

# Claude Kwe Yinda

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35  
papers

820  
citations

15  
h-index

28  
g-index

37  
ext. papers

1,330  
ext. citations

9.1  
avg. IF

4.38  
L-index

#	Paper	IF	Citations
35	Increased small particle aerosol transmission of B.1.1.7 compared with SARS-CoV-2 lineage A in vivo.. <i>Nature Microbiology</i> , <b>2022</b> ,	26.6	7
34	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> , <b>2022</b> , 18, e1009914	7.6	3
33	Efficacy of ChAdOx1 vaccines against SARS-CoV-2 Variants of Concern Beta, Delta and Omicron in the Syrian hamster model. <b>2022</b> ,		1
32	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> , <b>2022</b> , 119, e2114619119	11.5	2
31	OraSure IntelliSwab Rapid Antigen Test Performance with the SARS-CoV-2 Variants of Concern-Alpha, Beta, Gamma, Delta, and Omicron.. <i>Viruses</i> , <b>2022</b> , 14,	6.2	1
30	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> , <b>2021</b> , 7, eabj3627	14.3	9
29	ChAdOx1 nCoV-19 (AZD1222) protects Syrian hamsters against SARS-CoV-2 B.1.351 and B.1.1.7. <i>Nature Communications</i> , <b>2021</b> , 12, 5868	17.4	19
28	Mechanistic theory predicts the effects of temperature and humidity on inactivation of SARS-CoV-2 and other enveloped viruses. <i>ELife</i> , <b>2021</b> , 10,	8.9	55
27	Whole genome analysis of Aichivirus A, isolated from a child, suffering from gastroenteritis, in Pakistan. <i>Virus Research</i> , <b>2021</b> , 299, 198437	6.4	0
26	K18-hACE2 mice develop respiratory disease resembling severe COVID-19. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009195	7.6	96
25	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> , <b>2021</b> , 10, 1284-1292	18.9	13
24	Intranasal ChAdOx1 nCoV-19/AZD1222 vaccination reduces viral shedding after SARS-CoV-2 D614G challenge in preclinical models. <i>Science Translational Medicine</i> , <b>2021</b> , 13,	17.5	56
23	Increased aerosol transmission for B.1.1.7 (alpha variant) over lineage A variant of SARS-CoV-2 <b>2021</b> ,		3
22	SARS-CoV-2 disease severity and transmission efficiency is increased for airborne compared to fomite exposure in Syrian hamsters. <i>Nature Communications</i> , <b>2021</b> , 12, 4985	17.4	44
21	The B.1.427/1.429 (epsilon) SARS-CoV-2 variants are more virulent than ancestral B.1 (614G) in Syrian hamsters <b>2021</b> ,		5
20	Increased aerosol transmission for B.1.1.7 (alpha variant) over lineage A variant of SARS-CoV-2 <b>2021</b> ,		4
19	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , <b>2021</b> , 12,	7.8	13

18	Successional Stages in Infant Gut Microbiota Maturation.. <i>MBio</i> , <b>2021</b> , e0185721	7.8	7
17	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> , <b>2020</b> , 117, 10511-10519	11.5	16
16	Exploration of the virome of the European brown shrimp (). <i>Journal of General Virology</i> , <b>2020</b> , 101, 651-666	4.9	7
15	Mechanistic theory predicts the effects of temperature and humidity on inactivation of SARS-CoV-2 and other enveloped viruses <b>2020</b> ,		24
14	SARS-CoV-2 disease severity and transmission efficiency is increased for airborne but not fomite exposure in Syrian hamsters <b>2020</b> ,		14
13	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> , <b>2020</b> , 221, S383-S388	7	2
12	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , <b>2019</b> , 4,	5	35
11	Complete coding sequence of a novel picorna-like virus in a blackbird infected with Usutu virus. <i>Archives of Virology</i> , <b>2018</b> , 163, 1701-1703	2.6	2
10	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , <b>2018</b> , 4, vey008	3.7	58
9	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , <b>2017</b> , 6, e38	18.9	26
8	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , <b>2017</b> , 18, 249	4.5	32
7	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. <i>Virus Evolution</i> , <b>2017</b> , 3, vex024	3.7	20
6	Reassortment among picobirnaviruses found in wolves. <i>Archives of Virology</i> , <b>2016</b> , 161, 2859-62	2.6	21
5	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , <b>2016</b> , 6, 34209	4.9	34
4	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> , <b>2016</b> , 38, 1-7	4.5	9
3	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. <i>Virology Reports</i> , <b>2016</b> , 6, 74-80		7
2	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , <b>2015</b> , 5, 16532	4.9	168
1	Hymenoptera associated eukaryotic virome lacks host specificity		4

