

Coast-to-Coast Spread of SARS-CoV-2 during the Early

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City region. <i>Genome Research</i> , 2020, 30, 1781-1788.	2.4	66
2	Temporal Detection and Phylogenetic Assessment of SARS-CoV-2 in Municipal Wastewater. <i>Cell Reports Medicine</i> , 2020, 1, 100098.	3.3	424
3	COVID-19: facts and failures, a tale of two worlds. <i>European Journal of Epidemiology</i> , 2020, 35, 991-994.	2.5	6
4	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	203
5	COVID-19: US federal accountability for entry, spread, and inequitiesâ€”lessons for the future. <i>European Journal of Epidemiology</i> , 2020, 35, 995-1006.	2.5	38
6	Sensitive Recovery of Complete SARS-CoV-2 Genomes from Clinical Samples by Use of Swift Biosciencesâ€™ SARS-CoV-2 Multiplex Amplicon Sequencing Panel. <i>Journal of Clinical Microbiology</i> , 2020, 59, .	1.8	58
7	Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. <i>Nature Communications</i> , 2020, 11, 5558.	5.8	39
8	The Covid-19 Global Pandemic: A Natural Experiment in the Making. <i>Lifestyle Genomics</i> , 2020, 13, 135-137.	0.6	6
9	COVIDâ€™19 in Patients With Inflammatory Arthritis: A Prospective Study on the Effects of Comorbidities and Diseaseâ€™Modifying Antirheumatic Drugs on Clinical Outcomes. <i>Arthritis and Rheumatology</i> , 2020, 72, 1981-1989.	2.9	92
10	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , 2020, 182, 1295-1310.e20.	13.5	1,726
11	Understanding the complexities of SARS-CoV2 infection and its immunology: A road to immune-based therapeutics. <i>International Immunopharmacology</i> , 2020, 88, 106980.	1.7	31
12	High-Density Amplicon Sequencing Identifies Community Spread and Ongoing Evolution of SARS-CoV-2 in the Southern United States. <i>Cell Reports</i> , 2020, 33, 108352.	2.9	38
13	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	5.8	118
14	The SARS-CoV-2 Spike Glycoprotein Biosynthesis, Structure, Function, and Antigenicity: Implications for the Design of Spike-Based Vaccine Immunogens. <i>Frontiers in Immunology</i> , 2020, 11, 576622.	2.2	317
15	Genetic grouping of SARS-CoV-2 coronavirus sequences using informative subtype markers for pandemic spread visualization. <i>PLoS Computational Biology</i> , 2020, 16, e1008269.	1.5	38
16	Real-time public health communication of local SARS-CoV-2 genomic epidemiology. <i>PLoS Biology</i> , 2020, 18, e3000869.	2.6	15
17	Rapid multiplex MinION nanopore sequencing workflow for Influenza A viruses. <i>BMC Infectious Diseases</i> , 2020, 20, 648.	1.3	35
18	In vivo antiviral host transcriptional response to SARS-CoV-2 by viral load, sex, and age. <i>PLoS Biology</i> , 2020, 18, e3000849.	2.6	225

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19	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	6.0	331
20	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	6.0	217
21	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020, 11, 949.	1.0	65
22	SARS-CoV-2 Seroprevalence among a Southern U.S. Population Indicates Limited Asymptomatic Spread under Physical Distancing Measures. <i>MBio</i> , 2020, 11, .	1.8	25
23	Intra-host non-synonymous diversity at a neutralizing antibody epitope of SARS-CoV-2 spike protein N-terminal domain. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1350.e1-1350.e5.	2.8	20
24	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020, 11, 6272.	5.8	183
25	Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel. <i>Nature Communications</i> , 2020, 11, 5518.	5.8	115
26	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	1.8	29
27	SARS-CoV-2 and COVID-19: A genetic, epidemiological, and evolutionary perspective. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104384.	1.0	115
28	Introductions and early spread of SARS-CoV-2 in the New York City area. <i>Science</i> , 2020, 369, 297-301.	6.0	356
29	Ten recommendations for supporting open pathogen genomic analysis in public health. <i>Nature Medicine</i> , 2020, 26, 832-841.	15.2	63
30	A compendium answering 150 questions on COVID-19 and SARS-CoV-2. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2503-2541.	2.7	95
