Alexander Greninger

List of Publications by Year in descending order

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213 papers

14,612 citations

³⁸⁷²⁰ 50 h-index

27389 106 g-index

270 all docs

270 docs citations

times ranked

270

27013 citing authors

#	Article	IF	CITATIONS
1	Covid-19 in Critically Ill Patients in the Seattle Region — Case Series. New England Journal of Medicine, 2020, 382, 2012-2022.	13.9	2,120
2	Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing. New England Journal of Medicine, 2020, 383, 1492-1494.	13.9	506
3	Performance Characteristics of the Abbott Architect SARS-CoV-2 IgG Assay and Seroprevalence in Boise, Idaho. Journal of Clinical Microbiology, 2020, 58, .	1.8	496
4	Neutralizing Antibodies Correlate with Protection from SARS-CoV-2 in Humans during a Fishery Vessel Outbreak with a High Attack Rate. Journal of Clinical Microbiology, 2020, 58, .	1.8	494
5	Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. Genome Medicine, 2015, 7, 99.	3.6	456
6	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
7	Comparative Performance of SARS-CoV-2 Detection Assays Using Seven Different Primer-Probe Sets and One Assay Kit. Journal of Clinical Microbiology, 2020, 58, .	1.8	401
8	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
9	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. Cell, 2020, 181, 990-996.e5.	13.5	321
10	Characterization of orally efficacious influenza drug with high resistance barrier in ferrets and human airway epithelia. Science Translational Medicine, 2019, 11, .	5. 8	253
11	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. Science, 2020, 369, 582-587.	6.0	253
12	Recovery of divergent avian bornaviruses from cases of proventricular dilatation disease: Identification of a candidate etiologic agent. Virology Journal, 2008, 5, 88.	1.4	235
13	In vivo antiviral host transcriptional response to SARS-CoV-2 by viral load, sex, and age. PLoS Biology, 2020, 18, e3000849.	2.6	225
14	Cryptic transmission of SARS-CoV-2 in Washington state. Science, 2020, 370, 571-575.	6.0	217
15	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
16	Dynamics of Neutralizing Antibody Titers in the Months After Severe Acute Respiratory Syndrome Coronavirus 2 Infection. Journal of Infectious Diseases, 2021, 223, 197-205.	1.9	216
17	Comparison of Commercially Available and Laboratory-Developed Assays for <i>In Vitro</i> Detection of SARS-CoV-2 in Clinical Laboratories. Journal of Clinical Microbiology, 2020, 58, .	1.8	215
18	A human coronavirus evolves antigenically to escape antibody immunity. PLoS Pathogens, 2021, 17, e1009453.	2.1	183

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19	Affinity purification–mass spectrometry and network analysis to understand protein-protein interactions. Nature Protocols, 2014, 9, 2539-2554.	5.5	169
20	A Metagenomic Analysis of Pandemic Influenza A (2009 H1N1) Infection in Patients from North America. PLoS ONE, 2010, 5, e13381.	1.1	169
21	SARS-CoV-2 breakthrough infections elicit potent, broad, and durable neutralizing antibody responses. Cell, 2022, 185, 872-880.e3.	13.5	165
22	Orally Efficacious Broad-Spectrum Ribonucleoside Analog Inhibitor of Influenza and Respiratory Syncytial Viruses. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	162
23	De novo emergence of a remdesivir resistance mutation during treatment of persistent SARS-CoV-2 infection in an immunocompromised patient: a case report. Nature Communications, 2022, 13, 1547.	5 . 8	159
24	Identification of cardioviruses related to Theiler's murine encephalomyelitis virus in human infections. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14124-14129.	3. 3	152
25	The complete genome of klassevirus – a novel picornavirus in pediatric stool. Virology Journal, 2009, 6, 82.	1.4	152
26	The 3A Protein from Multiple Picornaviruses Utilizes the Golgi Adaptor Protein ACBD3 To Recruit PI4KIIIÎ ² . Journal of Virology, 2012, 86, 3605-3616.	1.5	144
27	The challenge of diagnostic metagenomics. Expert Review of Molecular Diagnostics, 2018, 18, 605-615.	1.5	130
28	A decade of RNA virus metagenomics is (not) enough. Virus Research, 2018, 244, 218-229.	1.1	129
29	Direct RT-qPCR detection of SARS-CoV-2 RNA from patient nasopharyngeal swabs without an RNA extraction step. PLoS Biology, 2020, 18, e3000896.	2.6	119
30	Discovery of a Novel Polyomavirus in Acute Diarrheal Samples from Children. PLoS ONE, 2012, 7, e49449.	1.1	110
31	Detection of SARS-CoV-2 Among Residents and Staff Members of an Independent and Assisted Living Community for Older Adults — Seattle, Washington, 2020. Morbidity and Mortality Weekly Report, 2020, 69, 416-418.	9.0	108
32	Rapid Metagenomic Next-Generation Sequencing during an Investigation of Hospital-Acquired Human Parainfluenza Virus 3 Infections. Journal of Clinical Microbiology, 2017, 55, 177-182.	1.8	106
33	Enhanced arbovirus surveillance with deep sequencing: Identification of novel rhabdoviruses and bunyaviruses in Australian mosquitoes. Virology, 2014, 448, 146-158.	1.1	103
34	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
35	Outbreak Investigation of COVID-19 Among Residents and Staff of an Independent and Assisted Living Community for Older Adults in Seattle, Washington. JAMA Internal Medicine, 2020, 180, 1101.	2.6	101
36	SARS-CoV-2 ORF6 Disrupts Bidirectional Nucleocytoplasmic Transport through Interactions with Rae1 and Nup98. MBio, 2021, 12, .	1.8	92

