

Charles Y Chiu

List of Publications by Year in descending order

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Version: 2024-02-01

167
papers

18,911
citations

16411

64
h-index

16605

123
g-index

242
all docs

242
docs citations

242
times ranked

25069
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR-Cas12-based detection of SARS-CoV-2. <i>Nature Biotechnology</i> , 2020, 38, 870-874.	9.4	1,884
2	Clinical metagenomics. <i>Nature Reviews Genetics</i> , 2019, 20, 341-355.	7.7	793
3	Actionable Diagnosis of Neuroleptospirosis by Next-Generation Sequencing. <i>New England Journal of Medicine</i> , 2014, 370, 2408-2417.	13.9	760
4	Clinical Metagenomic Next-Generation Sequencing for Pathogen Detection. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2019, 14, 319-338.	9.6	755
5	Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. <i>New England Journal of Medicine</i> , 2019, 380, 2327-2340.	13.9	644
6	Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 99.	3.6	456
7	Transmission, infectivity, and neutralization of a spike L452R SARS-CoV-2 variant. <i>Cell</i> , 2021, 184, 3426-3437.e8.	13.5	424
8	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. <i>Genome Research</i> , 2014, 24, 1180-1192.	2.4	421
9	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. <i>Archives of Pathology and Laboratory Medicine</i> , 2017, 141, 776-786.	1.2	404
10	Laboratory validation of a clinical metagenomic sequencing assay for pathogen detection in cerebrospinal fluid. <i>Genome Research</i> , 2019, 29, 831-842.	2.4	349
11	A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012-14): a retrospective cohort study. <i>Lancet Infectious Diseases</i> , 2015, 15, 671-682.	4.6	348
12	Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids. <i>Nature Medicine</i> , 2021, 27, 115-124.	15.2	329
13	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2587-2594.e7.	13.5	285
14	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. <i>Scientific Reports</i> , 2017, 7, 18022.	1.6	264
15	Diagnosis of Neuroinvasive Astrovirus Infection in an Immunocompromised Adult With Encephalitis by Unbiased Next-Generation Sequencing. <i>Clinical Infectious Diseases</i> , 2015, 60, 919-923.	2.9	262
16	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
17	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	9.4	251
18	Integrating host response and unbiased microbe detection for lower respiratory tract infection diagnosis in critically ill adults. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E12353-E12362.	3.3	249

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19	Recovery of divergent avian bornaviruses from cases of proventricular dilatation disease: Identification of a candidate etiologic agent. <i>Virology Journal</i> , 2008, 5, 88.	1.4	235
20	Viral Infection in Acute Exacerbation of Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 183, 1698-1702.	2.5	230
21	In vivo monoclonal antibody efficacy against SARS-CoV-2 variant strains. <i>Nature</i> , 2021, 596, 103-108.	13.7	222
22	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	6.0	217
23	The Perils of Pathogen Discovery: Origin of a Novel Parvovirus-Like Hybrid Genome Traced to Nucleic Acid Extraction Spin Columns. <i>Journal of Virology</i> , 2013, 87, 11966-11977.	1.5	216
24	An ensemble strategy that significantly improves de novo assembly of microbial genomes from metagenomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e46-e46.	6.5	213
25	Viral pathogen discovery. <i>Current Opinion in Microbiology</i> , 2013, 16, 468-478.	2.3	190
26	Metagenomic Sequencing Detects Respiratory Pathogens in Hematopoietic Cellular Transplant Patients. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 524-528.	2.5	187
27	A Novel Rhabdovirus Associated with Acute Hemorrhagic Fever in Central Africa. <i>PLoS Pathogens</i> , 2012, 8, e1002924.	2.1	181
28	A Metagenomic Analysis of Pandemic Influenza A (2009 H1N1) Infection in Patients from North America. <i>PLoS ONE</i> , 2010, 5, e13381.	1.1	169
29	Cryo-EM visualization of an exposed RGD epitope on adenovirus that escapes antibody neutralization. <i>EMBO Journal</i> , 1997, 16, 1189-1198.	3.5	165
30	A mouse model of paralytic myelitis caused by enterovirus D68. <i>PLoS Pathogens</i> , 2017, 13, e1006199.	2.1	158
31	Structure of Adenovirus Complexed with Its Internalization Receptor, α 5 β 1 Integrin. <i>Journal of Virology</i> , 1999, 73, 6759-6768.	1.5	155
32	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
33	Identification of cardioviruses related to Theiler's murine encephalomyelitis virus in human infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14124-14129.	3.3	152
34	The complete genome of klassevirus " a novel picornavirus in pediatric stool. <i>Virology Journal</i> , 2009, 6, 82.	1.4	152
35	Toward an Understanding of Changes in Diversity Associated with Fecal Microbiome Transplantation Based on 16S rRNA Gene Deep Sequencing. <i>MBio</i> , 2012, 3, .	1.8	151
36	Limited cross-variant immunity from SARS-CoV-2 Omicron without vaccination. <i>Nature</i> , 2022, 607, 351-355.	13.7	143

