

SNP-sites: rapid efficient extraction of SNPs from multi

Microbial Genomics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1388-1396.	2.4	96
2	Understanding pneumococcal serotype 1 biology through population genomic analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 649.	1.3	22
3	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
4	Genomic landscape of extended-spectrum β -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	1.3	46
5	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	3.4	121
6	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <i>Genome Research</i> , 2017, 27, 1437-1449.	2.4	231
7	<i>Brucella</i> Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. <i>Genome Biology and Evolution</i> , 2017, 9, 1901-1912.	1.1	26
8	Constraints on lateral gene transfer in promoting fimbrial usher protein diversity and function. <i>Open Biology</i> , 2017, 7, 170144.	1.5	10
9	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	6.0	128
10	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	2.8	46
11	Bacteriophages are the major drivers of <i>Shigella flexneri</i> serotype 1c genome plasticity: a complete genome analysis. <i>BMC Genomics</i> , 2017, 18, 722.	1.2	10
12	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , 2017, 23, 997-1000.	2.0	40
13	Rapid evolution of distinct <i>Helicobacter pylori</i> subpopulations in the Americas. <i>PLoS Genetics</i> , 2017, 13, e1006546.	1.5	73
14	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	2.0	32
15	Adaptation in a Fibronectin Binding Autolysin of <i>Staphylococcus saprophyticus</i> . <i>MSphere</i> , 2017, 2, .	1.3	9
16	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	1.0	478
17	Emergence of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. <i>MBio</i> , 2018, 9, .	1.8	434
18	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant <i>Staphylococcus aureus</i> . <i>MSphere</i> , 2018, 3, .	1.3	55

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19	Zoonotic Transfer of <i>Clostridium difficile</i> Harboring Antimicrobial Resistance between Farm Animals and Humans. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	102
20	Genomic epidemiology of the commercially important pathogen <i>Renibacterium salmoninarum</i> within the Chilean salmon industry. <i>Microbial Genomics</i> , 2018, 4, .	1.0	12
21	Evaluation of a Novel MALDI Biotyper Algorithm to Distinguish <i>Mycobacterium intracellulare</i> From <i>Mycobacterium chimaera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3140.	1.5	25
22	Genome sequence analysis of an extensively drug-resistant <i>Acinetobacter baumannii</i> indigo-pigmented strain depicts evidence of increase genome plasticity. <i>Scientific Reports</i> , 2018, 8, 16961.	1.6	28
23	Complement Susceptibility in Relation to Genome Sequence of Recent <i>Klebsiella pneumoniae</i> Isolates from Thai Hospitals. <i>MSphere</i> , 2018, 3, .	1.3	25
24	Virulence of <i>Mycobacterium tuberculosis</i> Clinical Isolates Is Associated With Sputum Pre-treatment Bacterial Load, Lineage, Survival in Macrophages, and Cytokine Response. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 417.	1.8	21
25	The Demographic History of African <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2338-2342.	1.1	26
26	Unveiling the Multilocus Sequence Typing (MLST) Schemes and Core Genome Phylogenies for Genotyping <i>Chlamydia trachomatis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1854.	1.5	23
27	The Complete Plastome Sequences of Eleven Capsicum Genotypes: Insights into DNA Variation and Molecular Evolution. <i>Genes</i> , 2018, 9, 503.	1.0	25
28	Signatures of Selection at Drug Resistance Loci in <i>Mycobacterium tuberculosis</i> . <i>MSystems</i> , 2018, 3, .	1.7	32
29	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018, 50, 951-955.	9.4	37
30	Global Scale Dissemination of ST93: A Divergent <i>Staphylococcus aureus</i> Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1453.	1.5	29
31	Genome-Wide Analysis of <i>Corynespora cassicola</i> Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018, 9, 276.	1.5	58
32	The evolution of ecological facilitation within mixed-species biofilms in the mouse gastrointestinal tract. <i>ISME Journal</i> , 2018, 12, 2770-2784.	4.4	34
33	Fast phylogenetic inference from typing data. <i>Algorithms for Molecular Biology</i> , 2018, 13, 4.	0.3	14
34	Phylogenomics and barcoding of <i>Panax</i> : toward the identification of ginseng species. <i>BMC Evolutionary Biology</i> , 2018, 18, 44.	3.2	45
35	Genomic epidemiology of <i>Shigella</i> in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. <i>Scientific Reports</i> , 2018, 8, 7389.	1.6	65
36	Pathogenic adaptations of <i>Colletotrichum</i> fungi revealed by genome wide gene family evolutionary analyses. <i>PLoS ONE</i> , 2018, 13, e0196303.	1.1	46