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37	Validation and Implementation of Clinical Laboratory Improvements Act-Compliant Whole-Genome Sequencing in the Public Health Microbiology Laboratory. Journal of Clinical Microbiology, 2017, 55, 2502-2520.	1.8	80
38	Occurrence and Timing of Subsequent Severe Acute Respiratory Syndrome Coronavirus 2 Reverse-transcription Polymerase Chain Reaction Positivity Among Initially Negative Patients. Clinical Infectious Diseases, 2021, 72, 323-326.	2.9	78
39	Oral prodrug of remdesivir parent GS-441524 is efficacious against SARS-CoV-2 in ferrets. Nature Communications, 2021, 12, 6415.	5.8	74
40	Hydroxychloroquine as Postexposure Prophylaxis to Prevent Severe Acute Respiratory Syndrome Coronavirus 2 Infection. Annals of Internal Medicine, 2021, 174, 344-352.	2.0	73
41	Identification of multiple large deletions in ORF7a resulting in in-frame gene fusions in clinical SARS-CoV-2 isolates. Journal of Clinical Virology, 2020, 129, 104523.	1.6	71
42	Analytical Sensitivity of the Abbott BinaxNOW COVID-19 Ag Card. Journal of Clinical Microbiology, 2021, 59, .	1.8	69
43	Validation of SARS-CoV-2 detection across multiple specimen types. Journal of Clinical Virology, 2020, 128, 104438.	1.6	66
44	Prolonged Shedding of Human Coronavirus in Hematopoietic Cell Transplant Recipients: Risk Factors and Viral Genome Evolution. Journal of Infectious Diseases, 2017, 216, 203-209.	1.9	64
45	Inhibition of Coronavirus Entry <i>In Vitro</i> and <i>Ex Vivo</i> by a Lipid-Conjugated Peptide Derived from the SARS-CoV-2 Spike Glycoprotein HRC Domain. MBio, 2020, 11, .	1.8	63
46	Metagenomic Analysis Reveals Clinical SARS-CoV-2 Infection and Bacterial or Viral Superinfection and Colonization. Clinical Chemistry, 2020, 66, 966-972.	1.5	63
47	CRISPR-Cas9 gene editing of hepatitis B virus in chronically infected humanized mice. Molecular Therapy - Methods and Clinical Development, 2021, 20, 258-275.	1.8	62
48	Prevalence of Coronavirus Disease 2019 Infection and Outcomes Among Symptomatic Healthcare Workers in Seattle, Washington. Clinical Infectious Diseases, 2020, 71, 2702-2707.	2.9	61
49	Clinical evaluation of the BioFire® Respiratory Panel 2.1 and detection of SARS-CoV-2. Journal of Clinical Virology, 2020, 129, 104538.	1.6	60
50	Sensitive Recovery of Complete SARS-CoV-2 Genomes from Clinical Samples by Use of Swift Biosciences' SARS-CoV-2 Multiplex Amplicon Sequencing Panel. Journal of Clinical Microbiology, 2020, 59, .	1.8	58
51	Validation and verification of the Abbott RealTime SARS-CoV-2 assay analytical and clinical performance. Journal of Clinical Virology, 2020, 129, 104474.	1.6	58
52	Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State. Science Translational Medicine, 2021, 13, .	5.8	58
53	Trajectory of Viral RNA Load Among Persons With Incident SARS-CoV-2 G614 Infection (Wuhan Strain) in Association With COVID-19 Symptom Onset and Severity. JAMA Network Open, 2022, 5, e2142796.	2.8	57
54	Hydroxychloroquine with or without azithromycin for treatment of early SARS-CoV-2 infection among high-risk outpatient adults: A randomized clinical trial. EClinicalMedicine, 2021, 33, 100773.	3.2	55