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37	Idiopathic pneumonia syndrome after hematopoietic cell transplantation: evidence of occult infectious etiologies. <i>Blood</i> , 2015, 125, 3789-3797.	0.6	137
38	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
39	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. <i>Nature Communications</i> , 2019, 10, 579.	5.8	131
40	Neutralizing immunity in vaccine breakthrough infections from the SARS-CoV-2 Omicron and Delta variants. <i>Cell</i> , 2022, 185, 1539-1548.e5.	13.5	126
41	Cross-Species Transmission of a Novel Adenovirus Associated with a Fulminant Pneumonia Outbreak in a New World Monkey Colony. <i>PLoS Pathogens</i> , 2011, 7, e1002155.	2.1	124
42	SARS-CoV-2 seroprevalence and neutralizing activity in donor and patient blood. <i>Nature Communications</i> , 2020, 11, 4698.	5.8	124
43	Acute Flaccid Myelitis of Unknown Etiology in California, 2012-2015. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 2663.	3.8	118
44	SARS-CoV-2 antibody magnitude and detectability are driven by disease severity, timing, and assay. <i>Science Advances</i> , 2021, 7, .	4.7	117
45	Metagenomics for the discovery of novel human viruses. <i>Future Microbiology</i> , 2010, 5, 177-189.	1.0	114
46	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
47	Discovery of a Novel Polyomavirus in Acute Diarrheal Samples from Children. <i>PLoS ONE</i> , 2012, 7, e49449.	1.1	110
48	The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. <i>Nature Medicine</i> , 2017, 23, 1080-1085.	15.2	109
49	Coinfections of Zika and Chikungunya Viruses in Bahia, Brazil, Identified by Metagenomic Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2348-2353.	1.8	106
50	Clinical metagenomic identification of <i>Balamuthia mandrillaris</i> encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. <i>Genome Medicine</i> , 2015, 7, 113.	3.6	102
51	A Helper-Independent Adenovirus Vector with E1, E3, and Fiber Deleted: Structure and Infectivity of Fiberless Particles. <i>Journal of Virology</i> , 1999, 73, 1601-1608.	1.5	96
52	Pan-viral serology implicates enteroviruses in acute flaccid myelitis. <i>Nature Medicine</i> , 2019, 25, 1748-1752.	15.2	93
53	Acute flaccid myelitis: cause, diagnosis, and management. <i>Lancet, The</i> , 2021, 397, 334-346.	6.3	88
54	Microarray Detection of Human Parainfluenzavirus 4 Infection Associated with Respiratory Failure in an Immunocompetent Adult. <i>Clinical Infectious Diseases</i> , 2006, 43, e71-e76.	2.9	87

