Nathan D Grubaugh

List of Publications by Year
in descending order

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103 papers	15,802 citations	47 h-index	99 g-index
		47006	33894
160 all docs	160 docs citations	160 times ranked	28256 citing authors

#	Article	IF	Citations
1	Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection: A Case Series From a 12-Month Longitudinal Occupational Cohort. Clinical Infectious Diseases, 2022, 74, 1682-1685.	5.8	9
2	Longitudinal Immune Profiling of a Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection in a Solid Organ Transplant Recipient. Journal of Infectious Diseases, 2022, 225, 374-384.	4.0	7
3	A stem-loop RNA RIG-I agonist protects against acute and chronic SARS-CoV-2 infection in mice. Journal of Experimental Medicine, 2022, 219, .	8.5	46
4	Sequencing SARS-CoV-2 genomes from saliva. Virus Evolution, 2022, 8, veab098.	4.9	4
5	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. Nature Communications, 2022, 13, 440.	12.8	100
6	An outbreak of SARSâ€CoVâ€2 on a transplant unit in the early vaccination era. Transplant Infectious Disease, 2022, 24, .	1.7	5
7	Neutralizing antibodies against the SARS-CoV-2 Delta and Omicron variants following heterologous CoronaVac plus BNT162b2 booster vaccination. Nature Medicine, 2022, 28, 481-485.	30.7	316
8	Clinical effectiveness of additional primary SARSâ€CoVâ€2 vaccine doses for solid organ transplant recipients. Clinical Transplantation, 2022, 36, e14601.	1.6	1
9	Comparative transmissibility of SARS-CoV-2 variants Delta and Alpha in New England, USA. Cell Reports Medicine, 2022, 3, 100583.	6.5	101
10	Evaluation of saliva self-collection devices for SARS-CoV-2 diagnostics. BMC Infectious Diseases, 2022, 22, 284.	2.9	9
11	Assessment of Clinical Effectiveness of BNT162b2 COVID-19 Vaccine in US Adolescents. JAMA Network Open, 2022, 5, e220935.	5.9	20
12	Rapid emergence of SARS-CoV-2 Omicron variant is associated with an infection advantage over Delta in vaccinated persons. Med, 2022, 3, 325-334.e4.	4.4	60
13	Translating virus evolution into epidemiology. Cell Host and Microbe, 2022, 30, 444-448.	11.0	4
14	Combining genomic and epidemiological data to compare the transmissibility of SARS-CoV-2 variants Alpha and Iota. Communications Biology, 2022, 5, 439.	4.4	9
15	Partial ORF1ab Gene Target Failure with Omicron BA.2.12.1. Journal of Clinical Microbiology, 2022, 60, e0060022.	3.9	11
16	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Outbreak at a College With High Coronavirus Disease 2019 (COVID-19) Vaccination Coverageâ€"Connecticut, August 2021â€"September 2021. Clinical Infectious Diseases, 2022, 75, S243-S250.	5.8	2
17	Omicron-specific mRNA vaccination alone and as a heterologous booster against SARS-CoV-2. Nature Communications, 2022, 13, .	12.8	40
18	Intrahost speciations and host switches played an important role in the evolution of herpesviruses. Virus Evolution, 2021, 7, veab025.	4.9	10