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55	Quantification of BK Virus Standards by Quantitative Real-Time PCR and Droplet Digital PCR Is Confounded by Multiple Virus Populations in the WHO BKV International Standard. Clinical Chemistry, 2017, 63, 761-769.	1.5	53
56	A SARS-CoV-2 Nucleocapsid Variant that Affects Antigen Test Performance. Journal of Clinical Virology, 2021, 141, 104900.	1.6	53
57	Whole-Genome Sequencing of Methicillin-Resistant Staphylococcus aureus Resistant to Fifth-Generation Cephalosporins Reveals Potential Non-mecA Mechanisms of Resistance. PLoS ONE, 2016, 11, e0149541.	1.1	53
58	ACBD3 Interaction with TBC1 Domain 22 Protein Is Differentially Affected by Enteroviral and Kobuviral 3A Protein Binding. MBio, 2013, 4, e00098-13.	1.8	52
59	The Laboratory Diagnosis of Coronavirus Disease 2019â€" Frequently Asked Questions. Clinical Infectious Diseases, 2020, 71, 2996-3001.	2.9	52
60	Pooling of SARS-CoV-2 samples to increase molecular testing throughput. Journal of Clinical Virology, 2020, 131, 104570.	1.6	51
61	Ultrasensitive Capture of Human Herpes Simplex Virus Genomes Directly from Clinical Samples Reveals Extraordinarily Limited Evolution in Cell Culture. MSphere, 2018, 3, .	1.3	49
62	Metagenomics to Assist in the Diagnosis of Bloodstream Infection. journal of applied laboratory medicine, The, 2019, 3, 643-653.	0.6	49
63	Anti-SARS-CoV-2 Antibody Levels Measured by the AdviseDx SARS-CoV-2 Assay Are Concordant with Previously Available Serologic Assays but Are Not Fully Predictive of Sterilizing Immunity. Journal of Clinical Microbiology, 2021, 59, e0098921.	1.8	48
64	VAPiD: a lightweight cross-platform viral annotation pipeline and identification tool to facilitate virus genome submissions to NCBI GenBank. BMC Bioinformatics, 2019, 20, 48.	1.2	47
65	Gene editing and elimination of latent herpes simplex virus in vivo. Nature Communications, 2020, 11, 4148.	5.8	46
66	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. Emerging Infectious Diseases, 2016, 22, 1788-1792.	2.0	45
67	Comparative genomic, transcriptomic, and proteomic reannotation of human herpesvirus 6. BMC Genomics, 2018, 19, 204.	1.2	45
68	DNA Microarray for Detection of Gastrointestinal Viruses. Journal of Clinical Microbiology, 2015, 53, 136-145.	1.8	41
69	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of Shigella sonnei with either Increased Virulence or Fluoroquinolone Resistance. MSphere, 2016, 1, .	1.3	40
70	Rule-Out Outbreak: 24-Hour Metagenomic Next-Generation Sequencing for Characterizing Respiratory Virus Source for Infection Prevention. Journal of the Pediatric Infectious Diseases Society, 2017, 6, 168-172.	0.6	38
71	Variants of Concern Are Overrepresented Among Postvaccination Breakthrough Infections of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Washington State. Clinical Infectious Diseases, 2022, 74, 1089-1092.	2.9	38
72	Predicting infectivity: comparing four PCRâ€based assays to detect culturable SARSâ€CoVâ€2 in clinical samples. EMBO Molecular Medicine, 2022, 14, e15290.	3.3	38