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55	Miscarriage and stillbirth following maternal Zika virus infection in nonhuman primates. <i>Nature Medicine</i> , 2018, 24, 1104-1107.	15.2	85
56	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	5.1	82
57	Cryo-EM imaging of the catalytic subunit of the DNA-dependent protein kinase. <i>Journal of Molecular Biology</i> , 1998, 284, 1075-1081.	2.0	79
58	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , 2021, 7, .	4.7	79
59	Longitudinal Transcriptome Analysis Reveals a Sustained Differential Gene Expression Signature in Patients Treated for Acute Lyme Disease. <i>MBio</i> , 2016, 7, e00100-16.	1.8	76
60	Viral Surveillance in Serum Samples From Patients With Acute Liver Failure By Metagenomic Next-Generation Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 65, 1477-1485.	2.9	76
61	Diagnosis of Fatal Human Case of St. Louis Encephalitis Virus Infection by Metagenomic Sequencing, California, 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 1964-1968.	2.0	76
62	Discovery of a Novel Human Pegivirus in Blood Associated with Hepatitis C Virus Co-Infection. <i>PLoS Pathogens</i> , 2015, 11, e1005325.	2.1	74
63	Direct Comparison of SARS-CoV-2 Analytical Limits of Detection across Seven Molecular Assays. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	73
64	Digital droplet PCR accurately quantifies SARS-CoV-2 viral load from crude lysate without nucleic acid purification. <i>Scientific Reports</i> , 2021, 11, 780.	1.6	72
65	Utility of DNA Microarrays for Detection of Viruses in Acute Respiratory Tract Infections in Children. <i>Journal of Pediatrics</i> , 2008, 153, 76-83.e1.	0.9	70
66	ReScan, a Multiplex Diagnostic Pipeline, Pans Human Sera for SARS-CoV-2 Antigens. <i>Cell Reports Medicine</i> , 2020, 1, 100123.	3.3	70
67	E-Predict: a computational strategy for species identification based on observed DNA microarray hybridization patterns. <i>Genome Biology</i> , 2005, 6, R78.	13.9	68
68	Diagnosis of a Critical Respiratory Illness Caused by Human Metapneumovirus by Use of a Pan-Virus Microarray. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2340-2343.	1.8	67
69	Experimental Zika Virus Infection in the Pregnant Common Marmoset Induces Spontaneous Fetal Loss and Neurodevelopmental Abnormalities. <i>Scientific Reports</i> , 2018, 8, 6851.	1.6	63
70	Neurobrucellosis: Unexpected Answer From Metagenomic Next-Generation Sequencing. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2017, 6, piw066.	0.6	62
71	Point-Counterpoint: Should We Be Performing Metagenomic Next-Generation Sequencing for Infectious Disease Diagnosis in the Clinical Laboratory?. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	62
72	Competitive SARS-CoV-2 Serology Reveals Most Antibodies Targeting the Spike Receptor-Binding Domain Compete for ACE2 Binding. <i>MSphere</i> , 2020, 5, .	1.3	62