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37	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	6.5	18
38	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal <i>Salmonella enterica</i> Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	1.7	21
39	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth <i>Brucella</i> sp. BCCN84.3. <i>Frontiers in Veterinary Science</i> , 2019, 6, 175.	0.9	18
40	Integrated genomic epidemiology and phenotypic profiling of <i>Clostridium difficile</i> across intra-hospital and community populations in Colombia. <i>Scientific Reports</i> , 2019, 9, 11293.	1.6	12
41	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019, 4, 1941-1950.	5.9	91
42	MARPLE, a point-of-care, strain-level disease diagnostics and surveillance tool for complex fungal pathogens. <i>BMC Biology</i> , 2019, 17, 65.	1.7	56
43	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	1.3	16
44	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in <i>Mycobacterium tuberculosis</i> in Southern India. <i>Scientific Reports</i> , 2019, 9, 10283.	1.6	32
45	Genomic Characterization of Jumbo <i>Salmonella</i> Phages That Effectively Target United Kingdom Pig-Associated <i>Salmonella</i> Serotypes. <i>Frontiers in Microbiology</i> , 2019, 10, 1491.	1.5	28
46	Gut Colonization Preceding Mucosal Barrier Injury Bloodstream Infection in Pediatric Hematopoietic Stem Cell Transplantation Recipients. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, 2274-2280.	2.0	36
47	Genomic Features of High-Priority <i>Salmonella enterica</i> Serovars Circulating in the Food Production Chain, Brazil, 2000–2016. <i>Scientific Reports</i> , 2019, 9, 11058.	1.6	61
48	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	6.5	36
49	Supporting evidence for a human reservoir of invasive non-Typhoidal <i>Salmonella</i> from household samples in Burkina Faso. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007782.	1.3	36
50	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	6.0	365
51	Genome-Wide Variation in Potyviruses. <i>Frontiers in Plant Science</i> , 2019, 10, 1439.	1.7	80
52	Developing Chloroplast Genomic Resources from 25 <i>Avena</i> Species for the Characterization of Oat Wild Relative Germplasm. <i>Plants</i> , 2019, 8, 438.	1.6	4
53	Large-scale genome analysis of bovine commensal <i>Escherichia coli</i> reveals that bovine-adapted <i>E. coli</i> lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains. <i>Genome Research</i> , 2019, 29, 1495-1505.	2.4	39
54	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	3.8	22

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55	Molecular characterization of carbapenem-resistant <i>Acinetobacter baumannii</i> using WGS revealed missed transmission events in Germany from 2012â€“15. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3473-3480.	1.3	15
56	Isolation of five Enterobacteriaceae species harbouring bla _{NDM-1} and mcr-1 plasmids from a single paediatric patient. <i>PLoS ONE</i> , 2019, 14, e0221960.	1.1	19
57	Genomic Analysis of <i>Clostridium perfringens</i> BEC/CPiLE-Positive, Toxinotype D and E Strains Isolated from Healthy Children. <i>Toxins</i> , 2019, 11, 543.	1.5	11
58	A Large-Scale Whole-Genome Comparison Shows that Experimental Evolution in Response to Antibiotics Predicts Changes in Naturally Evolved Clinical <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	31
59	An African <i>Salmonella</i> Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. <i>Nature Communications</i> , 2019, 10, 4280.	5.8	80
60	Geography Shapes the Population Genomics of <i>Salmonella enterica</i> Dublin. <i>Genome Biology and Evolution</i> , 2019, 11, 2220-2231.	1.1	23
61	'Candidatus <i>Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
62	Phylogenomic Approaches to DNA Barcoding of Herbal Medicines: Developing Clade-Specific Diagnostic Characters for Berberis. <i>Frontiers in Plant Science</i> , 2019, 10, 586.	1.7	28
63	Whole genome sequencing <i>Mycobacterium tuberculosis</i> directly from sputum identifies more genetic diversity than sequencing from culture. <i>BMC Genomics</i> , 2019, 20, 389.	1.2	56
64	Lineage specific histories of <i>Mycobacterium tuberculosis</i> dispersal in Africa and Eurasia. <i>Molecular Ecology</i> , 2019, 28, 3241-3256.	2.0	86
65	Diversification and Evolution of Vancomycin-Resistant <i>Enterococcus faecium</i> during Intestinal Domination. <i>Infection and Immunity</i> , 2019, 87, .	1.0	33
66	Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. <i>PLoS Biology</i> , 2019, 17, e3000244.	2.6	82
67	Local Diversification of Methicillin- Resistant <i>Staphylococcus aureus</i> ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019, 10, 82.	1.5	20
68	Inference of Convergent Gene Acquisition Among <i>Pseudomonas syringae</i> Strains Isolated From Watermelon, Cantaloupe, and Squash. <i>Frontiers in Microbiology</i> , 2019, 10, 270.	1.5	17
69	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019, 14, e0209395.	1.1	20
70	Livestock-Associated MRSA CC1 in Norway; Introduction to Pig Farms, Zoonotic Transmission, and Eradication. <i>Frontiers in Microbiology</i> , 2019, 10, 139.	1.5	30
71	The history, genome and biology of NCTC 30: a non-pandemic <i>Vibrio cholerae</i> isolate from World War One. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182025.	1.2	18
72	High quality reference genomes for toxigenic and non-toxigenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , 2019, 9, 5865.	1.6	13