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73	Associations Between Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants and Risk of Coronavirus Disease 2019 (COVID-19) Hospitalization Among Confirmed Cases in Washington State: A Retrospective Cohort Study. Clinical Infectious Diseases, 2022, 75, e536-e544.	2.9	38
74	Hamster organotypic modeling of SARS-CoV-2 lung and brainstem infection. Nature Communications, 2021, 12, 5809.	5.8	37
75	Two Rapidly Growing Mycobacterial Species Isolated from a Brain Abscess: First Whole-Genome Sequences of Mycobacterium immunogenum and Mycobacterium llatzerense. Journal of Clinical Microbiology, 2015, 53, 2374-2377.	1.8	36
76	Optimization and clinical validation of dual-target RT-LAMP for SARS-CoV-2. Journal of Virological Methods, 2020, 286, 113972.	1.0	36
77	Stability of SARS-CoV-2 in Phosphate-Buffered Saline for Molecular Detection. Journal of Clinical Microbiology, 2020, 58, .	1.8	36
78	Multiplexing primer/probe sets for detection of SARS-CoV-2 by qRT-PCR. Journal of Clinical Virology, 2020, 129, 104499.	1.6	35
79	Measuring infectious SARS-CoV-2 in clinical samples reveals a higher viral titer:RNA ratio for Delta and Epsilon vs. Alpha variants. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	35
80	In vivo disruption of latent HSV by designer endonuclease therapy. JCI Insight, 2016, 1, .	2.3	33
81	Low Prevalence of Severe Acute Respiratory Syndrome Coronavirus 2 Among Pregnant and Postpartum Patients With Universal Screening in Seattle, Washington. Clinical Infectious Diseases, 2021, 72, 869-872.	2.9	31
82	Evolutionary History of Endogenous Human Herpesvirus 6 Reflects Human Migration out of Africa. Molecular Biology and Evolution, 2021, 38, 96-107.	3.5	31
83	Specific allelic discrimination of N501Y and other SARS oVâ€2 mutations by ddPCR detects B.1.1.7 lineage in Washington State. Journal of Medical Virology, 2021, 93, 5931-5941.	2.5	31
84	SARS-CoV-2 Viral Load on Admission Is Associated With 30-Day Mortality. Open Forum Infectious Diseases, 2020, 7, ofaa535.	0.4	31
85	An optimized methodology for whole genome sequencing of RNA respiratory viruses from nasopharyngeal aspirates. PLoS ONE, 2018, 13, e0199714.	1.1	30
86	Treponema pallidum genome sequencing from six continents reveals variability in vaccine candidate genes and dominance of Nichols clade strains in Madagascar. PLoS Neglected Tropical Diseases, 2021, 15, e0010063.	1.3	30
87	Prevalent and Diverse Intratumoral Oncoprotein-Specific CD8+ T Cells within Polyomavirus-Driven Merkel Cell Carcinomas. Cancer Immunology Research, 2020, 8, 648-659.	1.6	28
88	The SARS-CoV-2 Omicron Variant Does Not Have Higher Nasal Viral Loads Compared to the Delta Variant in Symptomatic and Asymptomatic Individuals. Journal of Clinical Microbiology, 2022, 60, e0013922.	1.8	28
89	Viral Entry Properties Required for Fitness in Humans Are Lost through Rapid Genomic Change during Viral Isolation. MBio, 2018, 9, .	1.8	27
90	Inherited Chromosomally Integrated Human Herpesvirus 6 Demonstrates Tissue-Specific RNA Expression <i>In Vivo</i> That Correlates with an Increased Antibody Immune Response. Journal of Virology, 2019, 94, .	1.5	27