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73	Acute Liver Failure of Indeterminate Etiology: A Comprehensive Systematic Approach by An Expert Committee to Establish Causality. <i>American Journal of Gastroenterology</i> , 2018, 113, 1319.	0.2	61
74	Hepatitis E Virus-associated Meningoencephalitis in a Lung Transplant Recipient Diagnosed by Clinical Metagenomic Sequencing. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx121.	0.4	60
75	Clinical outcomes and serologic response in solid organ transplant recipients with COVID-19: A case series from the United States. <i>American Journal of Transplantation</i> , 2020, 20, 3225-3233.	2.6	60
76	The Role of Metagenomics and Next-Generation Sequencing in Infectious Disease Diagnosis. <i>Clinical Chemistry</i> , 2021, 68, 115-124.	1.5	60
77	Clinical features, diagnostics, and outcomes of patients presenting with acute respiratory illness: A retrospective cohort study of patients with and without COVID-19. <i>EClinicalMedicine</i> , 2020, 27, 100518.	3.2	59
78	Experimental Zika Virus Inoculation in a New World Monkey Model Reproduces Key Features of the Human Infection. <i>Scientific Reports</i> , 2017, 7, 17126.	1.6	58
79	Whole-Genome Sequencing of Methicillin-Resistant <i>Staphylococcus aureus</i> Resistant to Fifth-Generation Cephalosporins Reveals Potential Non-mecA Mechanisms of Resistance. <i>PLoS ONE</i> , 2016, 11, e0149541.	1.1	53
80	Using a Pan-Viral Microarray Assay (Virochip) to Screen Clinical Samples for Viral Pathogens. <i>Journal of Visualized Experiments</i> , 2011, . .	0.2	52
81	Cutting-Edge Infectious Disease Diagnostics with CRISPR. <i>Cell Host and Microbe</i> , 2018, 23, 702-704.	5.1	52
82	Structural Analysis of a Fiber-Pseudotyped Adenovirus with Ocular Tropism Suggests Differential Modes of Cell Receptor Interactions. <i>Journal of Virology</i> , 2001, 75, 5375-5380.	1.5	51
83	The Genome Sequence of Lone Star Virus, a Highly Divergent Bunyavirus Found in the <i>Amblyomma americanum</i> Tick. <i>PLoS ONE</i> , 2013, 8, e62083.	1.1	50
84	Thoracic CT findings of novel influenza A (H1N1) infection in immunocompromised patients. <i>Emergency Radiology</i> , 2010, 17, 299-307.	1.0	48
85	A Novel Adenovirus Species Associated with an Acute Respiratory Outbreak in a Baboon Colony and Evidence of Coincident Human Infection. <i>MBio</i> , 2013, 4, e00084.	1.8	48
86	A novel bocavirus in canine liver. <i>Virology Journal</i> , 2013, 10, 54.	1.4	47
87	Cultivation and Serological Characterization of a Human Theiler's-Like Cardiovirus Associated with Diarrheal Disease. <i>Journal of Virology</i> , 2010, 84, 4407-4414.	1.5	45
88	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	2.0	45
89	Identification of high-risk human papillomavirus and Rb/E2F pathway genomic alterations in mutually exclusive subsets of colorectal neuroendocrine carcinoma. <i>Modern Pathology</i> , 2019, 32, 290-305.	2.9	45
90	Upregulation of Human Endogenous Retrovirus-K Is Linked to Immunity and Inflammation in Pulmonary Arterial Hypertension. <i>Circulation</i> , 2017, 136, 1920-1935.	1.6	44