31	Nanopore Targeted Sequencing for the Accurate and Comprehensive Detection of SARS-CoV-2 and Other Respiratory Viruses. <i>Small</i> , 2020, 16, e2002169.	5.2	169
32	The laboratory's role in combating COVID-19. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2020, 57, 400-414.	2.7	42
33	COVID-19: test, trace and isolate new epidemiological data. <i>Environmental Microbiology</i> , 2020, 22, 2445-2456.	1.8	8
34	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
35	Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. <i>Cell</i> , 2020, 182, 812-827.e19.	13.5	3,551
36	Molecular mechanisms and epidemiology of COVID-19 from an allergist's perspective. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 285-299.	1.5	46

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37	Identification of multiple large deletions in ORF7a resulting in in-frame gene fusions in clinical SARS-CoV-2 isolates. <i>Journal of Clinical Virology</i> , 2020, 129, 104523.	1.6	71
38	On the founder effect in COVID-19 outbreaks: how many infected travelers may have started them all?. <i>National Science Review</i> , 2021, 8, nwaa246.	4.6	27
39	Correlating USA COVID-19 cases at epidemic onset days to domestic flights passenger inflows by state. <i>International Journal of Modern Physics C</i> , 2021, 32, 2150014.	0.8	3
40	SARS-CoV-2 infection in patients with a normal or abnormal liver. <i>Journal of Viral Hepatitis</i> , 2021, 28, 4-11.	1.0	29
41	Spike mutation D614G alters SARS-CoV-2 fitness. <i>Nature</i> , 2021, 592, 116-121.	13.7	1,380
42	<i>Coronapp</i>: A web application to annotate and monitor SARS-CoV-2 mutations. <i>Journal of Medical Virology</i> , 2021, 93, 3238-3245.	2.5	75
43	The D614G mutations in the SARS-CoV-2 spike protein: Implications for viral infectivity, disease severity and vaccine design. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 104-107.	1.0	85
44	Ravaging SARS-CoV-2: rudimentary diagnosis and puzzling immunological responses. <i>Current Medical Research and Opinion</i> , 2021, 37, 207-217.	0.9	5
45	Structural basis of severe acute respiratory syndrome coronavirus 2 infection. <i>Current Opinion in HIV and AIDS</i> , 2021, 16, 74-81.	1.5	7
46	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021, 103, 234-241.	1.5	63
47	Molecular epidemiology in the HIV and SARS-CoV-2 pandemics. <i>Current Opinion in HIV and AIDS</i> , 2021, 16, 11-24.	1.5	5
50	Validation of multiplex PCR sequencing assay of SIV. <i>Virology Journal</i> , 2021, 18, 21.	1.4	2
51	COVID-19 Dynamics: A Heterogeneous Model. <i>Frontiers in Public Health</i> , 2020, 8, 558368.	1.3	7
53	The Genetic Variant of SARS-CoV-2: Would it matter for Controlling the Devastating Pandemic?. <i>International Journal of Biological Sciences</i> , 2021, 17, 1476-1485.	2.6	23
54	Nanopore sequencing and its application to the study of microbial communities. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1497-1511.	1.9	106
55	SIR Model Parameter Fitting of SARS-CoV-2 Basic Reproduction Number in Venezuela and Ecuador Epidemic. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 94-108.	0.5	0
56	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
58	SARS-CoV-2 Genomic Variation in Space and Time in Hospitalized Patients in Philadelphia. <i>MBio</i> , 2021, 12, .	1.8	27

#	ARTICLE	IF	CITATIONS
59	Disease severity-specific neutrophil signatures in blood transcriptomes stratify COVID-19 patients. <i>Genome Medicine</i> , 2021, 13, 7.	3.6	193
60	Miniaturized DNA Sequencers for Personal Use: Unreachable Dreams or Achievable Goals. <i>Frontiers in Nanotechnology</i> , 2021, 3, .	2.4	7
61	Optimal inference of the start of COVID-19. <i>Physical Review Research</i> , 2021, 3, .	1.3	10
62	A streamlined clinical metagenomic sequencing protocol for rapid pathogen identification. <i>Scientific Reports</i> , 2021, 11, 4405.	1.6	15
63	The characteristics of multi-source mobility datasets and how they reveal the luxury nature of social distancing in the U.S. during the COVID-19 pandemic. <i>International Journal of Digital Earth</i> , 2021, 14, 424-442.	1.6	62
