i>Vibrio cholerae</i> Population Related to Toxicogenic Isolates. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7568-7575.	3.1	33
50	Influence of Seasonality on the Genetic Diversity of <i>Vibrio parahaemolyticus</i> in New Hampshire Shellfish Waters as Determined by Multilocus Sequence Analysis. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3778-3782.	3.1	31
51	Periodic Variation of Mutation Rates in Bacterial Genomes Associated with Replication Timing. <i>MBio</i> , 2018, 9, .	4.2	31
52	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.	5.6	31
53	New Insights from Elucidating the Role of LMP1 in Nasopharyngeal Carcinoma. <i>Cancers</i> , 2018, 10, 86.	3.8	30
54	Long-term experimental evolution in <i>Escherichia coli</i> . X. Quantifying the fundamental and realized niche. <i>BMC Evolutionary Biology</i> , 2002, 2, 12.	3.1	29

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55	Evolutionary Rates and Gene Dispensability Associate with Replication Timing in the Archaeon <i>Sulfolobus islandicus</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 859-869.	2.6	29
56	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, .	3.1	29
57	Environment changes epistasis to alter tradeoffs along alternative evolutionary paths. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2094-2105.	2.2	29
58	Evolutionary Effects of Translocations in Bacterial Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 1256-1262.	2.6	28
59	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.	2.2	28
60	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.	2.9	27
61	Experimental Adaptation of <i>Burkholderia cenocepacia</i> to Onion Medium Reduces Host Range. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2387-2396.	3.1	26
62	There and back again: consequences of biofilm specialization under selection for dispersal. <i>Frontiers in Genetics</i> , 2015, 6, 18.	2.3	26
63	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.	5.3	26
64	Sequence Type 631 <i>Vibrio parahaemolyticus</i> , an Emerging Foodborne Pathogen in North America. <i>Journal of Clinical Microbiology</i> , 2017, 55, 645-648.	4.3	25
65	Non-Uniform and Non-Random Binding of Nucleoprotein to Influenza A and B Viral RNA. <i>Viruses</i> , 2018, 10, 522.	3.4	25
66	Forecasting Seasonal <i>Vibrio parahaemolyticus</i> Concentrations in New England Shellfish. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 4341.	2.7	25
67	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.	7.4	25
68	The roles of history, chance, and natural selection in the evolution of antibiotic resistance. <i>ELife</i> , 2021, 10, .	5.8	25
69	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.	2.5	25
70	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.	6.2	25
71	High-Level Fosfomycin Resistance in Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>Emerging Infectious Diseases</i> , 2017, 23, 1902-1904.	4.3	24
72	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.	4.3	23

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73	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.	2.0	23
74	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.	9.0	23
75	The Origins of Specialization: Insights from Bacteria Held 25 Years in Captivity. <i>PLoS Biology</i> , 2014, 12, e1001790.	5.3	22
76	The Fitness Effects of Spontaneous Mutations Nearly Unseen by Selection in a Bacterium with Multiple Chromosomes. <i>Genetics</i> , 2016, 204, 1225-1238.	2.9	22
77	NADH Dehydrogenases in <i>Pseudomonas aeruginosa</i> Growth and Virulence. <i>Frontiers in Microbiology</i> , 2019, 10, 75.	3.5	22
78	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.	3.5	21
79	Quorum sensing provides a molecular mechanism for evolution to tune and maintain investment in cooperation. <i>ISME Journal</i> , 2021, 15, 1236-1247.	9.8	21
80	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.	12.7	21
81	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.	2.2	20
82	Experimental Evolution <i>In Vivo</i> To Identify Selective Pressures during Pneumococcal Colonization. <i>MSystems</i> , 2020, 5, .	3.9	20
83	EVOLUTION OF THERMAL DEPENDENCE OF GROWTH RATE OF ESCHERICHIA COLI POPULATIONS DURING 20,000 GENERATIONS IN A CONSTANT ENVIRONMENT. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 889-896.	2.2	19
84	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.	2.5	19
85	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.	2.5	19
86	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.	7.4	19
87	A method of processing nasopharyngeal swabs to enable multiple testing. <i>Pediatric Research</i> , 2019, 86, 651-654.	2.4	18
88	Rampant prophage movement among transient competitors drives rapid adaptation during infection. <i>Science Advances</i> , 2021, 7, .	10.7	17
89	Comparative genomics of <i>Burkholderia multivorans</i> , a ubiquitous pathogen with a highly conserved genomic structure. <i>PLoS ONE</i> , 2017, 12, e0176191.	2.5	17
90	Mutations that improve efficiency of a weak-link enzyme are rare compared to adaptive mutations elsewhere in the genome. <i>ELife</i> , 2019, 8, .	5.8	17

