P Richard Harrigan

List of Publications by Year
in descending order

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46 papers	2,119 citations	279487 23 h-index	233125 45 g-index
47 all docs	47 docs citations	47 times ranked	3280 citing authors

#	Article	IF	Citations
1	Predictors of HIV Drugâ€Resistance Mutations in a Large Antiretroviralâ€Naive Cohort Initiating Triple Antiretroviral Therapy. Journal of Infectious Diseases, 2005, 191, 339-347.	1.9	386
2	Expansion of HAART Coverage Is Associated with Sustained Decreases in HIV/AIDS Morbidity, Mortality and HIV Transmission: The â€œHIV Treatment as Preventionâ€• Experience in a Canadian Setting. PLoS ONE, 2014, 9, e87872.	1.1	272
3	Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study. Lancet HIV,the, 2016, 3, e231-e238.	2.1	168
4	Predicting HIV Coreceptor Usage on the Basis of Genetic and Clinical Covariates. Antiviral Therapy, 2007, 12, 1097-1106.	0.6	137
5	Significance and Clinical Management of Persistent Low-Level Viremia and Very-Low-Level Viremia in HIV-1-Infected Patients. Antimicrobial Agents and Chemotherapy, 2014, 58, 3585-3598.	1.4	105
6	A systematic review of the genetic mechanisms of dolutegravir resistance. Journal of Antimicrobial Chemotherapy, 2019, 74, 3135-3149.	1.3	95
7	The Impact of Clinical, Demographic and Risk Factors on Rates of HIV Transmission: A Population-based Phylogenetic Analysis in British Columbia, Canada. Journal of Infectious Diseases, 2015, 211, 926-935.	1.9	89
8	Early Initiation of Combination Antiretroviral Therapy in HIV-1-Infected Newborns Can Achieve Sustained Virologic Suppression With Low Frequency of CD4+ T Cells Carrying HIV in Peripheral Blood. Clinical Infectious Diseases, 2014, 59, 1012-1019.	2.9	77
9	Phylogenetic approach to recover integration dates of latent HIV sequences within-host. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8958-E8967.	3.3	50
10	Integrase strand transfer inhibitor (INSTI)-resistance mutations for the surveillance of transmitted HIV-1 drug resistance. Journal of Antimicrobial Chemotherapy, 2020, 75, 170-182.	1.3	50
11	Genotypic and Functional Impact of HIV-1 Adaptation to Its Host Population during the North American Epidemic. PLoS Genetics, 2014, 10, e1004295.	1.5	45
12	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. Scientific Reports, 2020, 10, 1634.	1.6	45
13	Global Origin and Transmission of Hepatitis C Virus Nonstructural Protein 3 Q80K Polymorphism. Journal of Infectious Diseases, 2015, 211, 1288-1295.	1.9	44
14	HIVâ€1 Drug Resistance: Degree of Underestimation by a Crossâ€Sectional versus a Longitudinal Testing Approach. Journal of Infectious Diseases, 2005, 191, 1325-1330.	1.9	42
15	The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study. Lancet Infectious Diseases, The, 2016, 16, 698-702.	4.6	41
16	Increased Prevalence of Controlled Viremia and Decreased Rates of HIV Drug Resistance Among HIV-Positive People Who Use Illicit Drugs During a Community-wide Treatment-as-Prevention Initiative. Clinical Infectious Diseases, 2016, 62, 640-647.	2.9	35
17	Bioinformatic data processing pipelines in support of nextâ€generation sequencingâ€based <scp>HIV</scp> drug resistance testing: the Winnipeg Consensus. Journal of the International AIDS Society, 2018, 21, e25193.	1.2	34
18	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. Viruses, 2020, 12, 694.	1.5	34