64	Dynamic Panel Data Modeling and Surveillance of COVID-19 in Metropolitan Areas in the United States: Longitudinal Trend Analysis. <i>Journal of Medical Internet Research</i> , 2021, 23, e26081.	2.1	14
65	Impact of domestic travel restrictions on transmission of COVID-19 infection using public transportation network approach. <i>Scientific Reports</i> , 2021, 11, 3109.	1.6	53
66	Molecular diagnostic assays for COVID-19: an overview. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2021, 58, 385-398.	2.7	47
69	Genomic sequencing effort for SARS-CoV-2 by country during the pandemic. <i>International Journal of Infectious Diseases</i> , 2021, 103, 305-307.	1.5	54
70	Evolutionary Dynamics and Dissemination Pattern of the SARS-CoV-2 Lineage B.1.1.33 During the Early Pandemic Phase in Brazil. <i>Frontiers in Microbiology</i> , 2020, 11, 615280.	1.5	62
71	Quantifying asymptomatic infection and transmission of COVID-19 in New York City using observed cases, serology, and testing capacity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	196
73	High Throughput Sequencing for the Detection and Characterization of RNA Viruses. <i>Frontiers in Microbiology</i> , 2021, 12, 621719.	1.5	28
74	Systematic Review of Mutations Associated with Isoniazid Resistance Points to Continuing Evolution and Subsequent Evasion of Molecular Detection, and Potential for Emergence of Multidrug Resistance in Clinical Strains of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	14
77	COVID-19: emergence and mutational diversification of SARS-CoV-2. <i>Microbial Biotechnology</i> , 2021, 14, 756-768.	2.0	17
78	Genomic monitoring of SARS-CoV-2 uncovers an Nsp1 deletion variant that modulates type I interferon response. <i>Cell Host and Microbe</i> , 2021, 29, 489-502.e8.	5.1	95
80	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 2021, 10, .	2.8	20
81	Japanese travel behavior trends and change under COVID-19 state-of-emergency declaration: Nationwide observation by mobile phone location data. <i>Transportation Research Interdisciplinary Perspectives</i> , 2021, 9, 100288.	1.6	41
82	Non-Pharmaceutical Interventions. <i>Cascade Journal of Knowledge</i> , 0, , 0-7:42 minutes.	0.0	0

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83	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	5.8	132
84	Case Study: Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient. , 2021, , .		3
86	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimoreâ€“Washington metropolitan area. <i>JCI Insight</i> , 2021, 6, .	2.3	31
87	Emergence of novel SARS-CoV-2 variants in the Netherlands. <i>Scientific Reports</i> , 2021, 11, 6625.	1.6	22
88	Whole-genome sequencing of SARS-CoV-2 reveals the detection of G614 variant in Pakistan. <i>PLoS ONE</i> , 2021, 16, e0248371.	1.1	34
89	Estimation of Secondary Household Attack Rates for Emergent Spike L452R Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants Detected by Genomic Surveillance at a Community-Based Testing Site in San Francisco. <i>Clinical Infectious Diseases</i> , 2022, 74, 32-39.	2.9	39
90	The role of weather conditions in COVID-19 transmission: A study of a global panel of 1236 regions. <i>Journal of Cleaner Production</i> , 2021, 292, 125987.	4.6	26
91	Introduction, Transmission Dynamics, and Fate of Early Severe Acute Respiratory Syndrome Coronavirus 2 Lineages in Santa Clara County, California. <i>Journal of Infectious Diseases</i> , 2021, 224, 207-217.	1.9	2
92	Temporal dynamics of SARS-CoV-2 mutation accumulation within and across infected hosts. <i>PLoS Pathogens</i> , 2021, 17, e1009499.	2.1	86
93	SARS-CoV-2 ORF6 Disrupts Bidirectional Nucleocytoplasmic Transport through Interactions with Rae1 and Nup98. <i>MBio</i> , 2021, 12, .	1.8	92
96	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. <i>Nature Communications</i> , 2021, 12, 2188.	5.8	23
97	Investigation and public health response to a COVID-19 outbreak in a rural resort communityâ€“Blaine County, Idaho, 2020. <i>PLoS ONE</i> , 2021, 16, e0250322.	1.1	4
99	Rapid High-Throughput Whole-Genome Sequencing of SARS-CoV-2 by Using One-Step Reverse Transcription-PCR Amplification with an Integrated Microfluidic System and Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	15
