

# My V T Phan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5700764/publications.pdf>

Version: 2024-02-01

41  
papers

1,450  
citations

430754

18  
h-index

377752

34  
g-index

51  
all docs

51  
docs citations

51  
times ranked

3156  
citing authors

#	ARTICLE	IF	CITATIONS
1	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
3	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
4	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.	5.9	82
5	Deep Sequencing of Norovirus Genomes Defines Evolutionary Patterns in an Urban Tropical Setting. <i>Journal of Virology</i> , 2014, 88, 11056-11069.	1.5	78
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, 1045-1052.	0.6	56
7	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018, 4, vey035.	2.2	56
8	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.	2.2	52
9	Virus Metagenomics in Farm Animals: A Systematic Review. <i>Viruses</i> , 2020, 12, 107.	1.5	47
10	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
11	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.	1.9	36
12	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.	1.5	35
13	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, 147-154.	1.5	32
14	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , 2016, 2, vew005.	2.2	26
15	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , 2019, 10, 2394.	1.5	26
16	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.	2.2	25
17	Alternate primers for whole-genome SARS-CoV-2 sequencing. <i>Virus Evolution</i> , 2021, 7, veab006.	2.2	25
18	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.	1.5	21

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19	Spike Protein Cleavage-Activation in the Context of the SARS-CoV-2 P681R Mutation: an Analysis from Its First Appearance in Lineage A.23.1 Identified in Uganda. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	20
20	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019, 9, 10076.	1.6	19
21	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, .	3.9	19
22	Notes from The Field: Ebola Virus Disease Cluster “ Northern Sierra Leone, January 2016. <i>Morbidity and Mortality Weekly Report</i> , 2016, 65, 681-682.	9.0	16
23	Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	14
24	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, .	3.9	9
25	Transmission networks of SARS-CoV-2 in Coastal Kenya during the first two waves: A retrospective genomic study. <i>ELife</i> , 0, 11, .	2.8	9
26	Complete Genome Sequences of Six Measles Virus Strains. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
27	Increased resolution of African swine fever virus genome patterns based on profile HMMs of protein domains. <i>Virus Evolution</i> , 2020, 6, veaa044.	2.2	7
28	Norovirus outbreak in a natural playground: A One Health approach. <i>Zoonoses and Public Health</i> , 2020, 67, 453-459.	0.9	7
29	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, 787.	1.2	7
30	Complete Genome Characterization of Eight Human Parainfluenza Viruses from the Netherlands. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
31	Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia. <i>BMC Genomics</i> , 2020, 21, 5.	1.2	4
32	Automated download and clean-up of family-specific databases for kmer-based virus identification. <i>Bioinformatics</i> , 2021, 37, 705-710.	1.8	4
33	Genome Sequence of a <i>Minacovirus</i> Strain from a Farmed Mink in The Netherlands. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
34	Genome Sequences of Seven <i>Megrivirus</i> Strains from Chickens in The Netherlands. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
35	SARS-CoV-2 Variants, South Sudan, January–March 2021. <i>Emerging Infectious Diseases</i> , 2021, 27, 3133-3136.	2.0	4
36	Complete Genome Characterization of Two Wild-Type Measles Viruses from Vietnamese Infants during the 2014 Outbreak. <i>Genome Announcements</i> , 2016, 4, .	0.8	2

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37	Genome Sequences of a Novel Vietnamese Bat Bunyavirus. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
38	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. <i>Viruses</i> , 2019, 11, 394.	1.5	2
39	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.	0.4	2
40	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. <i>Virus Evolution</i> , 2021, 7, veab067.	2.2	2
41	A64â€fViral sequence classification using deep learning algorithms. <i>Virus Evolution</i> , 2019, 5, .	2.2	0