

My V T Phan

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5700764/my-v-t-phan-publications-by-year.pdf>
Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

41 papers	917 citations	15 h-index	30 g-index
51 ext. papers	1,302 ext. citations	8.4 avg, IF	4.24 L-index

#	Paper	IF	Citations
41	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
40	SARS-CoV-2 Variants, South Sudan, January-March 2021. <i>Emerging Infectious Diseases</i> , 2021 , 27, 3133-3136.	36.2	2
39	No Evidence Known Viruses Play a Role in the Pathogenesis of Onchocerciasis-Associated Epilepsy. An Explorative Metagenomic Case-Control Study. <i>Pathogens</i> , 2021 , 10,	4.5	2
38	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. <i>Nature Microbiology</i> , 2021 , 6, 1094-1101	26.6	39
37	Automated download and clean-up of family-specific databases for kmer-based virus identification. <i>Bioinformatics</i> , 2021 , 37, 705-710	7.2	1
36	Spike protein cleavage-activation mediated by the SARS-CoV-2 P681R mutation: a case-study from its first appearance in variant of interest (VOI) A.23.1 identified in Uganda 2021 ,		14
35	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. <i>Virus Evolution</i> , 2021 , 7, veab063.	3.7	2
34	Alternate primers for whole-genome SARS-CoV-2 sequencing. <i>Virus Evolution</i> , 2021 , 7, veab006	3.7	8
33	Shedding of Yellow Fever Virus From an Imported Case in the Netherlands After Travel to Brazil. <i>Open Forum Infectious Diseases</i> , 2020 , 7, ofaa020	1	1
32	Norovirus outbreak in a natural playground: A One Health approach. <i>Zoonoses and Public Health</i> , 2020 , 67, 453-459	2.9	2
31	Virus Metagenomics in Farm Animals: A Systematic Review. <i>Viruses</i> , 2020 , 12,	6.2	21
30	Genome Sequences of Seven Strains from Chickens in The Netherlands. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
29	Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia. <i>BMC Genomics</i> , 2020 , 21, 5	4.5	1
28	Nosocomial outbreak of the Middle East Respiratory Syndrome coronavirus: A phylogenetic, epidemiological, clinical and infection control analysis. <i>Travel Medicine and Infectious Disease</i> , 2020 , 37, 101807	8.4	10
27	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020 , 10, 13748	4.9	15
26	Increased resolution of African swine fever virus genome patterns based on profile HMMs of protein domains. <i>Virus Evolution</i> , 2020 , 6, veaa044	3.7	4
25	Characterization of Norovirus and Other Human Enteric Viruses in Sewage and Stool Samples Through Next-Generation Sequencing. <i>Food and Environmental Virology</i> , 2019 , 11, 400-409	4	22

24	Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	9
23	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. <i>Viruses</i> , 2019 , 11,	6.2	1
22	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019 , 9, 10076	4.9	12
21	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , 2019 , 10, 2394	5.7	15
20	A64 Viral sequence classification using deep learning algorithms. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
19	Genomic sequence of yellow fever virus from a Dutch traveller returning from the Gambia-Senegal region, the Netherlands, November 2018. <i>Eurosurveillance</i> , 2019 , 24,	19.8	6
18	Complete Genome Sequences of Six Measles Virus Strains. <i>Genome Announcements</i> , 2018 , 6,		5
17	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018 , 4, vey035	3.7	35
16	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
15	Whole-Genome Next-Generation Sequencing to Study Within-Host Evolution of Norovirus (NoV) Among Immunocompromised Patients With Chronic NoV Infection. <i>Journal of Infectious Diseases</i> , 2017 , 216, 1513-1524	7	26
14	Characterization of Posa and Posa-like virus genomes in fecal samples from humans, pigs, rats, and bats collected from a single location in Vietnam. <i>Virus Evolution</i> , 2017 , 3, vex022	3.7	17
13	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016	3.7	89
12	Notes from The Field: Ebola Virus Disease Cluster - Northern Sierra Leone, January 2016. <i>Morbidity and Mortality Weekly Report</i> , 2016 , 65, 681-2	31.7	14
11	Severe acute respiratory infection caused by swine influenza virus in a child necessitating extracorporeal membrane oxygenation (ECMO), the Netherlands, October 2016. <i>Eurosurveillance</i> , 2016 , 21,	19.8	13
10	Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. <i>Virus Evolution</i> , 2016 , 2, vew027	3.7	35
9	Complete Genome Characterization of Two Wild-Type Measles Viruses from Vietnamese Infants during the 2014 Outbreak. <i>Genome Announcements</i> , 2016 , 4,		2
8	Genome Sequences of a Novel Vietnamese Bat Bunyavirus. <i>Genome Announcements</i> , 2016 , 4,		2
7	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , 2016 , 2, vew005	3.7	16

6	A prospective multi-center observational study of children hospitalized with diarrhea in Ho Chi Minh City, Vietnam. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015 , 92, 1045-52	3.2	4 ¹
5	The impact of environmental and climatic variation on the spatiotemporal trends of hospitalized pediatric diarrhea in Ho Chi Minh City, Vietnam. <i>Health and Place</i> , 2015 , 35, 147-54	4.6	20
4	Deep sequencing of norovirus genomes defines evolutionary patterns in an urban tropical setting. <i>Journal of Virology</i> , 2014 , 88, 11056-69	6.6	57
3	Increased resolution of African Swine Fever Virus genome patterns based on profile HMM protein domains		1
2	Alternate primers for whole-genome SARS-CoV-2 sequencing		2
1	Genomic surveillance reveals the spread patterns of SARS-CoV-2 in coastal Kenya during the first two waves		1