100	Fundamental evolution of all <i>Orthocoronavirinae</i> including three deadly lineages descendent from Chiropteraâ€“hosted coronaviruses: SARSâ€“CoV, MERSâ€“CoV and SARSâ€“CoVâ€“2. <i>Cladistics</i> , 2021, 37, 461-488.	1.5	16
101	An Evolutionary Portrait of the Progenitor SARS-CoV-2 and Its Dominant Offshoots in COVID-19 Pandemic. <i>Molecular Biology and Evolution</i> , 2021, 38, 3046-3059.	3.5	54
103	Testing at scale during the COVID-19 pandemic. <i>Nature Reviews Genetics</i> , 2021, 22, 415-426.	7.7	261
104	Retrospective Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Symptomatic Patients Prior to Widespread Diagnostic Testing in Southern California. <i>Clinical Infectious Diseases</i> , 2022, 74, 271-277.	2.9	4
105	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2595-2604.e13.	13.5	113

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108	Genomic epidemiology of SARS-CoV-2 in Esteio, Rio Grande do Sul, Brazil. <i>BMC Genomics</i> , 2021, 22, 371.	1.2	22
109	Epidemiology, pathogenesis, clinical presentations, diagnosis and treatment of COVID-19: a review of current evidence. <i>Expert Review of Clinical Pharmacology</i> , 2021, 14, 601-621.	1.3	144
112	Ultrafast Sample placement on Existing tRees (USHER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. <i>Nature Genetics</i> , 2021, 53, 809-816.	9.4	264
113	Experiences and Views of Domestic Summer Travelers During the COVID-19 Pandemic: Findings from a National Survey. <i>Health Security</i> , 2021, 19, 338-348.	0.9	2
114	New variants of SARS-CoV-2. <i>Revista Espanola De Quimioterapia</i> , 2021, 34, 419-428.	0.5	49
115	Visualizing and assessing US county-level COVID19 vulnerability. <i>American Journal of Infection Control</i> , 2021, 49, 678-684.	1.1	10
116	Rapid feedback on hospital onset SARS-CoV-2 infections combining epidemiological and sequencing data. <i>ELife</i> , 2021, 10, .	2.8	26
118	Molecular benchmarks of a SARS-CoV-2 epidemic. <i>Nature Communications</i> , 2021, 12, 3633.	5.8	3
119	The coSIR model predicts effective strategies to limit the spread of SARS-CoV-2 variants with low severity and high transmissibility. <i>Nonlinear Dynamics</i> , 2021, 105, 2757-2773.	2.7	6
120	Trends in COVID-19 cases and clinical management in Veterans Health Administration medical facilities: A national cohort study. <i>PLoS ONE</i> , 2021, 16, e0246217.	1.1	4
121	L-SIGN is a receptor on liver sinusoidal endothelial cells for SARS-CoV-2 virus. <i>JCI Insight</i> , 2021, 6, .	2.3	31
122	Emerging mutation in SARS-CoV-2 spike: Widening distribution over time in different geographic areas. <i>Biomedical Journal</i> , 2021, 44, 570-581.	1.4	6
123	How coronavirus disease will change the face of travel medicine. <i>Current Opinion in Infectious Diseases</i> , 2021, 34, 409-414.	1.3	2
124	Modification of the Spike Protein for Vaccines against Enveloped RNA Viruses. <i>Molecular Biology</i> , 2021, 55, 538-547.	0.4	2
125	Estimation of COVID-19 Dynamics in the Different States of the United States during the First Months of the Pandemic. <i>Engineering Proceedings</i> , 2021, 5, .	0.4	4
126	Temporal landscape of mutational frequencies in SARS-CoV-2 genomes of Bangladesh: possible implications from the ongoing outbreak in Bangladesh. <i>Virus Genes</i> , 2021, 57, 413-425.	0.7	7
127	The role of mask mandates, stay at home orders and school closure in curbing the COVID-19 pandemic prior to vaccination. <i>American Journal of Infection Control</i> , 2021, 49, 1036-1042.	1.1	32
128	SARS-CoV-2: Understanding the Transcriptional Regulation of ACE2 and TMPRSS2 and the Role of Single Nucleotide Polymorphism (SNP) at Codon 72 of p53 in the Innate Immune Response against Virus Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8660.	1.8	14

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130	Effect of mutation and vaccination on spread, severity, and mortality of COVID-19 disease. <i>Journal of Medical Virology</i> , 2022, 94, 197-204.	2.5	42
131	How COVID-19 has transformed my science. <i>Neuron</i> , 2021, 109, 3041-3044.	3.8	0
132	Patterns of within-host genetic diversity in SARS-CoV-2. <i>ELife</i> , 2021, 10, .	2.8	110
