

Charles Y Chiu

List of Publications by Year in descending order

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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	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
2	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
3	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
4	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
5	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
6	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
7	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
8	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
9	COVID-19 in vaccinated versus unvaccinated hematologic malignancy patients. <i>Transplant Infectious Disease</i> , 2022, 24, .	0.7	4
10	Limited cross-variant immunity from SARS-CoV-2 Omicron without vaccination. <i>Nature</i> , 2022, 607, 351-355.	13.7	143
11	COVID-19 Variant Detection with a High-Fidelity CRISPR-Cas12 Enzyme. <i>Journal of Clinical Microbiology</i> , 2022, 60, .	1.8	18
12	Metagenomic prediction of antimicrobial resistance in critically ill patients with lower respiratory tract infections. <i>Genome Medicine</i> , 2022, 14, .	3.6	25
13	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
14	Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids. <i>Nature Medicine</i> , 2021, 27, 115-124.	15.2	329
15	Acute flaccid myelitis: cause, diagnosis, and management. <i>Lancet, The</i> , 2021, 397, 334-346.	6.3	88
16	The Role of Metagenomics and Next-Generation Sequencing in Infectious Disease Diagnosis. <i>Clinical Chemistry</i> , 2021, 68, 115-124.	1.5	60
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	Detection of cryptogenic malignancies from metagenomic whole genome sequencing of body fluids. <i>Genome Medicine</i> , 2021, 13, 98.	3.6	16
26	In vivo monoclonal antibody efficacy against SARS-CoV-2 variant strains. <i>Nature</i> , 2021, 596, 103-108.	13.7	222
27	Transmission, infectivity, and neutralization of a spike L452R SARS-CoV-2 variant. <i>Cell</i> , 2021, 184, 3426-3437.e8.	13.5	424
28	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
29	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
30	SARS-CoV-2 antibody magnitude and detectability are driven by disease severity, timing, and assay. <i>Science Advances</i> , 2021, 7, .	4.7	117
31	Detection of Neoplasms by Metagenomic Next-Generation Sequencing of Cerebrospinal Fluid. <i>JAMA Neurology</i> , 2021, 78, 1355.	4.5	14
32	Timely intervention and control of a novel coronavirus (COVID-19) outbreak at a large skilled nursing facility in San Francisco, California, 2020. <i>Infection Control and Hospital Epidemiology</i> , 2021, 42, 1173-1180.	1.0	17
33	Connecting the Dots: Translating the Vaginal Microbiome Into a Drug. <i>Journal of Infectious Diseases</i> , 2021, 223, S296-S306.	1.9	18
34	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
35	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
36	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

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37	ReScan, a Multiplex Diagnostic Pipeline, Pans Human Sera for SARS-CoV-2 Antigens. <i>Cell Reports Medicine</i> , 2020, 1, 100123.	3.3	70
38	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
39	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
40	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
41	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	9.4	251
42	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
43	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
44	SARS-CoV-2 seroprevalence and neutralizing activity in donor and patient blood. <i>Nature Communications</i> , 2020, 11, 4698.	5.8	124
45	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	6.0	217
46	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
47	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
48	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
49	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
50	Human Tibroviruses: Commensals or Lethal Pathogens?. <i>Viruses</i> , 2020, 12, 252.	1.5	8
51	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
52	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
53	CRISPR-Cas12-based detection of SARS-CoV-2. <i>Nature Biotechnology</i> , 2020, 38, 870-874.	9.4	1,884
54	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

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55	Rapid deployment of SARS-CoV-2 testing: The CLIAHUB. <i>PLoS Pathogens</i> , 2020, 16, e1008966.	2.1	18
56	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
57	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
58	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
59	Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. <i>New England Journal of Medicine</i> , 2019, 380, 2327-2340.	13.9	644
60	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
61	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
62	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
63	Clinical metagenomics. <i>Nature Reviews Genetics</i> , 2019, 20, 341-355.	7.7	793
64	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. <i>Nature Communications</i> , 2019, 10, 579.	5.8	131
65	Severe Epididymo-Orchitis and Encephalitis Complicating Anti-PD-1 Therapy. <i>Oncologist</i> , 2019, 24, 872-876.	1.9	38
66	Pan-viral serology implicates enteroviruses in acute flaccid myelitis. <i>Nature Medicine</i> , 2019, 25, 1748-1752.	15.2	93
67	Clinical Metagenomic Next-Generation Sequencing for Pathogen Detection. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2019, 14, 319-338.	9.6	755
68	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
69	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
70	A Child With Intermittent Headaches and Eosinophilic Meningitis. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2018, 7, 355-357.	0.6	4
71	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
72	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

