

Jean Lutamyo Mbisa

List of Publications by Year in descending order

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48
papers

1,515
citations

430874

18
h-index

315739

38
g-index

50
all docs

50
docs citations

50
times ranked

2189
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Apolipoprotein B mRNA-editing Enzyme-catalytic Polypeptide-like 3G (APOBEC3G) Is Incorporated into HIV-1 Virions through Interactions with Viral and Nonviral RNAs. <i>Journal of Biological Chemistry</i> , 2004, 279, 35822-35828.	3.4	250
2	Human Immunodeficiency Virus Type 1 cDNAs Produced in the Presence of APOBEC3G Exhibit Defects in Plus-Strand DNA Transfer and Integration. <i>Journal of Virology</i> , 2007, 81, 7099-7110.	3.4	247
3	APOBEC3F and APOBEC3G Inhibit HIV-1 DNA Integration by Different Mechanisms. <i>Journal of Virology</i> , 2010, 84, 5250-5259.	3.4	115
4	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	3.9	112
5	Real-Time PCR Analysis of HIV-1 Replication Post-entry Events. <i>Methods in Molecular Biology</i> , 2009, 485, 55-72.	0.9	66
6	Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1051-1056.	7.1	65
7	Reovirus $\sigma 2$ Protein Determines Strain-Specific Differences in the Rate of Viral Inclusion Formation in L929 Cells. <i>Virology</i> , 2000, 272, 16-26.	2.4	45
8	De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. <i>PLoS ONE</i> , 2016, 11, e0157600.	2.5	43
9	Evidence of Self-Sustaining Drug Resistant HIV-1 Lineages Among Untreated Patients in the United Kingdom. <i>Clinical Infectious Diseases</i> , 2015, 61, 829-836.	5.8	34
10	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. <i>Viruses</i> , 2020, 12, 694.	3.3	34
11	Efficient and unbiased metagenomic recovery of RNA virus genomes from human plasma samples. <i>Scientific Reports</i> , 2017, 7, 4173.	3.3	31
12	Patterns of resistance development with integrase inhibitors in HIV. <i>Infection and Drug Resistance</i> , 2011, 4, 65.	2.7	30
13	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	3.3	29
14	Enhanced surveillance of HIV-1 drug resistance in recently infected MSM in the UK. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 227-234.	3.0	23
15	Consensus recommendations for resistance testing in the management of chronic hepatitis C virus infection: Public Health England HCV Resistance Group. <i>Journal of Infection</i> , 2019, 79, 503-512.	3.3	23
16	HIV-1 drug resistance mutations emerging on darunavir therapy in PI-naïve and -experienced patients in the UK. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3487-3494.	3.0	21
17	Molecular and epidemiological characterization of HIV-1 infection networks involving transmitted drug resistance mutations in Northern Greece. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 2831-2837.	3.0	19
18	Contribution of Gag and protease to variation in susceptibility to protease inhibitors between different strains of subtype B human immunodeficiency virus type 1. <i>Journal of General Virology</i> , 2014, 95, 190-200.	2.9	19