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91	Genetic engineering of Treponema pallidum subsp. pallidum, the Syphilis Spirochete. PLoS Pathogens, 2021, 17, e1009612.	2.1	27
92	The human clone ST22 SCCmec IV methicillin-resistant Staphylococcus aureus isolated from swine herds and wild primates in Nepal: is man the common source?. FEMS Microbiology Ecology, 2018, 94, .	1.3	26
93	Cooperating H3N2 Influenza Virus Variants Are Not Detectable in Primary Clinical Samples. MSphere, 2018, 3, .	1.3	26
94	Western Washington State COVID-19 Experience: Keys to Flattening the Curve and Effective Health System Response. Journal of the American College of Surgeons, 2020, 231, 316-324e1.	0.2	26
95	Pathogen or Bystander: Clinical Significance of Detecting Human Herpesvirus 6 in Pediatric Cerebrospinal Fluid. Journal of Clinical Microbiology, 2020, 58, .	1.8	26
96	T cell receptor sequencing identifies prior SARS-CoV-2 infection and correlates with neutralizing antibodies and disease severity. JCI Insight, 2022, 7, .	2.3	26
97	Changes in SARS-CoV-2 Positivity Rate in Outpatients in Seattle and Washington State, March 1–April 16, 2020. JAMA - Journal of the American Medical Association, 2020, 323, 2334.	3.8	25
98	Analysis of SARS-CoV-2 infection dynamic in vivo using reporter-expressing viruses. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
99	Serological Evidence of Human Klassevirus Infection. Vaccine Journal, 2010, 17, 1584-1588.	3.2	24
100	Detection of SARS-CoV-2 by bronchoscopy after negative nasopharyngeal testing: Stay vigilant for COVID-19. Respiratory Medicine Case Reports, 2020, 30, 101120.	0.2	24
101	Molecular Features of the Measles Virus Viral Fusion Complex That Favor Infection and Spread in the Brain. MBio, 2021, 12, e0079921.	1.8	24
102	The Unstructured Paramyxovirus Nucleocapsid Protein Tail Domain Modulates Viral Pathogenesis through Regulation of Transcriptase Activity. Journal of Virology, 2018, 92, .	1.5	23
103	Thermodynamically coupled biosensors for detecting neutralizing antibodies against SARS-CoV-2 variants. Nature Biotechnology, 2022, 40, 1336-1340.	9.4	23
104	In silico detection of SARS-CoV-2 specific B-cell epitopes and validation in ELISA for serological diagnosis of COVID-19. Scientific Reports, 2021, 11, 4290.	1.6	22
105	Development of the RealTime SARS-CoV-2 quantitative Laboratory Developed Test and correlation with viral culture as a measure of infectivity. Journal of Clinical Virology, 2021, 143, 104945.	1.6	22
106	Dual-strain genital herpes simplex virus type 2 (HSV-2) infection in the US, Peru, and 8 countries in sub-Saharan Africa: A nested cross-sectional viral genotyping study. PLoS Medicine, 2017, 14, e1002475.	3.9	22
107	Picornavirus–Host Interactions to Construct Viral Secretory Membranes. Progress in Molecular Biology and Translational Science, 2015, 129, 189-212.	0.9	21
108	Digital detection of endonuclease mediated gene disruption in the HIV provirus. Scientific Reports, 2016, 6, 20064.	1.6	21

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109	Copy Number Heterogeneity, Large Origin Tandem Repeats, and Interspecies Recombination in Human Herpesvirus 6A (HHV-6A) and HHV-6B Reference Strains. Journal of Virology, 2018, 92, .	1.5	21
110	Epidemiological and genomic characterization of community-acquired Clostridium difficile infections. BMC Infectious Diseases, 2018, 18, 443.	1.3	21
111	Large, Stable, Contemporary Interspecies Recombination Events in Circulating Human Herpes Simplex Viruses. Journal of Infectious Diseases, 2019, 221, 1271-1279.	1.9	21
112	Prospective, Real-time Metagenomic Sequencing During Norovirus Outbreak Reveals Discrete Transmission Clusters. Clinical Infectious Diseases, 2019, 69, 941-948.	2.9	21
113	International Spread of Multidrug-Resistant Campylobacter coli in Men Who Have Sex With Men in Washington State and Québec, 2015–2018. Clinical Infectious Diseases, 2020, 71, 1896-1904.	2.9	20
114	Clinical and Infection Prevention Applications of Severe Acute Respiratory Syndrome Coronavirus 2 Genotyping: An Infectious Diseases Society of America/American Society for Microbiology Consensus Review Document. Clinical Infectious Diseases, 2022, 74, 1496-1502.	2.9	20
115	Immunogenicity of a heterologous COVID-19 vaccine after failed vaccination in a lymphoma patient. Cancer Cell, 2021, 39, 1037-1038.	7.7	20
116	Copy Number Heterogeneity of JC Virus Standards. Journal of Clinical Microbiology, 2017, 55, 824-831.	1.8	19
117	Estimation of Full-Length TprK Diversity in Treponema pallidum subsp. <i>pallidum</i> . MBio, 2020, 11, .	1.8	19
118	Limited Marginal Utility of Deep Sequencing for HIV Drug Resistance Testing in the Age of Integrase Inhibitors. Journal of Clinical Microbiology, 2018, 56, .	1.8	18
119	Orally efficacious broad-spectrum allosteric inhibitor of paramyxovirus polymerase. Nature Microbiology, 2020, 5, 1232-1246.	5.9	18
120	Comparative genomics and full-length Tprk profiling of Treponema pallidum subsp. pallidum reinfection. PLoS Neglected Tropical Diseases, 2020, 14, e0007921.	1.3	18
121	Genomics and transcriptomics yields a system-level view of the biology of the pathogen Naegleria fowleri. BMC Biology, 2021, 19, 142.	1.7	18
122	Highly conserved intragenic HSV-2 sequences: Results from next-generation sequencing of HSV-2 UL and US regions from genital swabs collected from 3 continents. Virology, 2017, 510, 90-98.	1.1	17
123	Heterogeneous Antimicrobial Susceptibility Characteristics in Pseudomonas aeruginosa Isolates from Cystic Fibrosis Patients. MSphere, 2018, 3, .	1.3	17
124	Complete genome sequence of sequential Pandoraea apista isolates from the same cystic fibrosis patient supports a model of chronic colonization with in vivo strain evolution over time. Diagnostic Microbiology and Infectious Disease, 2017, 87, 1-6.	0.8	16
125	Prolonged persistence of PCR-detectable virus during an outbreak of SARS-CoV-2 in an inpatient geriatric psychiatry unit in King County, Washington. American Journal of Infection Control, 2021, 49, 293-298.	1.1	16
126	Performance characteristics of the Abbott Alinity m SARS-CoV-2 assay. Journal of Clinical Virology, 2021, 140, 104869.	1.6	16

