

Soo-Yon Rhee

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

4,736
citations

147801

31
h-index

149698

56
g-index

59
all docs

59
docs citations

59
times ranked

4552
citing authors

#	ARTICLE	IF	CITATIONS
1	Public availability of HIV-1 drug resistance sequence and treatment data: a systematic review. <i>Lancet Microbe</i> , The, 2022, 3, e392-e398.	7.3	14
2	Adherence to contemporary antiretroviral treatment regimens and impact on immunological and virologic outcomes in a US healthcare system. <i>PLoS ONE</i> , 2022, 17, e0263742.	2.5	9
3	Spectrum of Atazanavir-Selected Protease Inhibitor-Resistance Mutations. <i>Pathogens</i> , 2022, 11, 546.	2.8	3
4	Integrase Strand Transfer Inhibitor Resistance in Integrase Strand Transfer Inhibitor-Naive Persons. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 736-743.	1.1	13
5	Temporal Trends in HIV-1 Mutations Used for the Surveillance of Transmitted Drug Resistance. <i>Viruses</i> , 2021, 13, 879.	3.3	10
6	Comparing mutational pathways to lopinavir resistance in HIV-1 subtypes B versus C. <i>PLoS Computational Biology</i> , 2021, 17, e1008363.	3.2	2
7	Development of HIV Drug Resistance in a Cohort of Adults on First-Line Antiretroviral Therapy in Tanzania during the Stavudine Era. <i>Microbiology Research</i> , 2021, 12, 847-861.	1.9	5
8	Integrase strand transfer inhibitor (INSTI)-resistance mutations for the surveillance of transmitted HIV-1 drug resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 170-182.	3.0	50
9	Coronavirus Antiviral Research Database (CoV-RDB): An Online Database Designed to Facilitate Comparisons between Candidate Anti-Coronavirus Compounds. <i>Viruses</i> , 2020, 12, 1006.	3.3	60
10	Virological Failure and Acquired Genotypic Resistance Associated With Contemporary Antiretroviral Treatment Regimens. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa316.	0.9	8
11	HIV-1 transmitted drug resistance surveillance: shifting trends in study design and prevalence estimates. <i>Journal of the International AIDS Society</i> , 2020, 23, e25611.	3.0	33
12	Predictors of first-line antiretroviral therapy failure among adults and adolescents living with HIV/AIDS in a large prevention and treatment program in Nigeria. <i>AIDS Research and Therapy</i> , 2020, 17, 64.	1.7	5
13	Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2. <i>Journal of Infectious Diseases</i> , 2020, 221, 1962-1972.	4.0	14
14	Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted Human Immunodeficiency Virus Type 1 Drug Resistance in a Large US Clinic Population. <i>Clinical Infectious Diseases</i> , 2019, 68, 213-221.	5.8	46
15	A systematic review of the genetic mechanisms of dolutegravir resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3135-3149.	3.0	95
16	Amino Acid Prevalence of HIV-1 <i>crf01_AG05</i> Mutations by Direct Polymerase Chain Reaction and Single Genome Sequencing. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 924-929.	1.1	3
17	National and International Dimensions of Human Immunodeficiency Virus-1 Sequence Clusters in a Northern California Clinical Cohort. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz135.	0.9	6
18	Trends in Pretreatment HIV-1 Drug Resistance in Antiretroviral Therapy-naive Adults in South Africa, 2000-2016: A Pooled Sequence Analysis. <i>EClinicalMedicine</i> , 2019, 9, 26-34.	7.1	51

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19	Moderate-to-High Levels of Pretreatment HIV Drug Resistance in KwaZulu-Natal Province, South Africa. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 129-138.	1.1	21
20	Selection analyses of paired HIV-1 gag and gp41 sequences obtained before and after antiretroviral therapy. <i>Scientific Data</i> , 2018, 5, 180147.	5.3	1
21	Geographically-stratified HIV-1 group M pol subtype and circulating recombinant form sequences. <i>Scientific Data</i> , 2018, 5, 180148.	5.3	7
22	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. <i>EBioMedicine</i> , 2017, 18, 225-235.	6.1	28
23	Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1-Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing. <i>Journal of Infectious Diseases</i> , 2017, 216, 387-391.	4.0	28
24	Genetic Variability of HIV-1 for Drug Resistance Assay Development. <i>Viruses</i> , 2016, 8, 48.	3.3	14
25	Surveillance of HIV Transmitted Drug Resistance in Latin America and the Caribbean: A Systematic Review and Meta-Analysis. <i>PLoS ONE</i> , 2016, 11, e0158560.	2.5	35
26	HIV-1 Protease, Reverse Transcriptase, and Integrase Variation. <i>Journal of Virology</i> , 2016, 90, 6058-6070.	3.4	72
27	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 565-575.	9.1	217
28	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. <i>ELife</i> , 2016, 5, .	6.0	70
29	Geographic and Temporal Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted HIV-1 Drug Resistance: An Individual-Patient- and Sequence-Level Meta-Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001810.	8.4	188
30	Impact of Drug Resistance-Associated Amino Acid Changes in HIV-1 Subtype C on Susceptibility to Newer Nonnucleoside Reverse Transcriptase Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 960-971.	3.2	48
31	HIV-1 Drug Resistance Mutations: Potential Applications for Point-of-Care Genotypic Resistance Testing. <i>PLoS ONE</i> , 2015, 10, e0145772.	2.5	72
32	Non-nucleoside reverse transcriptase inhibitor (NNRTI) cross-resistance: implications for preclinical evaluation of novel NNRTIs and clinical genotypic resistance testing. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 12-20.	3.0	98
33	Nucleoside Reverse Transcriptase Inhibitor Resistance Mutations Associated with First-Line Stavudine-Containing Antiretroviral Therapy: Programmatic Implications for Countries Phasing Out Stavudine. <i>Journal of Infectious Diseases</i> , 2013, 207, S70-S77.	4.0	30
34	Functional conservation of HIV-1 Gag: implications for rational drug design. <i>Retrovirology</i> , 2013, 10, 126.	2.0	56
35	Standardized Comparison of the Relative Impacts of HIV-1 Reverse Transcriptase (RT) Mutations on Nucleoside RT Inhibitor Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2305-2313.	3.2	48
36	Standardized representation, visualization and searchable repository of antiretroviral treatment-change episodes. <i>AIDS Research and Therapy</i> , 2012, 9, 13.	1.7	3