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73	Satellite tracking of gulls and genomic characterization of faecal bacteria reveals environmentally mediated acquisition and dispersal of antimicrobial-resistant <i>Escherichia coli</i> on the Kenai Peninsula, Alaska. <i>Molecular Ecology</i> , 2019, 28, 2531-2545.	2.0	29
74	Loss and Gain in the Evolution of the <i>Salmonella enterica</i> Serovar Gallinarum Biovar Pullorum Genome. <i>MSphere</i> , 2019, 4, .	1.3	23
75	Pleiotropy Modulates the Efficacy of Selection in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 500-515.	3.5	20
76	Multidisciplinary evaluation of <i>Clostridium butyricum</i> clonality isolated from preterm neonates with necrotizing enterocolitis in South France between 2009 and 2017. <i>Scientific Reports</i> , 2019, 9, 2077.	1.6	10
77	Resistance mechanisms and population structure of highly drug resistant <i>Klebsiella</i> in Pakistan during the introduction of the carbapenemase NDM-1. <i>Scientific Reports</i> , 2019, 9, 2392.	1.6	45
78	Dispersal of <i>Mycobacterium tuberculosis</i> Driven by Historical European Trade in the South Pacific. <i>Frontiers in Microbiology</i> , 2019, 10, 2778.	1.5	28
79	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: <i>Neisseria meningitidis</i> as a Proof of Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 2897.	1.5	8
80	Genomic analysis on broiler-associated <i>Clostridium perfringens</i> strains and exploratory caecal microbiome investigation reveals key factors linked to poultry necrotic enteritis. <i>Animal Microbiome</i> , 2019, 1, 12.	1.5	29
81	Genomic Analysis of Fluoroquinolone- and Tetracycline-Resistant <i>Campylobacter jejuni</i> Sequence Type 6964 in Humans and Poultry, New Zealand, 2014–2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 2226-2234.	2.0	27
82	Genetic Features of <i>mcr-1</i> Mediated Colistin Resistance in CMY-2-Producing <i>Escherichia coli</i> From Romanian Poultry. <i>Frontiers in Microbiology</i> , 2019, 10, 2267.	1.5	29
83	Isolation and comparative genomics of <i>Mycobacterium tuberculosis</i> isolates from cattle and their attendants in South India. <i>Scientific Reports</i> , 2019, 9, 17892.	1.6	14
84	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	2.0	19
85	Residual Variation Intolerance Score Detects Loci Under Selection in Neuroinvasive <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2702.	1.5	1
86	Persistence of Nasopharyngeal Pneumococcal Vaccine Serotypes and Increase of Nonvaccine Serotypes Among Vaccinated Infants and Their Mothers 5 Years After Introduction of Pneumococcal Conjugate Vaccine 13 in The Gambia. <i>Clinical Infectious Diseases</i> , 2019, 68, 1512-1521.	2.9	41
87	Co-circulation of Multidrug-resistant <i>Shigella</i> Among Men Who Have Sex With Men in Australia. <i>Clinical Infectious Diseases</i> , 2019, 69, 1535-1544.	2.9	77
88	A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new sub-population of <i>Helicobacter pylori</i> from Australia. <i>Evolutionary Applications</i> , 2020, 13, 278-289.	1.5	6
89	Complete plastome assemblies from a panel of 13 diverse potato taxa. <i>PLoS ONE</i> , 2020, 15, e0240124.	1.1	17
90	Understanding and predicting ciprofloxacin minimum inhibitory concentration in <i>Escherichia coli</i> with machine learning. <i>Scientific Reports</i> , 2020, 10, 15026.	1.6	24