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19	Asynchronicity of endemic and emerging mosquito-borne disease outbreaks in the Dominican Republic. Nature Communications, 2021, 12, 151.	12.8	22
20	Multiple Transmission Chains within COVID-19 Cluster, Connecticut, USA, 20201. Emerging Infectious Diseases, 2021, 27, 2669-2672.	4.3	5
21	SalivaDirect: A simplified and flexible platform to enhance SARS-CoV-2 testing capacity. Med, 2021, 2, 263-280.e6.	4.4	211
22	Abstract S03-03: Cancer patients display diminished viral RNA clearance and altered T cell responses during SARS-CoV-2 infection. , 2021, , .		0
23	Public health actions to control new SARS-CoV-2 variants. Cell, 2021, 184, 1127-1132.	28.9	149
24	Tracking smell loss to identify healthcare workers with SARS-CoV-2 infection. PLoS ONE, 2021, 16, e0248025.	2.5	10
25	Case Study: Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient. , 2021, , .		3
26	Evidence for SARS-CoV-2 Spike Protein in the Urine of COVID-19 Patients. Kidney360, 2021, 2, 924-936.	2.1	34
27	Maternal respiratory SARS-CoV-2 infection in pregnancy is associated with a robust inflammatory response at the maternal-fetal interface. Med, 2021, 2, 591-610.e10.	4.4	122
28	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. Cell Reports Medicine, 2021, 2, 100288.	6.5	121
29	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. Cell, 2021, 184, 2595-2604.e13.	28.9	113
30	Delayed production of neutralizing antibodies correlates with fatal COVID-19. Nature Medicine, 2021, 27, 1178-1186.	30.7	183
31	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	5.6	200
32	MOG-associated encephalitis following SARS-COV-2 infection. Multiple Sclerosis and Related Disorders, 2021, 50, 102857.	2.0	45
33	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil. Nature Communications, 2021, 12, 2619.	12.8	43
34	COVID-19 one year into the pandemic: from genetics and genomics to therapy, vaccination, and policy. Human Genomics, 2021, 15, 27.	2.9	39
35	Diverse functional autoantibodies in patients with COVID-19. Nature, 2021, 595, 283-288.	27.8	619
36	Viral dynamics of acute SARS-CoV-2 infection and applications to diagnostic and public health strategies. PLoS Biology, 2021, 19, e3001333.	5.6	133

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37	COVID-19 vaccines: Keeping pace with SARS-CoV-2 variants. Cell, 2021, 184, 5077-5081.	28.9	114
38	Emergence of an early SARS-CoV-2 epidemic in the United States. Cell, 2021, 184, 4939-4952.e15.	28.9	31
39	Reply to: A finding of sex similarities rather than differences in COVID-19 outcomes. Nature, 2021, 597, E10-E11.	27.8	4
40	Zika Virus Non-Structural Protein 1 Antigen-Capture Immunoassay. Viruses, 2021, 13, 1771.	3.3	5
41	Impact of circulating SARS-CoV-2 variants on mRNA vaccine-induced immunity. Nature, 2021, 600, 523-529.	27.8	194
42	Tracing the Origin, Spread, and Molecular Evolution of Zika Virus in Puerto Rico, 2016â€“2017. Emerging Infectious Diseases, 2021, 27, 2971-2973.	4.3	4
43	COVID-19 Outcomes and Genomic Characterization of SARS-CoV-2 Isolated From Veterans in New England States: Retrospective Analysis. Jmirx Med, 2021, 2, e31503.	0.4	5
44	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. New England Journal of Medicine, 2021, 385, 2489-2491.	27.0	216
45	Authors' Response to Peer Reviews of â€œCOVID-19 Outcomes and Genomic Characterization of SARS-CoV-2 Isolated From Veterans in New England States: Retrospective Analysisâ€• Jmirx Med, 2021, 2, e35515.	0.4	0
46	301. Detection of Pneumococcal Pneumonia During SARS-CoV-2 Infection. Open Forum Infectious Diseases, 2021, 8, S257-S257.	0.9	0
47	362. Saliva as a Reliable Sample Type for Mass SARS-CoV-2 Testing Strategies. Open Forum Infectious Diseases, 2021, 8, S284-S284.	0.9	0
48	Of variants and vaccines. Cell, 2021, 184, 6222-6223.	28.9	18
49	Detection of SARS-CoV-2 RNA by multiplex RT-qPCR. PLoS Biology, 2020, 18, e3000867.	5.6	64
50	Sex differences in immune responses that underlie COVID-19 disease outcomes. Nature, 2020, 588, 315-320.	27.8	1,035
51	Analytical sensitivity and efficiency comparisons of SARS-CoV-2 RTâ€“qPCR primerâ€“probe sets. Nature Microbiology, 2020, 5, 1299-1305.	13.3	661
52	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. Nature Communications, 2020, 11, 5620.	12.8	35
53	Longitudinal analyses reveal immunological misfiring in severe COVID-19. Nature, 2020, 584, 463-469.	27.8	1,710
54	Measurement of SARS-CoV-2 RNA in wastewater tracks community infection dynamics. Nature Biotechnology, 2020, 38, 1164-1167.	17.5	785