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37	A multifaceted analysis of HIV-1 protease multidrug resistance phenotypes. BMC Bioinformatics, 2011, 12, 477.	2.6	15
38	HIV-1 Integrase Inhibitor Resistance and Its Clinical Implications. Journal of Infectious Diseases, 2011, 203, 1204-1214.	4.0	194
39	Hepatitis B virus reverse transcriptase sequence variant database for sequence analysis and mutation discovery. Antiviral Research, 2010, 88, 269-275.	4.1	45
40	HIV-1 Protease Mutations and Protease Inhibitor Cross-Resistance. Antimicrobial Agents and Chemotherapy, 2010, 54, 4253-4261.	3.2	169
41	HIV-1 Integrase Sequence Variability in Antiretroviral Naïve Patients and in Triple-Class Experienced Patients Subsequently Treated with Raltegravir. AIDS Research and Human Retroviruses, 2010, 26, 1323-1326.	1.1	31
42	Drug Resistance Mutations for Surveillance of Transmitted HIV-1 Drug-Resistance: 2009 Update. PLoS ONE, 2009, 4, e4724.	2.5	823
43	Nonpolymorphic Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Treatment-Selected Mutations. Antimicrobial Agents and Chemotherapy, 2009, 53, 4869-4878.	3.2	32
44	Predictive Value of HIV-1 Genotypic Resistance Test Interpretation Algorithms. Journal of Infectious Diseases, 2009, 200, 453-463.	4.0	39
45	The calibrated population resistance tool: standardized genotypic estimation of transmitted HIV-1 drug resistance. Bioinformatics, 2009, 25, 1197-1198.	4.1	159
46	Predicting the Response to Combination Antiretroviral Therapy: Retrospective Validation of geno2pheno on a Large Clinical Database. Journal of Infectious Diseases, 2009, 199, 999-1006.	4.0	40
47	Natural variation of HIV-1 group M integrase: Implications for a new class of antiretroviral inhibitors. Retrovirology, 2008, 5, 74.	2.0	102
48	Sequence editing by Apolipoprotein B RNA-editing catalytic component-B and epidemiological surveillance of transmitted HIV-1 drug resistance. Aids, 2008, 22, 717-725.	2.2	21
49	HIV-1 Subtype B Protease and Reverse Transcriptase Amino Acid Covariation. PLoS Computational Biology, 2007, 3, e87.	3.2	92
50	HIV-1 protease and reverse transcriptase mutations for drug resistance surveillance. Aids, 2007, 21, 215-223.	2.2	277
51	HIV-1 pol mutation frequency by subtype and treatment experience: extension of the HIVseq program to seven non-B subtypes. Aids, 2006, 20, 643-651.	2.2	78
52	Genotypic predictors of human immunodeficiency virus type 1 drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17355-17360.	7.1	211
53	A COMBINED DATA MINING APPROACH FOR INFREQUENT EVENTS: ANALYZING HIV MUTATION CHANGES BASED ON TREATMENT HISTORY. , 2006, , .		3
54	HIV-1 Protease and Reverse Transcriptase Mutations: Correlations with Antiretroviral Therapy in Subtype B Isolates and Implications for Drug Resistance Surveillance. Journal of Infectious Diseases, 2005, 192, 456-465.	4.0	104

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55	Distribution of Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Mutation Patterns in 4,183 Persons Undergoing Genotypic Resistance Testing. <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 3122-3126.	3.2	93
56	Human immunodeficiency virus reverse transcriptase and protease sequence database. <i>Nucleic Acids Research</i> , 2003, 31, 298-303.	14.5	730