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91	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020, 183, 739-751.e8.	13.5	924
92	Clinical and molecular characteristics of carbapenem non-susceptible <i>Escherichia coli</i> : A nationwide survey from Oman. <i>PLoS ONE</i> , 2020, 15, e0239924.	1.1	18
93	Microbiota Supplementation with <i>Bifidobacterium</i> and <i>Lactobacillus</i> Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. <i>Cell Reports Medicine</i> , 2020, 1, 100077.	3.3	119
94	Genomic and Phenotypic Analysis of an ESBL-Producing <i>E. coli</i> ST1159 Clonal Lineage From Wild Birds in Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1699.	1.5	7
95	Within-host microevolution of <i>Streptococcus pneumoniae</i> is rapid and adaptive during natural colonisation. <i>Nature Communications</i> , 2020, 11, 3442.	5.8	39
96	Epstein-Barr Virus Genomes Reveal Population Structure and Type 1 Association with Endemic Burkitt Lymphoma. <i>Journal of Virology</i> , 2020, 94, .	1.5	20
97	Complete Mitochondrial Genome and a Set of 10 Novel Kompetitive Allele-Specific PCR Markers in Ginseng (<i>Panax ginseng</i> C. A. Mey.). <i>Agronomy</i> , 2020, 10, 1868.	1.3	10
98	Genetic Determinants of Resistance to Extended-Spectrum Cephalosporin and Fluoroquinolone in <i>Escherichia coli</i> Isolated from Diseased Pigs in the United States. <i>MSphere</i> , 2020, 5, .	1.3	23
99	Insights from Population Genomics to Enhance and Sustain Biological Control of Insect Pests. <i>Insects</i> , 2020, 11, 462.	1.0	19
100	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	1.7	82
101	De Novo Assembly-Based Analysis of RPGR Exon ORF15 in an Indigenous African Cohort Overcomes Limitations of a Standard Next-Generation Sequencing (NGS) Data Analysis Pipeline. <i>Genes</i> , 2020, 11, 800.	1.0	9
102	High relatedness of invasive multi-drug resistant non-typhoidal <i>Salmonella</i> genotypes among patients and asymptomatic carriers in endemic informal settlements in Kenya. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008440.	1.3	40
103	Microevolution of acquired colistin resistance in Enterobacteriaceae from ICU patients receiving selective decontamination of the digestive tract. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3135-3143.	1.3	18
104	Strain-Level Metagenomic Data Analysis of Enriched In Vitro and In Silico Spiked Food Samples: Paving the Way towards a Culture-Free Foodborne Outbreak Investigation Using STEC as a Case Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5688.	1.8	14
105	Genomic Diversification, Structural Plasticity, and Hybridization in <i>Leishmania</i> (<i>Viannia</i>) <i>braziliensis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 582192.	1.8	21
106	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	2.0	11
107	Multidrug-Resistant CTX-M and CMY-2 Producing <i>Escherichia coli</i> Isolated from Healthy Household Dogs from the Great Metropolitan Area, Costa Rica. <i>Microbial Drug Resistance</i> , 2020, 26, 1421-1428.	0.9	7
108	The level of antimicrobial resistance of sewage isolates is higher than that of river isolates in different <i>Escherichia coli</i> lineages. <i>Scientific Reports</i> , 2020, 10, 17880.	1.6	12