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91	Metagenomic-based Surveillance of Pacific Coast tick <i>Dermacentor occidentalis</i> Identifies Two Novel Bunyaviruses and an Emerging Human Rickettsial Pathogen. <i>Scientific Reports</i> , 2017, 7, 12234.	1.6	42
92	DNA Microarray for Detection of Gastrointestinal Viruses. <i>Journal of Clinical Microbiology</i> , 2015, 53, 136-145.	1.8	41
93	Cell-free DNA tissues of origin by methylation profiling reveals significant cell, tissue, and organ-specific injury related to COVID-19 severity. <i>Med</i> , 2021, 2, 411-422.e5.	2.2	41
94	STROBE-metagenomics: a STROBE extension statement to guide the reporting of metagenomics studies. <i>Lancet Infectious Diseases</i> , The, 2020, 20, e251-e260.	4.6	40
95	Genomic Assays for Identification of Chikungunya Virus in Blood Donors, Puerto Rico, 2014. <i>Emerging Infectious Diseases</i> , 2015, 21, 1409-1413.	2.0	39
96	Severe Epididymo-Orchitis and Encephalitis Complicating Anti-PD-1 Therapy. <i>Oncologist</i> , 2019, 24, 872-876.	1.9	38
97	Utility of Metagenomic Next-Generation Sequencing for Characterization of HIV and Human Pegivirus Diversity. <i>PLoS ONE</i> , 2015, 10, e0141723.	1.1	37
98	Predominance of antibody-resistant SARS-CoV-2 variants in vaccine breakthrough cases from the San Francisco Bay Area, California. <i>Nature Microbiology</i> , 2022, 7, 277-288.	5.9	37
99	The Mitochondrial Genome and a 60-kb Nuclear DNA Segment from <i>Naegleria fowleri</i> , the Causative Agent of Primary Amoebic Meningoencephalitis. <i>Journal of Eukaryotic Microbiology</i> , 2013, 60, 179-191.	0.8	36
100	Two Rapidly Growing Mycobacterial Species Isolated from a Brain Abscess: First Whole-Genome Sequences of <i>Mycobacterium immunogenum</i> and <i>Mycobacterium llutzerense</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 2374-2377.	1.8	36
101	Optimization and clinical validation of dual-target RT-LAMP for SARS-CoV-2. <i>Journal of Virological Methods</i> , 2020, 286, 113972.	1.0	36
102	In-Depth Investigation of Archival and Prospectively Collected Samples Reveals No Evidence for XMRV Infection in Prostate Cancer. <i>PLoS ONE</i> , 2012, 7, e44954.	1.1	35
103	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
104	Concerns over the origin of NIH-CQV, a novel virus discovered in Chinese patients with seronegative hepatitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E976-E976.	3.3	34
105	Development of a candidate reference material for adventitious virus detection in vaccine and biologicals manufacturing by deep sequencing. <i>Vaccine</i> , 2016, 34, 2035-2043.	1.7	34
106	Detection of SARS-CoV-2 variants by Abbott molecular, antigen, and serological tests. <i>Journal of Clinical Virology</i> , 2022, 147, 105080.	1.6	28
107	Differentiation enhances Zika virus infection of neuronal brain cells. <i>Scientific Reports</i> , 2018, 8, 14543.	1.6	26
108	The B.1.427/1.429 (epsilon) SARS-CoV-2 variants are more virulent than ancestral B.1 (614G) in Syrian hamsters. <i>PLoS Pathogens</i> , 2022, 18, e1009914.	2.1	26

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109	The Long March: A Sample Preparation Technique that Enhances Contig Length and Coverage by High-Throughput Short-Read Sequencing. <i>PLoS ONE</i> , 2008, 3, e3495.	1.1	25
110	Polyoma virus-associated carcinomas of the urologic tract: a clinicopathologic and molecular study. <i>Modern Pathology</i> , 2018, 31, 1429-1441.	2.9	25
111	Metagenomic prediction of antimicrobial resistance in critically ill patients with lower respiratory tract infections. <i>Genome Medicine</i> , 2022, 14, .	3.6	25
112	Antibodies to the Novel Human Pegivirus 2 Are Associated with Active and Resolved Infections. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2023-2030.	1.8	23
113	Digitally collected cryo-electron micrographs for single particle reconstruction. , 2000, 49, 224-232.		22
114	Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing. <i>PLoS ONE</i> , 2019, 14, e0212193.	1.1	22
115	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. <i>Clinical Infectious Diseases</i> , 2017, 64, 476-481.	2.9	21
116	Epidemiological and genomic characterization of community-acquired <i>Clostridium difficile</i> infections. <i>BMC Infectious Diseases</i> , 2018, 18, 443.	1.3	21
117	Experimental Cross-Species Infection of Common Marmosets by Titi Monkey Adenovirus. <i>PLoS ONE</i> , 2013, 8, e68558.	1.1	20
118	Bacteriologic features of surgical site infections following breast surgery. <i>American Journal of Surgery</i> , 2009, 198, 529-531.	0.9	19
119	Pandemic (H1N1) 2009 Infection in Patients with Hematologic Malignancy. <i>Emerging Infectious Diseases</i> , 2010, 16, 1910-1917.	2.0	18
120	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	1.7	18
121	Connecting the Dots: Translating the Vaginal Microbiome Into a Drug. <i>Journal of Infectious Diseases</i> , 2021, 223, S296-S306.	1.9	18
122	Rapid deployment of SARS-CoV-2 testing: The CLIAHUB. <i>PLoS Pathogens</i> , 2020, 16, e1008966.	2.1	18
123	COVID-19 Variant Detection with a High-Fidelity CRISPR-Cas12 Enzyme. <i>Journal of Clinical Microbiology</i> , 2022, 60, .	1.8	18
124	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	17
125	Fatal Case of Chronic Jamestown Canyon Virus Encephalitis Diagnosed by Metagenomic Sequencing in Patient Receiving Rituximab. <i>Emerging Infectious Diseases</i> , 2021, 27, 238-242.	2.0	17
126	Use of Metagenomic Next-Generation Sequencing to Identify Pathogens in Pediatric Osteoarticular Infections. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab346.	0.4	17

