

# Claude Kwe Yinda

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4882971/publications.pdf>

Version: 2024-02-01

28  
papers

1,737  
citations

361045

20  
h-index

500791

28  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3285  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532.	1.6	277
2	K18-hACE2 mice develop respiratory disease resembling severe COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009195.	2.1	227
3	Intranasal ChAdOx1 nCoV-19/AZD1222 vaccination reduces viral shedding after SARS-CoV-2 D614G challenge in preclinical models. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	180
4	Mechanistic theory predicts the effects of temperature and humidity on inactivation of SARS-CoV-2 and other enveloped viruses. <i>ELife</i> , 2021, 10, .	2.8	158
5	SARS-CoV-2 disease severity and transmission efficiency is increased for airborne compared to fomite exposure in Syrian hamsters. <i>Nature Communications</i> , 2021, 12, 4985.	5.8	94
6	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , 2018, 4, vey008.	2.2	90
7	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
8	ChAdOx1 nCoV-19 (AZD1222) protects Syrian hamsters against SARS-CoV-2 B.1.351 and B.1.1.7. <i>Nature Communications</i> , 2021, 12, 5868.	5.8	52
9	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	1.8	48
10	Increased small particle aerosol transmission of B.1.1.7 compared with SARS-CoV-2 lineage A in vivo. <i>Nature Microbiology</i> , 2022, 7, 213-223.	5.9	45
11	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	1.6	44
12	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	44
13	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249.	1.2	42
14	Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519.	3.3	36
15	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021, 12, .	1.8	31
16	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. <i>Virus Evolution</i> , 2017, 3, vex024.	2.2	30
17	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	3.3	30
18	The B.1.427/1.429 (epsilon) SARS-CoV-2 variants are more virulent than ancestral B.1 (614G) in Syrian hamsters. <i>PLoS Pathogens</i> , 2022, 18, e1009914.	2.1	26

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19	Prior aerosol infection with lineage A SARS-CoV-2 variant protects hamsters from disease, but not reinfection with B.1.351 SARS-CoV-2 variant. <i>Emerging Microbes and Infections</i> , 2021, 10, 1284-1292.	3.0	25
20	Reassortment among picobirnaviruses found in wolves. <i>Archives of Virology</i> , 2016, 161, 2859-2862.	0.9	24
21	Subtle differences in the pathogenicity of SARS-CoV-2 variants of concern B.1.1.7 and B.1.351 in rhesus macaques. <i>Science Advances</i> , 2021, 7, eabj3627.	4.7	24
22	OraSure InteliSwabâ„¢ Rapid Antigen Test Performance with the SARS-CoV-2 Variants of Concernâ€”Alpha, Beta, Gamma, Delta, and Omicron. <i>Viruses</i> , 2022, 14, 543.	1.5	14
23	Complete genome analyses of the first porcine rotavirus group H identified from a South African pig does not provide evidence for recent interspecies transmission events. <i>Infection, Genetics and Evolution</i> , 2016, 38, 1-7.	1.0	13
24	Exploration of the virome of the European brown shrimp ( <i>Crangon crangon</i> ). <i>Journal of General Virology</i> , 2020, 101, 651-666.	1.3	13
25	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. <i>Virology Reports</i> , 2016, 6, 74-80.	0.4	8
26	A Novel Field-Deployable Method for Sequencing and Analyses of Henipavirus Genomes From Complex Samples on the MinION Platform. <i>Journal of Infectious Diseases</i> , 2020, 221, S383-S388.	1.9	5
27	Complete coding sequence of a novel picorna-like virus in a blackbird infected with Usutu virus. <i>Archives of Virology</i> , 2018, 163, 1701-1703.	0.9	4
28	Whole genome analysis of Aichivirus A, isolated from a child, suffering from gastroenteritis, in Pakistan. <i>Virus Research</i> , 2021, 299, 198437.	1.1	2