133	Recovery of Deleted Deep Sequencing Data Sheds More Light on the Early Wuhan SARS-CoV-2 Epidemic. <i>Molecular Biology and Evolution</i> , 2021, 38, 5211-5224.	3.5	24
134	Factors associated with SARS-CoV2 infection and care pathways among the most vulnerable populations living in Marseille: a case control study. <i>BMC Public Health</i> , 2021, 21, 1704.	1.2	1
137	SARS-CoV-2 transmission dynamics in Belarus in 2020 revealed by genomic and incidence data analysis. <i>Communications Medicine</i> , 2021, 1, .	1.9	7
138	Phylogenetic estimates of SARS-CoV-2 introductions into Washington State. <i>The Lancet Regional Health Americas</i> , 2021, 1, 100018.	1.5	8
139	Investigating the first stage of the COVID-19 pandemic in Ukraine using epidemiological and genomic data. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105087.	1.0	10
140	Decomposing the sources of SARS-CoV-2 fitness variation in the United States. <i>Virus Evolution</i> , 2021, 7, veab073.	2.2	14
141	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
142	Clinical outcomes in patients infected with different SARS-CoV-2 variants at one hospital during three phases of the COVID-19 epidemic in Marseille, France. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105092.	1.0	22
143	Immune response variables and viral mutations impact on COVID-19 reinfection and relapse. <i>International Immunopharmacology</i> , 2021, 100, 108108.	1.7	7
144	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021, 89, 134-145.	0.8	9
145	Geographic Patterns of the Pandemic in the United States: Covid-19 Response Within a Disunified Federal System. , 2021, , 451-467.		1
146	Microsecond molecular dynamics suggest that a non-synonymous mutation, frequently observed in patients with mild symptoms in Tokyo, alters dynamics of the SARS-CoV-2 main protease. <i>Biophysics and Physicobiology</i> , 2021, 18, 215-222.	0.5	3
148	Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. <i>MBio</i> , 2021, 12, .	1.8	284
149	How do we share data in COVID-19 research? A systematic review of COVID-19 datasets in PubMed Central Articles. <i>Briefings in Bioinformatics</i> , 2021, 22, 800-811.	3.2	22
186	Molecular-Level Anatomy of SARS-CoV-2 for the Battle against the COVID-19 Pandemic. <i>Bulletin of the Chemical Society of Japan</i> , 2021, 94, 1478-1490.	2.0	24

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187	Genomic epidemiology reveals multiple introductions and spread of SARS-CoV-2 in the Indian state of Karnataka. <i>PLoS ONE</i> , 2020, 15, e0243412.	1.1	26
188	Evidence for Limited Early Spread of COVID-19 Within the United States, January–February 2020. <i>Morbidity and Mortality Weekly Report</i> , 2020, 69, 680-684.	9.0	141
190	The Role of Weather Conditions in COVID-19 Transmission: A Study of a Global Panel of 1236 Regions. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
191	Longitudinal Surveillance for SARS-CoV-2 Among Staff in Six Colorado Long Term Care Facilities: Epidemiologic, Virologic and Sequence Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4
192	Risk Assessment of Importation and Local Transmission of COVID-19 in South Korea: Statistical Modeling Approach. <i>JMIR Public Health and Surveillance</i> , 2021, 7, e26784.	1.2	12
193	SARS-Cov-2 genome sequence analysis suggests rapid spread followed by epidemic slowdown in France. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	1
195	Epidemiological Model Suggests D614G Spike Protein Mutation Accelerates Transmission of COVID-19 – Worldwide, 2020. <i>China CDC Weekly</i> , 2020, 2, 946-947.	1.0	5
196	Impact of computational approaches in the fight against COVID-19: an AI guided review of 17 000 studies. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	20
197	Cryptic transmission of SARS-CoV-2 and the first COVID-19 wave. <i>Nature</i> , 2021, 600, 127-132.	13.7	61
198	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	1.7	26
199	Noninvasive Technologies for Primate Conservation in the 21st Century. <i>International Journal of Primatology</i> , 2022, 43, 133-167.	0.9	16