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127	Timely intervention and control of a novel coronavirus (COVID-19) outbreak at a large skilled nursing facility—San Francisco, California, 2020. <i>Infection Control and Hospital Epidemiology</i> , 2021, 42, 1173-1180.	1.0	17
128	Complete genome sequence of sequential <i>Pandoraea apista</i> isolates from the same cystic fibrosis patient supports a model of chronic colonization with in vivo strain evolution over time. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 87, 1-6.	0.8	16
129	Detection of cryptogenic malignancies from metagenomic whole genome sequencing of body fluids. <i>Genome Medicine</i> , 2021, 13, 98.	3.6	16
130	Individualized Constellation of Killer Cell Immunoglobulin-Like Receptors and Cognate HLA Class I Ligands that Controls Natural Killer Cell Antiviral Immunity Predisposes COVID-19. <i>Frontiers in Genetics</i> , 2022, 13, 845474.	1.1	15
131	Detection of Neoplasms by Metagenomic Next-Generation Sequencing of Cerebrospinal Fluid. <i>JAMA Neurology</i> , 2021, 78, 1355.	4.5	14
132	Characterization of the Bas-Congo Virus Glycoprotein and Its Function in Pseudotyped Viruses. <i>Journal of Virology</i> , 2013, 87, 9558-9568.	1.5	13
133	Efficacy of an inactivated Zika vaccine against virus infection during pregnancy in mice and marmosets. <i>Npj Vaccines</i> , 2022, 7, 9.	2.9	13
134	Review: Resolution Issues in Single-Particle Reconstruction. <i>Journal of Structural Biology</i> , 1999, 128, 58-64.	1.3	12
135	Contact-Tracing Outcomes Among Household Contacts of Fully Vaccinated Coronavirus Disease 2019 (COVID-19) Patients: San Francisco, California, 29 January—2 July 2021. <i>Clinical Infectious Diseases</i> , 2022, 75, e267-e275.	2.9	12
136	Rosavirus: the prototype of a proposed new genus of the Picornaviridae family. <i>Virus Genes</i> , 2013, 47, 556-558.	0.7	10
137	Bas-Congo virus: another deadly virus?. <i>Future Microbiology</i> , 2013, 8, 139-141.	1.0	10
138	Exploratory analysis of the potential for advanced diagnostic testing to reduce healthcare expenditures of patients hospitalized with meningitis or encephalitis. <i>PLoS ONE</i> , 2020, 15, e0226895.	1.1	10
139	Two Sides of a Coin: a Zika Virus Mutation Selected in Pregnant Rhesus Macaques Promotes Fetal Infection in Mice but at a Cost of Reduced Fitness in Nonpregnant Macaques and Diminished Transmissibility by Vectors. <i>Journal of Virology</i> , 2020, 94, .	1.5	10
140	Universal Polymerase Chain Reaction and Antibody Testing Demonstrate Little to No Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 in a Rural Community. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofaa531.	0.4	9
141	Magnitude and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Household Transmission: A Longitudinal Cohort Study. <i>Clinical Infectious Diseases</i> , 2022, 75, S193-S204.	2.9	9
142	No Viral Association Found in a Set of Differentiated Vulvar Intraepithelial Neoplasia Cases by Human Papillomavirus and Pan-Viral Microarray Testing. <i>PLoS ONE</i> , 2015, 10, e0125292.	1.1	8
143	Genome Sequence of Bivens Arm Virus, a Tibrovirus Belonging to the Species <i>Tibrogargan virus</i> () Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.8	0.8	8
144	Two human immunodeficiency virus Type 2 cases in US blood donors including serologic, molecular, and genomic characterization of an epidemiologically unusual case. <i>Transfusion</i> , 2016, 56, 1560-1568.	0.8	8

