

Deogratus Ssemwanga

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2238943/publications.pdf>

Version: 2024-02-01

26
papers

726
citations

759233

12
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

1315
citing authors

#	ARTICLE	IF	CITATIONS
1	HIV subtype diversity worldwide. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 153-160.	3.8	182
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
3	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183.	4.7	59
4	Phylogeography of HIV-1 suggests that Ugandan fishing communities are a sink for, not a source of, virus from general populations. <i>Scientific Reports</i> , 2019, 9, 1051.	3.3	43
5	Update on HIV-1 acquired and transmitted drug resistance in Africa. <i>AIDS Reviews</i> , 2015, 17, 3-20.	1.0	41
6	Analysis of the history and spread of HIV-1 in Uganda using phylodynamics. <i>Journal of General Virology</i> , 2015, 96, 1890-1898.	2.9	34
7	HIV Type 1 Subtype Distribution, Multiple Infections, Sexual Networks, and Partnership Histories in Female Sex Workers in Kampala, Uganda. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 357-365.	1.1	27
8	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016, 6, 39489.	3.3	23
9	HIV-1 transmission networks in high risk fishing communities on the shores of Lake Victoria in Uganda: A phylogenetic and epidemiological approach. <i>PLoS ONE</i> , 2017, 12, e0185818.	2.5	23
10	Rates of HIV-1 superinfection and primary HIV-1 infection are similar in female sex workers in Uganda. <i>Aids</i> , 2014, 28, 2147-2152.	2.2	20
11	Phylogenetic and Demographic Characterization of Directed HIV-1 Transmission Using Deep Sequences from High-Risk and General Population Cohorts/Groups in Uganda. <i>Viruses</i> , 2020, 12, 331.	3.3	17
12	Rates of HIV-1 virological suppression and patterns of acquired drug resistance among fisherfolk on first-line antiretroviral therapy in Uganda. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3021-3029.	3.0	16
13	HIV-1 Subtype Distribution Trends and Evidence of Transmission Clusters Among Incident Cases in a Rural Clinical Cohort in Southwest Uganda, 2004–2010. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 520-527.	1.1	13
14	Sustained virological response and drug resistance among female sex workers living with HIV on antiretroviral therapy in Kampala, Uganda: a cross-sectional study. <i>Sexually Transmitted Infections</i> , 2019, 95, 405-411.	1.9	12
15	Transmitted Antiretroviral Drug Resistance Among Drug-Naive Female Sex Workers With Recent Infection in Kampala, Uganda. <i>Clinical Infectious Diseases</i> , 2012, 54, S339-S342.	5.8	11
16	Prevalence of viral load suppression, predictors of virological failure and patterns of HIV drug resistance after 12 and 48 months on first-line antiretroviral therapy: a national cross-sectional survey in Uganda. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1280-1289.	3.0	11
17	Low Drug Resistance Levels Among Drug-Naive Individuals with Recent HIV Type 1 Infection in a Rural Clinical Cohort in Southwestern Uganda. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1784-1787.	1.1	10
18	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	4.9	9

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19	HIV drug resistance among adults initiating antiretroviral therapy in Uganda. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2407-2414.	3.0	8
20	Phylogenetic Networks and Parameters Inferred from HIV Nucleotide Sequences of High-Risk and General Population Groups in Uganda: Implications for Epidemic Control. <i>Viruses</i> , 2021, 13, 970.	3.3	5
21	HIV-1 superinfection can occur in the presence of broadly neutralizing antibodies. <i>Vaccine</i> , 2018, 36, 578-586.	3.8	4
22	The Molecular Epidemiology and Transmission Dynamics of HIV Type 1 in a General Population Cohort in Uganda. <i>Viruses</i> , 2020, 12, 1283.	3.3	4
23	Short Communication: Choosing the Right Program for the Identification of HIV-1 Transmission Networks from Nucleotide Sequences Sampled from Different Populations. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 948-951.	1.1	3
24	Employing phylogenetic tree shape statistics to resolve the underlying host population structure. <i>BMC Bioinformatics</i> , 2021, 22, 546.	2.6	3
25	HIV-1 drug resistance genotyping success rates and correlates of Dried-blood spots and plasma specimen genotyping failure in a resource-limited setting. <i>BMC Infectious Diseases</i> , 2022, 22, 474.	2.9	2
26	High Levels of Acquired HIV Drug Resistance Following Virological Nonsuppression in HIV-Infected Women from a High-Risk Cohort in Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 782-791.	1.1	1