200	A Comprehensive Overview of the Newly Emerged COVID-19 Pandemic: Features, Origin, Genomics, Epidemiology, Treatment, and Prevention. <i>Biologics</i> , 2021, 1, 357-383.	2.3	8
202	Switchover phenomenon induced by epidemic seeding on geometric networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5
204	Scalable Reconstruction of SARS-CoV-2 Phylogeny with Recurrent Mutations. <i>Journal of Computational Biology</i> , 2021, 28, 1130-1141.	0.8	2
205	Interventions to Disrupt Coronavirus Disease Transmission at a University, Wisconsin, USA, August–October 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 2776-2785.	2.0	24
206	Strength and Weakness of Molecular Identification Strategies Against Causative Viral Agent from Emerging COVID-19. <i>Journal of Bacteriology and Virology</i> , 2020, 50, 65-75.	0.0	0
210	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 followed by community and nosocomial spread, Germany, February to May 2020. <i>Eurosurveillance</i> , 2021, 26, .	3.9	11
211	Longitudinal Immune Profiling of a Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection in a Solid Organ Transplant Recipient. <i>Journal of Infectious Diseases</i> , 2022, 225, 374-384.	1.9	7

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212	Comprehensive analyses of bioinformatics applications in the fight against COVID-19 pandemic. <i>Computational Biology and Chemistry</i> , 2021, 95, 107599.	1.1	21
213	A reconstruction of early cryptic COVID spread. <i>Nature</i> , 2021, 600, 40-41.	13.7	3
215	Narrative review of the novel coronavirus SARS-CoV-2: update on genomic characteristics, transmissions and animal model. <i>Journal of Thoracic Disease</i> , 2020, 12, 7454-7466.	0.6	1
219	Contagion Modeling and Simulation in Transport and Air Travel Networks During the COVID-19 Pandemic: A Survey. <i>IEEE Access</i> , 2021, 9, 149529-149541.	2.6	6
220	COVID-19 Vaccination, Herd Immunity and The Transition Toward Normalcy: Challenges with The Upcoming Sports Events. <i>Annals of Applied Sport Science</i> , 2021, 9, 0-0.	0.4	17
221	Analysis of SARS-COV2 spike protein variants among Iraqi isolates. <i>Gene Reports</i> , 2022, 26, 101420.	0.4	12
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228	Algorithm for Preventing the Spread of COVID-19 in Airports and Air Routes by Applying Fuzzy Logic and a Markov Chain. <i>Mathematics</i> , 2021, 9, 3040.	1.1	3
229	A machine learning model for nowcasting epidemic incidence. <i>Mathematical Biosciences</i> , 2022, 343, 108677.	0.9	8
230	Early Adoption of Longitudinal Surveillance for SARS-CoV-2 among Staff in Long-Term Care Facilities: Prevalence, Virologic and Sequence Analysis. <i>Microbiology Spectrum</i> , 2021, 9, e0100321.	1.2	18
231	InterARTIC: an interactive web application for whole-genome nanopore sequencing analysis of SARS-CoV-2 and other viruses. <i>Bioinformatics</i> , 2022, 38, 1443-1446.	1.8	8
232	A symbiosis between cellular automata and dynamic weighted multigraph with application on virus spread modeling. <i>Chaos, Solitons and Fractals</i> , 2022, 155, 111660.	2.5	5
235	Measures to prevent nosocomial transmissions of COVID-19 based on interpersonal contact data. <i>Primary Health Care Research and Development</i> , 2022, 23, e4.	0.5	3
237	Of vascular defense, hemostasis, cancer, and platelet biology: an evolutionary perspective. <i>Cancer and Metastasis Reviews</i> , 2022, 41, 147-172.	2.7	6
239	Mutations in viral nucleocapsid protein and endoRNase are discovered to associate with COVID19 hospitalization risk. <i>Scientific Reports</i> , 2022, 12, 1206.	1.6	12
240	The first three waves of the Covid-19 pandemic hint at a limited genetic repertoire for SARS-CoV-2. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	11
241	Distinct mutations and lineages of SARSâ€CoVâ€2 virus in the early phase of COVIDâ€19 pandemic and subsequent 1â€year global expansion. <i>Journal of Medical Virology</i> , 2022, 94, 2035-2049.	2.5	7
242	SARS-CoV-2 introductions and early dynamics of the epidemic in Portugal. <i>Communications Medicine</i> , 2022, 2, .	1.9	5

#	ARTICLE	IF	CITATIONS
243	COVID-19 in Southeast Asia: current status and perspectives. <i>Bioengineered</i> , 2022, 13, 3797-3809.	1.4	36