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19	Challenges of aciclovir-resistant HSV infection in allogeneic bone marrow transplant recipients. <i>Journal of Clinical Virology</i> , 2020, 128, 104421.	3.1	19
20	Dynamics of HIV Type 1 Recombination Following Superinfection. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 963-970.	1.1	18
21	Intercontinental Dispersal of HIV-1 Subtype B Associated with Transmission among Men Who Have Sex with Men in Japan. <i>Journal of Virology</i> , 2014, 88, 9864-9876.	3.4	18
22	HIV-1 subtype influences susceptibility and response to monotherapy with the protease inhibitor lopinavir/ritonavir. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 243-248.	3.0	18
23	Mutations in the RNase H Primer Grip Domain of Murine Leukemia Virus Reverse Transcriptase Decrease Efficiency and Accuracy of Plus-Strand DNA Transfer. <i>Journal of Virology</i> , 2005, 79, 419-427.	3.4	16
24	Phenotypic characterization of virological failure following lopinavir/ritonavir monotherapy using full-length gag-protease genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 3340-3348.	3.0	16
25	Real world SOF/VEL/VOX retreatment outcomes and viral resistance analysis for HCV patients with prior failure to DAA therapy. <i>Journal of Viral Hepatitis</i> , 2021, 28, 1256-1264.	2.0	16
26	Surveillance of HIV-1 transmitted integrase strand transfer inhibitor resistance in the UK. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3311-3318.	3.0	15
27	Inpatient Variation of the Respiratory Syncytial Virus Attachment Protein Gene. <i>Journal of Virology</i> , 2010, 84, 10425-10428.	3.4	13
28	Low frequency of genotypic resistance in HIV-1-infected patients failing an atazanavir-containing regimen: a clinical cohort study. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2339-43.	3.0	13
29	A European multi-centre External Quality Assessment (EQA) study on phenotypic and genotypic methods used for Herpes Simplex Virus (HSV) drug resistance testing. <i>Journal of Clinical Virology</i> , 2017, 96, 89-93.	3.1	13
30	Presence, persistence and effects of pre-treatment HIV-1 drug resistance variants detected using next generation sequencing: A Retrospective longitudinal study from rural coastal Kenya. <i>PLoS ONE</i> , 2019, 14, e0210559.	2.5	13
31	Technical Validation of a Hepatitis C Virus Whole Genome Sequencing Assay for Detection of Genotype and Antiviral Resistance in the Clinical Pathway. <i>Frontiers in Microbiology</i> , 2020, 11, 576572.	3.5	13
32	The evolution of HIV-1 reverse transcriptase in route to acquisition of Q151M multi-drug resistance is complex and involves mutations in multiple domains. <i>Retrovirology</i> , 2011, 8, 31.	2.0	12
33	Seroprevalence of HCV, HBV and HIV in two inner-city London emergency departments. <i>Epidemiology and Infection</i> , 2019, 147, e145.	2.1	11
34	Subtype-specific differences in the development of accessory mutations associated with high-level resistance to HIV-1 nucleoside reverse transcriptase inhibitors. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1220-1236.	3.0	10
35	Enhanced Detection of DNA Viruses in the Cerebrospinal Fluid of Encephalitis Patients Using Metagenomic Next-Generation Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 1879.	3.5	10
36	Phylogenetic and Phylogeographic Patterns of the HIV Type 1 Subtype F1 Parenteral Epidemic in Romania. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1161-1166.	1.1	9

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37	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. Wellcome Open Research, 2019, 4, 155.	1.8	9
38	Next generation sequencing of HIV-1 protease in the PIVOT trial of protease inhibitor monotherapy. Journal of Clinical Virology, 2018, 101, 63-65.	3.1	8
39	Impact of Interferon- β Receptor-1 Promoter Polymorphisms on the Transcriptome of the Hepatitis B Virus-Associated Hepatocellular Carcinoma. Frontiers in Immunology, 2018, 9, 777.	4.8	8
40	An Innovative Study Design to Assess the Community Effect of Interventions to Mitigate HIV Epidemics Using Transmission-Chain Phylodynamics. American Journal of Epidemiology, 2018, 187, 2615-2622.	3.4	7
41	Determining the Origins of Human Immunodeficiency Virus Type 1 Drug-resistant Minority Variants in People Who Are Recently Infected Using Phylogenetic Reconstruction. Clinical Infectious Diseases, 2018, 69, 1136-1143.	5.8	5
42	Resolution by deep sequencing of a dual hepatitis E virus infection transmitted via blood components. Journal of General Virology, 2019, 100, 1491-1500.	2.9	5
43	Protease mutations emerging on darunavir in protease inhibitor-naïve and experienced patients in the UK. Journal of the International AIDS Society, 2014, 17, 19739.	3.0	4
44	Manipulation of both virus- and cell-specific factors is required for robust transient replication of a hepatitis C virus genotype 3a sub-genomic replicon. Journal of General Virology, 2017, 98, 2495-2506.	2.9	4
45	Inpatient Evolutionary Dynamics of Human Immunodeficiency Virus Type 1 in Individuals Undergoing Alternative Treatment Strategies with Reverse Transcriptase Inhibitors. AIDS Research and Human Retroviruses, 2015, 31, 749-756.	1.1	2
46	Clinical evaluation of a Hepatitis C Virus whole-genome sequencing pipeline for genotyping and resistance testing. Clinical Microbiology and Infection, 2021, , .	6.0	1
47	Coevolved Multidrug-Resistant HIV-1 Protease and Reverse Transcriptase Influences Integrase Drug Susceptibility and Replication Fitness. Pathogens, 2021, 10, 1070.	2.8	1
48	LBP-34-Effect of Resistance Associated Substitutions on Retreatment of HCV infected patients with prior failure to Direct Acting Antiviral Therapy. Journal of Hepatology, 2019, 70, e158-e159.	3.7	0