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19	Cohort Profile: HAART Observational Medical Evaluation and Research (HOMER) Cohort. International Journal of Epidemiology, 2015, 44, 58-67.	0.9	31
20	Relative effects of antiretroviral therapy and harm reduction initiatives on HIV incidence in British Columbia, Canada, 1996â€“2013: a modelling study. Lancet HIV,the, 2017, 4, e303-e310.	2.1	31
21	Longitudinal study of surrogate aging measures during human immunodeficiency virus seroconversion. Aging, 2017, 9, 687-705.	1.4	31
22	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. Nucleic Acids Research, 2014, 42, e98-e98.	6.5	29
23	Mitochondrial DNA somatic mutation burden and heteroplasmy are associated with chronological age, smoking, and HIV infection. Aging Cell, 2019, 18, e13018.	3.0	27
24	Temporal trends in the discontinuation of first-line antiretroviral therapy. Journal of Antimicrobial Chemotherapy, 2014, 69, 2202-2209.	1.3	24
25	Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. Journal of Hepatology, 2016, 64, 1247-1255.	1.8	18
26	Are We Ready for NGS HIV Drug Resistance Testing? The Second â€œWinnipeg Consensusâ€• Symposium. Viruses, 2020, 12, 586.	1.5	18
27	Blood mitochondrial DNA mutations in HIV-infected women and their infants exposed to HAART during pregnancy. Aids, 2012, 26, 675-683.	1.0	17
28	Genotypic and Mechanistic Characterization of Subtype-Specific HIV Adaptation to Host Cellular Immunity. Journal of Virology, 2019, 93, .	1.5	17
29	Prevalence and clinical implications of insertions in the HIV-1 p6^{Gag} N-terminal region in drug-naive individuals initiating antiretroviral therapy. Antiviral Therapy, 2003, 8, 91-96.	0.6	16
30	Improving the clinical relevance of a mouse pregnancy model of antiretroviral toxicity; a pharmacokinetic dosing-optimization study of current HIV antiretroviral regimens. Antiviral Research, 2018, 159, 45-54.	1.9	15
31	Population-Level Immune-Mediated Adaptation in HIV-1 Polymerase during the North American Epidemic. Journal of Virology, 2016, 90, 1244-1258.	1.5	13
32	Increasing Prevalence of HIV Pretreatment Drug Resistance in Women But Not Men in Rural Uganda During 2005â€“2013. AIDS Patient Care and STDs, 2018, 32, 257-264.	1.1	13
33	Prevalence of Human Immunodeficiency Virus-1 Integrase Strand Transfer Inhibitor Resistance in British Columbia, Canada Between 2009 and 2016: A Longitudinal Analysis. Open Forum Infectious Diseases, 2019, 6, ofz060.	0.4	11
34	â€œDeepâ€• Sequencing Accuracy and Reproducibility Using Roche/454 Technology for Inferring Co-Receptor Usage in HIV-1. PLoS ONE, 2014, 9, e99508.	1.1	10
35	Quality Control of Next-Generation Sequencing-Based HIV-1 Drug Resistance Data in Clinical Laboratory Information Systems Framework. Viruses, 2020, 12, 645.	1.5	7
36	Association of the CCR5Î”32 Mutation with Clinical Response and >5-year Survival following Initiation of First Triple Antiretroviral Regimen. Antiviral Therapy, 2005, 10, 849-853.	0.6	7

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37	A systematic, deep sequencing-based methodology for identification of mixed-genotype hepatitis C virus infections. Infection, Genetics and Evolution, 2019, 69, 76-84.	1.0	6
38	SHARED: An International Collaboration to Unravel Hepatitis C Resistance. Viruses, 2021, 13, 1580.	1.5	6
39	GWATCH: a web platform for automated gene association discovery analysis. GigaScience, 2014, 3, 18.	3.3	5
40	Sociodemographic correlates of HIV drug resistance and access to drug resistance testing in British Columbia, Canada. PLoS ONE, 2017, 12, e0184848.	1.1	5
41	Phylogenetic surveillance of travel-related Zika virus infections through whole-genome sequencing methods. Scientific Reports, 2019, 9, 16433.	1.6	4
42	HIV-1 phylodynamic analysis among people who inject drugs in Pakistan correlates with trends in illicit opioid trade. PLoS ONE, 2020, 15, e0237560.	1.1	4
43	Tenofovir and emtricitabine resistance among antiretroviral-naive patients in the Canadian Observational Cohort Collaboration: implications for PrEP. Antiviral Therapy, 2019, 24, 211-220.	0.6	2
44	Discordance between Etravirine Phenotype and Genotype-Based Predicted Phenotype for Subtype C HIV-1 from First-Line Antiretroviral Therapy Failures in South Africa. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	1
45	Intra-host evolutionary dynamics of the hepatitis C virus among people who inject drugs. Scientific Reports, 2021, 11, 9986.	1.6	1
46	Validation of a Genotype-Independent Hepatitis C Virus Near-Whole Genome Sequencing Assay. Viruses, 2021, 13, 1721.	1.5	1