

Debra A Wadford

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

4,728
citations

566801

15
h-index

752256

20
g-index

29
all docs

29
docs citations

29
times ranked

9419
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	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
3	Limited cross-variant immunity from SARS-CoV-2 Omicron without vaccination. <i>Nature</i> , 2022, 607, 351-355.	13.7	143
4	Acute Fulminant Cerebral Edema: A Newly Recognized Phenotype in Children With Suspected Encephalitis. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, 289-294.	0.6	20
5	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
6	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
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	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
9	366. Abbott BinaxNOW Rapid Antigen Test Performance in Detecting SARS-CoV-2 Infections in a COVID-19 Outbreak Among Horse Racetrack Workers. <i>Open Forum Infectious Diseases</i> , 2021, 8, S286-S286.	0.4	0
10	Rotavirus Vaccination Coverage During a Rotavirus Outbreak Resulting in a Fatality at a Subacute Care Facility. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2020, 9, 287-292.	0.6	6
11	Identification of a Polymorphism in the N Gene of SARS-CoV-2 That Adversely Impacts Detection by Reverse Transcription-PCR. <i>Journal of Clinical Microbiology</i> , 2020, 59, .	1.8	66
12	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
13	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
14	CRISPR-Cas12-based detection of SARS-CoV-2. <i>Nature Biotechnology</i> , 2020, 38, 870-874.	9.4	1,884
15	Public Health Responses to COVID-19 Outbreaks on Cruise Ships — Worldwide, February–March 2020. <i>Morbidity and Mortality Weekly Report</i> , 2020, 69, 347-352.	9.0	301
16	LB14. Cerebrospinal Fluid Profiling of the Human Host Response Reveals Species-Specific Enterovirus Biosignatures in Acute Flaccid Myelitis Cases. <i>Open Forum Infectious Diseases</i> , 2019, 6, S998-S999.	0.4	0
17	Pan-viral serology implicates enteroviruses in acute flaccid myelitis. <i>Nature Medicine</i> , 2019, 25, 1748-1752.	15.2	93
18	Nearly Complete Genome Sequence of an Echovirus 30 Strain from a Cluster of Aseptic Meningitis Cases in California, September 2017. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0

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19	Genome Sequences of Rhinovirus Genotype C56 Detected in Three Patients with Acute Respiratory Illness, California, 2016 to 2017. Microbiology Resource Announcements, 2018, 7, .	0.3	2
20	Whole-Genome Sequence of Human Rhinovirus C47, Isolated from an Adult Respiratory Illness Outbreak in Butte County, California, 2017. Genome Announcements, 2018, 6, .	0.8	1
21	Acute Flaccid Myelitis of Unknown Etiology in California, 2012-2015. JAMA - Journal of the American Medical Association, 2015, 314, 2663.	3.8	118
22	A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012â€“14): a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 671-682.	4.6	348
23	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