244	SARS-CoV-2 Variants Associated with Vaccine Breakthrough in the Delaware Valley through Summer 2021. <i>MBio</i> , 2022, 13, e0378821.	1.8	11
245	Spatial analysis of socio-economic factors and their relationship with the cases of COVID-19 in Pernambuco, Brazil. <i>Tropical Medicine and International Health</i> , 2022, 27, 397-407.	1.0	9
246	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021, 600, 408-418.	13.7	249
249	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	3.3	18
250	Unrecognized introductions of SARS-CoV-2 into the US state of Georgia shaped the early epidemic. <i>Virus Evolution</i> , 2022, 8, veac011.	2.2	2
251	A Bayesian Spatiotemporal Nowcasting Model for Public Health Decision-Making and Surveillance. <i>American Journal of Epidemiology</i> , 2022, , .	1.6	3
252	Mutations and Phylogenetic Analyses of SARS-CoV-2 Among Imported COVID-19 From Abroad in Nanjing, China. <i>Frontiers in Microbiology</i> , 2022, 13, 851323.	1.5	4
253	Nonfatal opioid overdoses before and after Covid-19: Regional variation in rates of change. <i>PLoS ONE</i> , 2022, 17, e0263893.	1.1	7
254	Travel ban effects on SARS-CoV-2 transmission lineages in the UAE as inferred by genomic epidemiology. <i>PLoS ONE</i> , 2022, 17, e0264682.	1.1	3
256	Using genomic epidemiology of SARS-CoV-2 to support contact tracing and public health surveillance in rural Humboldt County, California. <i>BMC Public Health</i> , 2022, 22, 456.	1.2	10
257	Evolutionary history and introduction of SARS-CoV-2 Alpha VOC/B.1.1.7 in Pakistan through international travelers. <i>Virus Evolution</i> , 2022, 8, veac020.	2.2	8
258	New Insights for Biosensing: Lessons from Microbial Defense Systems. <i>Chemical Reviews</i> , 2022, 122, 8126-8180.	23.0	15
259	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
260	Genomic epidemiology of the Los Angeles COVID-19 outbreak and the early history of the B.1.43 strain in the USA. <i>BMC Genomics</i> , 2022, 23, 260.	1.2	0
261	Role of genomics in combating COVID-19 pandemic. <i>Gene</i> , 2022, 823, 146387.	1.0	20
262	The spike glycoprotein of SARS-CoV-2: A review of how mutations of spike glycoproteins have driven the emergence of variants with high transmissibility and immune escape. <i>International Journal of Biological Macromolecules</i> , 2022, 208, 105-125.	3.6	41
263	Describing, Modelling and Forecasting the Spatial and Temporal Spread of COVID-19: A Short Review. <i>Fields Institute Communications</i> , 2022, , 25-51.	0.6	13

#	ARTICLE	IF	CITATIONS
264	Diverse Local Epidemics Reveal the Distinct Effects of Population Density, Demographics, Climate, Depletion of Susceptibles, and Intervention in the First Wave of COVID-19 in the United States. <i>Fields Institute Communications</i> , 2022, , 1-23.	0.6	2
265	EXTENT OF ANXIETY AND STRESS IN DIFFERENT GROUPS OF HEALTH CARE WORKERS OF SIKKIM BASED ON THEIR EXTENT OF INSOMNIA. , 2021, , 93-95.		0
268	Viral surface geometry shapes influenza and coronavirus spike evolution through antibody pressure. <i>PLoS Computational Biology</i> , 2021, 17, e1009664.	1.5	4
269	Translating virus evolution into epidemiology. <i>Cell Host and Microbe</i> , 2022, 30, 444-448.	5.1	4
270	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. <i>Nature Reviews Genetics</i> , 2022, 23, 547-562.	7.7	70
271	Extracorporeal membrane oxygenation for respiratory failure in phases of COVID-19 variants. <i>Journal of Cardiac Surgery</i> , 2022, 37, 2972-2979.	0.3	5
272	Evolution and Epidemiology of SARS-CoV-2 Virus. <i>Methods in Molecular Biology</i> , 2022, 2452, 3-18.	0.4	0
273	An Electrostatically-steered Conformational Selection Mechanism Promotes SARS-CoV-2 Spike Protein Variation. <i>Journal of Molecular Biology</i> , 2022, 434, 167637.	2.0	1
274	A measure to estimate the risk of imported COVID-19 cases and its application for evaluating travel-related control measures. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
276	Before you go: a packing list for portable DNA sequencing of microbiomes and metagenomes. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	4