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127	Sensitive Identification of Bacterial DNA in Clinical Specimens by Broad-Range 16S rRNA Gene Enrichment. Journal of Clinical Microbiology, 2020, 58, .	1.8	15
128	Cell free DNA from respiratory pathogens is detectable in the blood plasma of Cystic Fibrosis patients. Scientific Reports, 2020, 10, 6903.	1.6	15
129	Longitudinal TprK profiling of in vivo and in vitro-propagated Treponema pallidum subsp. pallidum reveals accumulation of antigenic variants in absence of immune pressure. PLoS Neglected Tropical Diseases, 2021, 15, e0009753.	1.3	15
130	Retrospective clinical evaluation of 4 lateral flow assays for the detection of SARS-CoV-2 IgG. Diagnostic Microbiology and Infectious Disease, 2020, 98, 115161.	0.8	14
131	CrAssphage and its bacterial host in cat feces. Scientific Reports, 2021, 11, 815.	1.6	14
132	Evaluating Antibody Mediated Protection against Alpha, Beta, and Delta SARS-CoV-2 Variants of Concern in K18-hACE2 Transgenic Mice. Journal of Virology, 2022, 96, jvi0218421.	1.5	14
133	A Method for Variant Agnostic Detection of SARS-CoV-2, Rapid Monitoring of Circulating Variants, and Early Detection of Emergent Variants Such as Omicron. Journal of Clinical Microbiology, 2022, 60,	1.8	14
134	Whole-genome analysis of extraintestinal pathogenic Escherichia coli (ExPEC) MDR ST73 and ST127 isolated from endangered southern resident killer whales (Orcinus orca). Journal of Antimicrobial Chemotherapy, 2019, 74, 2176-2180.	1.3	13
135	Expedited SARS-CoV-2 screening of donors and recipients supports continued solid organ transplantation. American Journal of Transplantation, 2020, 20, 3106-3112.	2.6	13
136	A Bifluorescent-Based Assay for the Identification of Neutralizing Antibodies against SARS-CoV-2 Variants of Concern <i>In Vitro</i> and <i>In Vivo</i> Journal of Virology, 2021, 95, e0112621.	1.5	13
137	Clinical and Infection Prevention Applications of Severe Acute Respiratory Syndrome Coronavirus 2 Genotyping: an Infectious Diseases Society of America/American Society for Microbiology Consensus Review Document. Journal of Clinical Microbiology, 2022, 60, JCM0165921.	1.8	13
138	A Novel, Widespread <i>qacA</i> Allele Results in Reduced Chlorhexidine Susceptibility in <i>Staphylococcus epidermidis</i> Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	12
139	The First Quarter of SARS-CoV-2 Testing: the University of Washington Medicine Experience. Journal of Clinical Microbiology, 2020, 58, .	1.8	12
140	Estimating the False-Positive Rate of Highly Automated SARS-CoV-2 Nucleic Acid Amplification Testing. Journal of Clinical Microbiology, 2021, 59, e0108021.	1.8	12
141	Human parainfluenza virus evolution during lung infection of immunocompromised individuals promotes viral persistence. Journal of Clinical Investigation, 2021, 131, .	3.9	12
142	Mutations in viral nucleocapsid protein and endoRNase are discovered to associate with COVID19 hospitalization risk. Scientific Reports, 2022, 12, 1206.	1.6	12
143	Rapid and accurate identification of SARS-CoV-2 Omicron variants using droplet digital PCR (RT-ddPCR). Journal of Clinical Virology, 2022, 154, 105218.	1.6	12
144	Draft Genome Sequences of Four NDM-1-Producing Klebsiella pneumoniae Strains from a Health Care Facility in Northern California. Genome Announcements, 2015, 3, .	0.8	11