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55	Real-time public health communication of local SARS-CoV-2 genomic epidemiology. PLoS Biology, 2020, 18, e3000869.	5.6	15
56	Saliva or Nasopharyngeal Swab Specimens for Detection of SARS-CoV-2. New England Journal of Medicine, 2020, 383, 1283-1286.	27.0	823
57	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. Cell, 2020, 181, 990-996.e5.	28.9	321
58	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
59	Why does Japan have so few cases of COVIDâ€19?. EMBO Molecular Medicine, 2020, 12, e12481.	6.9	133
60	Acute encephalopathy with elevated CSF inflammatory markers as the initial presentation of COVID-19. BMC Neurology, 2020, 20, 248.	1.8	108
61	Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear. Cell, 2020, 182, 794-795.	28.9	353
62	We shouldnâ€™t worry when a virus mutates during disease outbreaks. Nature Microbiology, 2020, 5, 529-530.	13.3	136
63	456. Implementing an At-Home Smell Test for Early Assessment of COVID-19 in High-Risk Healthcare Workers. Open Forum Infectious Diseases, 2020, 7, S295-S296.	0.9	2
64	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. Journal of Virology, 2020, 94, .	3.4	10
65	SARSâ€“CoV-2 infection of the placenta. Journal of Clinical Investigation, 2020, 130, 4947-4953.	8.2	387
66	Endless Forms: Within-Host Variation in the Structure of the West Nile Virus RNA Genome during Serial Passage in Bird Hosts. MSphere, 2019, 4, .	2.9	5
67	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. PLoS Pathogens, 2019, 15, e1008042.	4.7	87
68	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. Cell, 2019, 178, 1057-1071.e11.	28.9	68
69	Arbovirus coinfection and co-transmission: A neglected public health concern?. PLoS Biology, 2019, 17, e3000130.	5.6	106
70	Small RNA responses of Culex mosquitoes and cell lines during acute and persistent virus infection. Insect Biochemistry and Molecular Biology, 2019, 109, 13-23.	2.7	47
71	Precision epidemiology for infectious disease control. Nature Medicine, 2019, 25, 206-211.	30.7	94
72	Misperceived Risks of Zika-related Microcephaly in India. Trends in Microbiology, 2019, 27, 381-383.	7.7	28