277	Rapid and Affordable High Throughput Screening of SARS-CoV-2 Variants Using Denaturing High-Performance Liquid Chromatography Analysis. <i>Frontiers in Virology</i> , 0, 2, .	0.7	0
279	Clinical Performance Characteristics of the Swift Normalase Amplicon Panel for Sensitive Recovery of Severe Acute Respiratory Syndrome Coronavirus 2 Genomes. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 963-976.	1.2	7
280	New Phylogenetic Models Incorporating Interval-Specific Dispersal Dynamics Improve Inference of Disease Spread. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
281	covSampler: A subsampling method with balanced genetic diversity for large-scale SARS-CoV-2 genome data sets. <i>Virus Evolution</i> , 2022, 8, .	2.2	3
282	The SARS-CoV-2 Variants and their Impacts. <i>Journal of Pure and Applied Microbiology</i> , 2022, 16, 1409-1424.	0.3	3
283	Genomic surveillance of SARS-CoV-2 in Puerto Rico enabled early detection and tracking of variants. <i>Communications Medicine</i> , 2022, 2, .	1.9	4
284	STARs (STrain-Amplicon-Seq), a targeted Nanopore sequencing workflow for SARS-CoV-2 diagnostics and genotyping. <i>Biology Methods and Protocols</i> , 0, , .	1.0	0
285	SARS-COV-2/COVID-19: scenario, epidemiology, adaptive mutations, and environmental factors. <i>Environmental Science and Pollution Research</i> , 2022, 29, 69117-69136.	2.7	7

#	ARTICLE	IF	CITATIONS
287	NanoCoV19: An analytical pipeline for rapid detection of severe acute respiratory syndrome coronavirus 2. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
288	Phylodynamic analysis of SARS-CoV-2 spread in Rio de Janeiro, Brazil, highlights how metropolitan areas act as dispersal hubs for new variants. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
289	New rules for genomics-informed COVID-19 responsesâ€“Lessons learned from the first waves of the Omicron variant in Australia. <i>PLoS Genetics</i> , 2022, 18, e1010415.	1.5	9
290	Associations Between Mobility Indices and the COVID-19 Pandemic in Thailand. <i>Nakhara: Journal of Environmental Design and Planning</i> , 2022, 21, 215.	0.0	0
291	Amino acid variants of SARS-CoV-2 papain-like protease have impact on drug binding. <i>PLoS Computational Biology</i> , 2022, 18, e1010667.	1.5	3
292	Social vulnerability amplifies the disparate impact of mobility on COVID-19 transmissibility across the United States. <i>Humanities and Social Sciences Communications</i> , 2022, 9, .	1.3	4
293	Nasal host response-based screening for undiagnosed respiratory viruses: a pathogen surveillance and detection study. <i>Lancet Microbe</i> , The, 2023, 4, e38-e46.	3.4	10
294	Sentinel Surveillance System Implementation and Evaluation for SARS-CoV-2 Genomic Data, Washington, USA, 2020â€“2021. <i>Emerging Infectious Diseases</i> , 2023, 29, 242-251.	2.0	4
295	One Health Investigation of SARS-CoV-2 in People and Animals on Multiple Mink Farms in Utah. <i>Viruses</i> , 2023, 15, 96.	1.5	4
296	Accelerated SARS-CoV-2 intrahost evolution leading to distinct genotypes during chronic infection. <i>Cell Reports Medicine</i> , 2023, 4, 100943.	3.3	31
297	Correlated substitutions reveal SARS-like coronaviruses recombine frequently with a diverse set of structured gene pools. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	4
298	The DataHarmonizer: a tool for faster data harmonization, validation, aggregation and analysis of pathogen genomics contextual information. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
299	Using metagenomics to detect West Nile virus in mosquitoes collected in Oklahoma. <i>Bios</i> , 2023, 93, .	0.0	2
300	The effect of changing COVID-19 restrictions on the transmission rate in a veterinary clinic. <i>Infectious Disease Modelling</i> , 2023, 8, 294-308.	1.2	0
301	Dissecting Phenotype from Genotype with Clinical Isolates of SARS-CoV-2 First Wave Variants. <i>Viruses</i> , 2023, 15, 611.	1.5	1
303	Estimating the undetected emergence of COVID-19 in the US. <i>PLoS ONE</i> , 2023, 18, e0284025.	1.1	0
304	Maximum likelihood pandemic-scale phylogenetics. <i>Nature Genetics</i> , 2023, 55, 746-752.	9.4	11
319	Bioinformatics in the study of microbial infections. , 2024, , 1975-1992.		0

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