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145	Establishment and characterization of an oral tongue squamous cell carcinoma cell line from a never-smoking patient. <i>Oral Oncology</i> , 2017, 69, 1-10.	0.8	8
146	Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. <i>Frontiers in Microbiology</i> , 2019, 10, 856.	1.5	8
147	Gastroenteritis, Hepatitis, Encephalopathy, and Human Herpesvirus 6 Detection in an Immunocompetent Child: Benefits and Risks of Syndromic Multiplex Molecular Panel Testing. <i>Journal of Pediatrics</i> , 2019, 212, 228-231.	0.9	8
148	Associations of Early COVID-19 Cases in San Francisco With Domestic and International Travel. <i>Clinical Infectious Diseases</i> , 2020, 71, 2976-2980.	2.9	8
149	Human Tibroviruses: Commensals or Lethal Pathogens?. <i>Viruses</i> , 2020, 12, 252.	1.5	8
150	Acute Zika virus infection in an asymptomatic blood donor at the onset of the Puerto Rico epidemic. <i>Transfusion</i> , 2019, 59, 3164-3170.	0.8	7
151	New Genomes from the Congo Basin Expand History of CRF01_AE Origin and Dissemination. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 574-582.	0.5	7
152	Beatrice Hill Virus Represents a Novel Species in the Genus Tibrovirus (Mononegavirales :) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td	0.8	6
153	Metagenomic sequencing of stool samples in Bangladeshi infants: virome association with poliovirus shedding after oral poliovirus vaccination. <i>Scientific Reports</i> , 2020, 10, 15392.	1.6	6
154	Draft Genome Sequence of Mycobacterium heraklionense Strain Davo. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
155	Draft Genome Sequence of Mycobacterium obuense Strain UC1, Isolated from Patient Sputum. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
156	A Child With Intermittent Headaches and Eosinophilic Meningitis. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2018, 7, 355-357.	0.6	4
157	COVID-19 in vaccinated versus unvaccinated hematologic malignancy patients. <i>Transplant Infectious Disease</i> , 2022, 24, .	0.7	4
158	Bas-Congo Virus. , 2014, , 13-24.		3
159	First Complete Genome Sequence of Corynebacterium riegellii. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
160	The hidden threat of unidentified agents of disease in human and veterinary biologicals. <i>Biologicals</i> , 2013, 41, 129-130.	0.5	2
161	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
162	Draft Genome Sequence of Mycobacterium elephantis Strain Lipa. <i>Genome Announcements</i> , 2015, 3, .	0.8	1

#	ARTICLE	IF	CITATIONS
163	Draft Genome Sequence of <i>Mycobacterium heckeshornense</i> Strain RLE. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
164	First Draft Genome Sequences of <i>Neisseria</i> sp. Strain 83E34 and <i>Neisseria</i> sp. Strain 74A18 Previously Identified as CDC Eugonic Fermenter 4b Species. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
165	Draft Genome Sequence of <i>Mycobacterium arupense</i> Strain GUC1. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
166	Metagenomic Next-Generation Sequencing for Pathogen Detection and Identification. , 2018, , 617-632.		0
167	Pathologic Findings Associated With a Case of Acute Flaccid Myelitis. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 484-487.	0.9	0