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91	The OmpR Regulator of <i>Burkholderia multivorans</i> Controls Mucoïd-to-Nonmucoïd Transition and Other Cell Envelope Properties Associated with Persistence in the Cystic Fibrosis Lung. <i>Journal of Bacteriology</i> , 2018, 200, .	2.3	16
92	Genomic Diversity of Hospital-Acquired Infections Revealed through Prospective Whole-Genome Sequencing-Based Surveillance. <i>MSystems</i> , 2022, 7, .	3.9	15
93	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.	4.1	14
94	Phage therapy in a lung transplant recipient with cystic fibrosis infected with multidrug-resistant <i>Burkholderia multivorans</i> . <i>Transplant Infectious Disease</i> , 2023, 25, .	1.6	14
95	<i>Clostridioides difficile</i> : a potential source of NpmA in the clinical environment. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 521-523.	3.1	13
96	Negative frequency-dependent selection maintains coexisting genotypes during fluctuating selection. <i>Molecular Ecology</i> , 2020, 29, 138-148.	3.5	13
97	Complete Genome Sequences of 13 <i>Bacillus subtilis</i> Soil Isolates for Studying Secondary Metabolite Diversity. <i>Microbiology Resource Announcements</i> , 2020, 9, .	1.0	13
98	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.	3.3	12
99	High-Level Carbapenem Resistance in OXA-232-Producing <i>Raoultella ornithinolytica</i> Triggered by Ertapenem Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 64, .	3.3	12
100	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.	3.3	10
101	Evolutionary Divergence of the Wsp Signal Transduction Systems in Beta- and Gammaproteobacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0130621.	3.1	10
102	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.	3.5	9
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.	0.9	8
104	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.	2.3	8
105	Evolved resistance to a novel cationic peptide antibiotic requires high mutation supply. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 266-276.	2.5	8
106	<i>Staphylococcus aureus</i> genotype variation among and within periprosthetic joint infections. <i>Journal of Orthopaedic Research</i> , 2022, 40, 420-428.	2.4	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.	0.8	5
108	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.	3.1	5

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109	Use of a cohorting-unit and systematic surveillance cultures to control a <i>Klebsiella pneumoniae</i> carbapenemase (KPC)â€‘producing Enterobacteriaceae outbreak. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 767-773.	2.0	5
110	SprayNPray: user-friendly taxonomic profiling of genome and metagenome contigs. <i>BMC Genomics</i> , 2022, 23, 202.	2.9	5
111	Evolution towards Virulence in a <i>Burkholderia</i> Two-Component System. <i>MBio</i> , 2021, 12, e0182321.	4.2	4
112	The Study of Microbial Adaptation by Long-Term Experimental Evolution. , 0, , 55-81.		2
113	Novel Requirement for Staphylococcal Cell Wall-Anchored Protein SasD in Pulmonary Infection. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
114	Adaptation to Overflow Metabolism by Mutations That Impair tRNA Modification in Experimentally Evolved Bacteria. <i>MBio</i> , 2023, 14, .	4.2	2
115	Precise measurement of the fitness effects of spontaneous mutations by droplet digital PCR in <i>Burkholderia cenocepacia</i> . <i>Genetics</i> , 2021, 219, .	2.9	1
116	<i>Inoviridae</i> prophage and bacterial host dynamics during diversification, succession, and Atlantic invasion of Pacific-native <i>Vibrio parahaemolyticus</i> . <i>MBio</i> , 2024, 15, .	4.2	1
117	Persistence and evolution of <i>Pseudomonas aeruginosa</i> following initiation of highly effective modulator therapy in cystic fibrosis. <i>MBio</i> , 2024, 15, .	4.2	1
118	Experimental Evolution of Pathogens. , 0, , 215-224.		0
119	AUTORIA, AUTORIDADE E AUTONOMIA NO TRABALHO ACADÃŠMICO-PROFISSIONAL: UMA REFLEXÃƒO BIOGRÃƒFICA. <i>Revista Interinstitucional Artes De Educar</i> , 2021, 7, .	0.0	0
120	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, , .	0.6	0
121	Genomic characterization of SARS-CoV-2 from vaccine breakthrough cases in Allegheny County, Pennsylvania. <i>PLoS ONE</i> , 2022, 17, e0272954.	2.5	0
122	The contribution of DNA repair pathways to <i>Staphylococcus aureus</i> fitness and fidelity during nitric oxide stress. <i>MBio</i> , 0, , .	4.2	0
123	Draft genomes of seven isolates from Danish wastewater facilities belonging to <i>Pseudomonas</i> , <i>Bacillus</i> , <i>Pseudochromobacterium</i> , <i>Brevundimonas</i> , and <i>Pandoraea</i> . <i>Microbiology Resource Announcements</i> , 2023, 12, .	1.0	0
124	<i>Streptococcus pneumoniae</i> favors tolerance via metabolic adaptation over resistance to circumvent fluoroquinolones. <i>MBio</i> , 2024, 15, .	4.2	0
125	Harnessing the Diversity of <i>Burkholderia</i> spp. Prophages for Therapeutic Potential. <i>Cells</i> , 2024, 13, 428.	4.2	0
126	Cystic fibrosis pathogens persist in the upper respiratory tract following initiation of elxacaftor/tezacaftor/ivacaftor therapy. <i>Microbiology Spectrum</i> , 0, , .	3.0	0