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73	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. Genome Biology, 2019, 20, 8.	8.8	712
74	Tracking virus outbreaks in the twenty-first century. Nature Microbiology, 2019, 4, 10-19.	13.3	305
75	Genomic Insights into Zika Virus Emergence and Spread. Cell, 2018, 172, 1160-1162.	28.9	56
76	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. Nature Communications, 2018, 9, 1624.	12.8	68
77	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. Cell, 2018, 173, 443-455.e12.	28.9	176
78	Adventitious viruses persistently infect three commonly used mosquito cell lines. Virology, 2018, 521, 175-180.	2.4	29
79	Inferring the risk factors behind the geographical spread and transmission of Zika in the Americas. PLoS Neglected Tropical Diseases, 2018, 12, e0006194.	3.0	67
80	Mosquitoes Transmit Unique West Nile Virus Populations during Each Feeding Episode. Cell Reports, 2017, 19, 709-718.	6.4	67
81	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	27.8	298
82	Zika virus evolution and spread in the Americas. Nature, 2017, 546, 411-415.	27.8	323
83	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 2017, 12, 1261-1276.	12.0	898
84	Experimental Evolution to Study Virus Emergence. Cell, 2017, 169, 1-3.	28.9	39
85	Neutralizing human monoclonal antibodies prevent Zika virus infection in macaques. Science Translational Medicine, 2017, 9, .	12.4	89
86	Ontogeny of the B- and T-cell response in a primary Zika virus infection of a dengue-naÃ¯ve individual during the 2016 outbreak in Miami, FL. PLoS Neglected Tropical Diseases, 2017, 11, e0006000.	3.0	48
87	The Use of Xenosurveillance to Detect Human Bacteria, Parasites, and Viruses in Mosquito Bloodmeals. American Journal of Tropical Medicine and Hygiene, 2017, 97, 324-329.	1.4	26
88	Transmission bottlenecks and RNAi collectively influence tick-borne flavivirus evolution. Virus Evolution, 2016, 2, vew033.	4.9	35
89	Genetic Drift during Systemic Arbovirus Infection of Mosquito Vectors Leads to Decreased Relative Fitness during Host Switching. Cell Host and Microbe, 2016, 19, 481-492.	11.0	125
90	West African Anopheles gambiae mosquitoes harbor a taxonomically diverse virome including new insect-specific flaviviruses, mononegaviruses, and totiviruses. Virology, 2016, 498, 288-299.	2.4	112

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91	Dynamics of West Nile virus evolution in mosquito vectors. Current Opinion in Virology, 2016, 21, 132-138.	5.4	39
92	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013â€“2016 Epidemic. Cell, 2016, 167, 1088-1098.e6.	28.9	173
93	West Nile Virus Population Structure, Injury, and Interferon-Stimulated Gene Expression in the Brain From a Fatal Case of Encephalitis. Open Forum Infectious Diseases, 2016, 3, ofv182.	0.9	11
94	Isolation of a Novel Insect-Specific Flavivirus fromCuliseta melanurain the Northeastern United States. Vector-Borne and Zoonotic Diseases, 2016, 16, 181-190.	1.5	15
95	Temporal and Spatial Variability of Entomological Risk Indices for West Nile Virus Infection in Northern Colorado: 2006â€“2013. Journal of Medical Entomology, 2016, 53, 425-434.	1.8	16
96	Navigating the Zika panic. F1000Research, 2016, 5, 1914.	1.6	1
97	Sampling Host-Seeking Anthropophilic Mosquito Vectors in West Africa: Comparisons of an Active Human-Baited Tent-Trap Against Gold Standard Methods. American Journal of Tropical Medicine and Hygiene, 2015, 92, 415-421.	1.4	11
98	Experimental Evolution of an RNA Virus in Wild Birds: Evidence for Host-Dependent Impacts on Population Structure and Competitive Fitness. PLoS Pathogens, 2015, 11, e1004874.	4.7	51
99	Xenosurveillance: A Novel Mosquito-Based Approach for Examining the Human-Pathogen Landscape. PLoS Neglected Tropical Diseases, 2015, 9, e0003628.	3.0	67
100	Evaluation of ivermectin mass drug administration for malaria transmission control across different West African environments. Malaria Journal, 2014, 13, 417.	2.3	93
101	Evaluation of a Field-Portable DNA Microarray Platform and Nucleic Acid Amplification Strategies for the Detection of Arboviruses, Arthropods, and Bloodmeals. American Journal of Tropical Medicine and Hygiene, 2013, 88, 245-253.	1.4	17
102	Isolation and genomic characterization of Chaoyang virus strain ROK144 from Aedes vexans nipponii from the Republic of Korea. Virology, 2013, 435, 220-224.	2.4	39
103	Multi-Gene Detection and Identification of Mosquito-Borne RNA Viruses Using an Oligonucleotide Microarray. PLoS Neglected Tropical Diseases, 2013, 7, e2349.	3.0	11