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73	Metagenomic Next-Generation Sequencing for Pathogen Detection and Identification. , 2018, , 617-632.		0
74	Integrating host response and unbiased microbe detection for lower respiratory tract infection diagnosis in critically ill adults. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12353-E12362.	3.3	249
75	Differentiation enhances Zika virus infection of neuronal brain cells. Scientific Reports, 2018, 8, 14543.	1.6	26
76	Epidemiological and genomic characterization of community-acquired Clostridium difficile infections. BMC Infectious Diseases, 2018, 18, 443.	1.3	21
77	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. Cell Host and Microbe, 2018, 23, 855-864.e7.	5.1	82
78	Polyoma virus-associated carcinomas of the urologic tract: a clinicopathologic and molecular study. Modern Pathology, 2018, 31, 1429-1441.	2.9	25
79	Miscarriage and stillbirth following maternal Zika virus infection in nonhuman primates. Nature Medicine, 2018, 24, 1104-1107.	15.2	85
80	Acute Liver Failure of Indeterminate Etiology: A Comprehensive Systematic Approach by An Expert Committee to Establish Causality. American Journal of Gastroenterology, 2018, 113, 1319.	0.2	61
81	Cutting-Edge Infectious Disease Diagnostics with CRISPR. Cell Host and Microbe, 2018, 23, 702-704.	5.1	52
82	Neurobrucellosis: Unexpected Answer From Metagenomic Next-Generation Sequencing. Journal of the Pediatric Infectious Diseases Society, 2017, 6, piw066.	0.6	62
83	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. Archives of Pathology and Laboratory Medicine, 2017, 141, 776-786.	1.2	404
84	First Complete Genome Sequence of Corynebacterium riegellii. Genome Announcements, 2017, 5, .	0.8	3
85	Establishment and characterization of an oral tongue squamous cell carcinoma cell line from a never-smoking patient. Oral Oncology, 2017, 69, 1-10.	0.8	8
86	Metagenomic-based Surveillance of Pacific Coast tick Dermacentor occidentalis Identifies Two Novel Bunyaviruses and an Emerging Human Rickettsial Pathogen. Scientific Reports, 2017, 7, 12234.	1.6	42
87	Upregulation of Human Endogenous Retrovirus-K Is Linked to Immunity and Inflammation in Pulmonary Arterial Hypertension. Circulation, 2017, 136, 1920-1935.	1.6	44
88	Viral Surveillance in Serum Samples From Patients With Acute Liver Failure By Metagenomic Next-Generation Sequencing. Clinical Infectious Diseases, 2017, 65, 1477-1485.	2.9	76
89	The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. Nature Medicine, 2017, 23, 1080-1085.	15.2	109
90	Beatrice Hill Virus Represents a Novel Species in the Genus Tibrovirus (Mononegavirales :) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Td (0.8	6

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91	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
92	Complete genome sequence of sequential <i>Pandora</i> apista 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
93	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. <i>Scientific Reports</i> , 2017, 7, 18022.	1.6	264
94	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
95	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
96	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
97	A mouse model of paralytic myelitis caused by enterovirus D68. <i>PLoS Pathogens</i> , 2017, 13, e1006199.	2.1	158
98	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	2.0	45
99	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
100	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
101	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
102	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
103	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
104	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
105	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
106	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
107	Idiopathic pneumonia syndrome after hematopoietic cell transplantation: evidence of occult infectious etiologies. <i>Blood</i> , 2015, 125, 3789-3797.	0.6	137
108	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

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109	Utility of Metagenomic Next-Generation Sequencing for Characterization of HIV and Human Pegivirus Diversity. PLoS ONE, 2015, 10, e0141723.	1.1	37
110	Discovery of a Novel Human Pegivirus in Blood Associated with Hepatitis C Virus Co-Infection. PLoS Pathogens, 2015, 11, e1005325.	2.1	74
111	Genomic Assays for Identification of Chikungunya Virus in Blood Donors, Puerto Rico, 2014. Emerging Infectious Diseases, 2015, 21, 1409-1413.	2.0	39
112	Draft Genome Sequence of Mycobacterium arupense Strain GUC1. Genome Announcements, 2015, 3, .	0.8	0
113	Draft Genome Sequence of Mycobacterium elephantis Strain Lipa. Genome Announcements, 2015, 3, .	0.8	1
114	Draft Genome Sequence of Mycobacterium heraklionense Strain Davo. Genome Announcements, 2015, 3, .	0.8	4
115	Draft Genome Sequence of Mycobacterium heckeshornense Strain RLE. Genome Announcements, 2015, 3, .	0.8	1
116	Clinical metagenomic identification of Balamuthia mandrillaris encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. Genome Medicine, 2015, 7, 113.	3.6	102
117	Acute Flaccid Myelitis of Unknown Etiology in California, 2012-2015. JAMA - Journal of the American Medical Association, 2015, 314, 2663.	3.8	118
118	Diagnosis of Neuroinvasive Astrovirus Infection in an Immunocompromised Adult With Encephalitis by Unbiased Next-Generation Sequencing. Clinical Infectious Diseases, 2015, 60, 919-923.	2.9	262
119	An ensemble strategy that significantly improves de novo assembly of microbial genomes from metagenomic next-generation sequencing data. Nucleic Acids Research, 2015, 43, e46-e46.	6.5	213
120	Two Rapidly Growing Mycobacterial Species Isolated from a Brain Abscess: First Whole-Genome Sequences of Mycobacterium immunogenum and Mycobacterium llutzerense. Journal of Clinical Microbiology, 2015, 53, 2374-2377.	1.8	36
121	A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012-14): a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 671-682.	4.6	348
122	Genome Sequence of Bivens Arm Virus, a Tibrovirus Belonging to the Species Tibrogargan virus () Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 2	0.8	8
123	Draft Genome Sequence of Mycobacterium obuense Strain UC1, Isolated from Patient Sputum. Genome Announcements, 2015, 3, .	0.8	4
124	DNA Microarray for Detection of Gastrointestinal Viruses. Journal of Clinical Microbiology, 2015, 53, 136-145.	1.8	41
125	Concerns over the origin of NIH-CQV, a novel virus discovered in Chinese patients with seronegative hepatitis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E976-E976.	3.3	34
126	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. Genome Research, 2014, 24, 1180-1192.	2.4	421