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109	Cultivated Tomato (<i>Solanum lycopersicum</i> L.) Suffered a Severe Cytoplasmic Bottleneck during Domestication: Implications from Chloroplast Genomes. <i>Plants</i> , 2020, 9, 1443.	1.6	11
110	Multi-omic Analysis of the Interaction between <i>Clostridioides difficile</i> Infection and Pediatric Inflammatory Bowel Disease. <i>Cell Host and Microbe</i> , 2020, 28, 422-433.e7.	5.1	45
111	Cereulide Synthetase Acquisition and Loss Events within the Evolutionary History of Group III <i>Bacillus cereus</i> Sensu Lato Facilitate the Transition between Emetic and Diarrheal Foodborne Pathogens. <i>MBio</i> , 2020, 11, .	1.8	23
112	Genetic Diversity, Pedigree Relationships, and A Haplotype-Based DNA Fingerprinting System of Red Bayberry Cultivars. <i>Frontiers in Plant Science</i> , 2020, 11, 563452.	1.7	5
113	Pandemic <i>Vibrio cholerae</i> shuts down site-specific recombination to retain an interbacterial defence mechanism. <i>Nature Communications</i> , 2020, 11, 6246.	5.8	17
114	Multiple Introductions Followed by Ongoing Community Spread of SARS-CoV-2 at One of the Largest Metropolitan Areas of Northeast Brazil. <i>Viruses</i> , 2020, 12, 1414.	1.5	47
115	Selective Sweeps Lead to Evolutionary Success in an Amazonian Hyperdominant Palm. <i>Frontiers in Genetics</i> , 2020, 11, 596662.	1.1	4
116	Whole-Genome Sequence Analysis of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Agona Isolate from an Australian Silver Gull (<i>Chroicocephalus novaehollandiae</i>) Reveals the Acquisition of Multidrug Resistance Plasmids. <i>MSphere</i> , 2020, 5, .	1.3	22
117	A whole-genome worldwide molecular epidemiology approach for contagious caprine pleuropneumonia. <i>Heliyon</i> , 2020, 6, e05146.	1.4	10
118	Mitochondrial DNAs provide insight into trypanosome phylogeny and molecular evolution. <i>BMC Evolutionary Biology</i> , 2020, 20, 161.	3.2	25
119	A <i>Klebsiella pneumoniae</i> ST307 outbreak clone from Germany demonstrates features of extensive drug resistance, hypermucoviscosity, and enhanced iron acquisition. <i>Genome Medicine</i> , 2020, 12, 113.	3.6	82
120	Trends of mutation accumulation across global SARS-CoV-2 genomes: Implications for the evolution of the novel coronavirus. <i>Genomics</i> , 2020, 112, 5331-5342.	1.3	32
121	Amino Acid k-mer Feature Extraction for Quantitative Antimicrobial Resistance (AMR) Prediction by Machine Learning and Model Interpretation for Biological Insights. <i>Biology</i> , 2020, 9, 365.	1.3	21
122	Population Genomic Analysis of <i>Mycoplasma bovis</i> Elucidates Geographical Variations and Genes associated with Host-Types. <i>Microorganisms</i> , 2020, 8, 1561.	1.6	13
123	Restricted Sequence Variation in <i>Streptococcus pyogenes</i> Penicillin Binding Proteins. <i>MSphere</i> , 2020, 5, .	1.3	18
124	Dissemination of Quinolone-Resistant <i>Escherichia coli</i> in the Norwegian Broiler and Pig Production Chains and Possible Persistence in the Broiler Production Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
125	Epidemiological and Genomic Characterization of <i>Campylobacter jejuni</i> Isolates from a Foodborne Outbreak at Hangzhou, China. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3001.	1.8	33
126	Extended-Spectrum-β-Lactamase- and Plasmid AmpC-Producing <i>Escherichia coli</i> Causing Community-Onset Bloodstream Infection: Association of Bacterial Clones and Virulence Genes with Septic Shock, Source of Infection, and Recurrence. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	17

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127	Discordant evolution of mitochondrial and nuclear yeast genomes at population level. <i>BMC Biology</i> , 2020, 18, 49.	1.7	42
128	Global Distribution and Evolution of <i>Mycobacterium bovis</i> Lineages. <i>Frontiers in Microbiology</i> , 2020, 11, 843.	1.5	37
129	Complete Genome Sequences, Derived by Next-Generation Sequencing, of JC Polyomavirus Strains Isolated from Vietnamese Renal Transplant Recipients. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
130	Genome Dynamics of <i>Vibrio cholerae</i> Isolates Linked to Seasonal Outbreaks of Cholera in Dhaka, Bangladesh. <i>MBio</i> , 2020, 11, .	1.8	39
131	Evolution of the Insecticide Target <i>Rdl</i> in African <i>Anopheles</i> Is Driven by Interspecific and Interkaryotypic Introgression. <i>Molecular Biology and Evolution</i> , 2020, 37, 2900-2917.	3.5	31
132	Molecular characterization of <i>Brucella ovis</i> in Argentina. <i>Veterinary Microbiology</i> , 2020, 245, 108703.	0.8	2
133	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
134	Comparative Genome Analyses of Wild Type- and Quinolone Resistant <i>Escherichia coli</i> Indicate Dissemination of QREC in the Norwegian Broiler Breeding Pyramid. <i>Frontiers in Microbiology</i> , 2020, 11, 938.	1.5	5
135	Crucial Role of the Accessory Genome in the Evolutionary Trajectory of <i>Acinetobacter baumannii</i> Global Clone 1. <i>Frontiers in Microbiology</i> , 2020, 11, 342.	1.5	16
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