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145	Genome Sequences of Three Novel Bunyaviruses, Two Novel Rhabdoviruses, and One Novel Nyamivirus from Washington State Moths. Genome Announcements, 2017, 5, .	0.8	11
146	Distribution of Staphylococcus species in dairy cows, workers and shared farm environments. FEMS Microbiology Letters, 2018, 365, .	0.7	11
147	Mycobacterium grossiae sp. nov., a rapidly growing, scotochromogenic species isolated from human clinical respiratory and blood culture specimens. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4345-4351.	0.8	11
148	The Impact of Bâ€eell Directed Therapy on SARSâ€CoVâ€2 Vaccine Efficacy in CLL. British Journal of Haematology, 2022, , .	1.2	11
149	Reliability of Self-Sampling for Accurate Assessment of Respiratory Virus Viral and Immunologic Kinetics. Journal of Infectious Diseases, 2022, 226, 278-286.	1.9	10
150	Draft Genome Sequences of Ciliovirus and Brinovirus from San Francisco Wastewater. Genome Announcements, 2015, 3, .	0.8	9
151	Draft Genome Sequence of Goose Dicistrovirus. Genome Announcements, 2016, 4, .	0.8	9
152	<i>In Vivo</i> Generation of BK and JC Polyomavirus Defective Viral Genomes in Human Urine Samples Associated with Higher Viral Loads. Journal of Virology, 2021, 95, .	1.5	9
153	Rapid adaptation to human protein kinase R by a unique genomic rearrangement in rhesus cytomegalovirus. PLoS Pathogens, 2021, 17, e1009088.	2.1	9
154	Evaluation of Genotypic Antiviral Resistance Testing as an Alternative to Phenotypic Testing in a Patient with DOCK8 Deficiency and Severe HSV-1 Disease. Journal of Infectious Diseases, 2020, 221, 2035-2042.	1.9	9
155	Isolation and characterization of the fall Chinook aquareovirus. Virology Journal, 2017, 14, 170.	1.4	8
156	Private collection: high correlation of sample collection and patient admission date in clinical microbiological testing complicates sharing of phylodynamic metadata. Virus Evolution, 2018, 4, vey005.	2.2	8
157	Reducing COVID-19 quarantine with SARS-CoV-2 testing: a simulation study. BMJ Open, 2021, 11, e050473.	0.8	8
158	Fast SARS-CoV-2 Variant Detection Using Snapback Primer High-Resolution Melting. Diagnostics, 2021, 11, 1788.	1.3	8
159	Phylogenetic estimates of SARS-CoV-2 introductions into Washington State. The Lancet Regional Health Americas, 2021, 1, 100018.	1.5	8
160	Myeloablation-associated deletion of ORF4 in a human coronavirus 229E infection. Npj Genomic Medicine, 2017, 2, 30.	1.7	7
161	Societal Implications of the Internet of Pathogens. Journal of Clinical Microbiology, 2019, 57, .	1.8	7
162	High-resolution profiling of human cytomegalovirus cell-free DNA in human plasma highlights its exceptionally fragmented nature. Scientific Reports, 2020, 10, 3734.	1.6	7

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163	Identification of Mycobacterium porcinum in patients with cystic Fibrosis: Pathogen or contaminant?. Journal of Cystic Fibrosis, 2020, 19, 580-586.	0.3	7
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165	Test it earlier, result it faster, makes us stronger: how rapid viral diagnostics enable therapeutic success. Current Opinion in Virology, 2021, 49, 111-116.	2.6	7
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