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127	Bas-Congo Virus. , 2014, , 13-24.		3
128	Actionable Diagnosis of Neuroleptospirosis by Next-Generation Sequencing. New England Journal of Medicine, 2014, 370, 2408-2417.	13.9	760
129	A novel bocavirus in canine liver. Virology Journal, 2013, 10, 54.	1.4	47
130	Rosavirus: the prototype of a proposed new genus of the Picornaviridae family. Virus Genes, 2013, 47, 556-558.	0.7	10
131	Viral pathogen discovery. Current Opinion in Microbiology, 2013, 16, 468-478.	2.3	190
132	The hidden threat of unidentified agents of disease in human and veterinary biologicals. Biologicals, 2013, 41, 129-130.	0.5	2
133	The Mitochondrial Genome and a 60â€b Nuclear DNA Segment from <i>Naegleria fowleri</i> , the Causative Agent of Primary Amoebic Meningoencephalitis. Journal of Eukaryotic Microbiology, 2013, 60, 179-191.	0.8	36
134	A Novel Adenovirus Species Associated with an Acute Respiratory Outbreak in a Baboon Colony and Evidence of Coincident Human Infection. MBio, 2013, 4, e00084.	1.8	48
135	Bas-Congo virus: another deadly virus?. Future Microbiology, 2013, 8, 139-141.	1.0	10
136	The Perils of Pathogen Discovery: Origin of a Novel Parvovirus-Like Hybrid Genome Traced to Nucleic Acid Extraction Spin Columns. Journal of Virology, 2013, 87, 11966-11977.	1.5	216
137	Characterization of the Bas-Congo Virus Glycoprotein and Its Function in Pseudotyped Viruses. Journal of Virology, 2013, 87, 9558-9568.	1.5	13
138	The Genome Sequence of Lone Star Virus, a Highly Divergent Bunyavirus Found in the Amblyomma americanum Tick. PLoS ONE, 2013, 8, e62083.	1.1	50
139	Experimental Cross-Species Infection of Common Marmosets by Titi Monkey Adenovirus. PLoS ONE, 2013, 8, e68558.	1.1	20
140	A Novel Rhabdovirus Associated with Acute Hemorrhagic Fever in Central Africa. PLoS Pathogens, 2012, 8, e1002924.	2.1	181
141	Toward an Understanding of Changes in Diversity Associated with Fecal Microbiome Transplantation Based on 16S rRNA Gene Deep Sequencing. MBio, 2012, 3, .	1.8	151
142	In-Depth Investigation of Archival and Prospectively Collected Samples Reveals No Evidence for XMRV Infection in Prostate Cancer. PLoS ONE, 2012, 7, e44954.	1.1	35
143	Discovery of a Novel Polyomavirus in Acute Diarrheal Samples from Children. PLoS ONE, 2012, 7, e49449.	1.1	110
144	Viral Infection in Acute Exacerbation of Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2011, 183, 1698-1702.	2.5	230

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145	Using a Pan-Viral Microarray Assay (Virochip) to Screen Clinical Samples for Viral Pathogens. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	52
146	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
147	Thoracic CT findings of novel influenza A (H1N1) infection in immunocompromised patients. <i>Emergency Radiology</i> , 2010, 17, 299-307.	1.0	48
148	Pandemic (H1N1) 2009 Infection in Patients with Hematologic Malignancy. <i>Emerging Infectious Diseases</i> , 2010, 16, 1910-1917.	2.0	18
149	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
150	Metagenomics for the discovery of novel human viruses. <i>Future Microbiology</i> , 2010, 5, 177-189.	1.0	114
151	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
152	Bacteriologic features of surgical site infections following breast surgery. <i>American Journal of Surgery</i> , 2009, 198, 529-531.	0.9	19
153	The complete genome of klassevirus " a novel picornavirus in pediatric stool. <i>Virology Journal</i> , 2009, 6, 82.	1.4	152
154	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
155	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
156	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
157	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
158	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
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