

Ricardo J Camacho

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

4,845
citations

159358

30
h-index

95083

68
g-index

82
all docs

82
docs citations

82
times ranked

4093
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential patterns of post-migration HIV-1 infection acquisition among Portuguese immigrants of different geographical origin. <i>Aids</i> , 2022, Publish Ahead of Print, .	1.0	6
2	Human Immunodeficiency Virus-2 (HIV-2): A Summary of the Present Standard of Care and Treatment Options for Individuals Living with HIV-2 in Western Europe. <i>Clinical Infectious Diseases</i> , 2021, 72, 503-509.	2.9	13
3	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.	0.8	5
4	Increasing Prevalence of HIV-1 Transmitted Drug Resistance in Portugal: Implications for First Line Treatment Recommendations. <i>Viruses</i> , 2020, 12, 1238.	1.5	7
5	Molecular Epidemiology of HIV-1 Infected Migrants Followed Up in Portugal: Trends between 2001-2017. <i>Viruses</i> , 2020, 12, 268.	1.5	12
6	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	1.9	23
7	Collaborative update of a rule-based expert system for HIV-1 genotypic resistance test interpretation. <i>PLoS ONE</i> , 2017, 12, e0181357.	1.1	31
8	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	1.0	60
9	Sub-Epidemics Explain Localized High Prevalence of Reduced Susceptibility to Rilpivirine in Treatment-Naïve HIV-1-Infected Patients: Subtype and Geographic Compartmentalization of Baseline Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 427-433.	0.5	19
10	EPICE-HIV: An Epidemiologic Cost-Effectiveness Model for HIV Treatment. <i>PLoS ONE</i> , 2016, 11, e0149007.	1.1	6
11	Assessing transmissibility of HIV-1 drug resistance mutations from treated and from drug-naïve individuals. <i>Aids</i> , 2015, 29, 2045-2052.	1.0	21
12	Development of Nevirapine Resistance in Children Exposed to the Prevention of Mother-to-Child HIV-1 Transmission Programme in Maputo, Mozambique. <i>PLoS ONE</i> , 2015, 10, e0131994.	1.1	10
13	HIV-2EU- Supporting Standardized HIV-2 Drug-Resistance Interpretation in Europe: An Update: Table 1.. <i>Clinical Infectious Diseases</i> , 2015, 61, 1346-1347.	2.9	23
14	Discordant predictions of residual activity could impact dolutegravir prescription upon raltegravir failure. <i>Journal of Clinical Virology</i> , 2015, 70, 120-127.	1.6	6
15	Global Dispersal Pattern of HIV Type 1 Subtype CRF01_AE: A Genetic Trace of Human Mobility Related to Heterosexual Sexual Activities Centralized in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 1735-1744.	1.9	62
16	HIV-1 Diversity, Transmission Dynamics and Primary Drug Resistance in Angola. <i>PLoS ONE</i> , 2014, 9, e113626.	1.1	17
17	Time on drug analysis based on real life data. <i>Journal of the International AIDS Society</i> , 2014, 17, 19790.	1.2	0
18	Pharmacy refill adherence outperforms self-reported methods in predicting HIV therapy outcome in resource-limited settings. <i>BMC Public Health</i> , 2014, 14, 1035.	1.2	82

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19	Possible Footprints of APOBEC3F and/or Other APOBEC3 Deaminases, but Not APOBEC3G, on HIV-1 from Patients with Acute/Early and Chronic Infections. <i>Journal of Virology</i> , 2014, 88, 12882-12894.	1.5	21
20	Increase in transmitted resistance to non-nucleoside reverse transcriptase inhibitors among newly diagnosed HIV-1 infections in Europe. <i>BMC Infectious Diseases</i> , 2014, 14, 407.	1.3	43
21	A near-full length genotypic assay for HCV1b. <i>Journal of Virological Methods</i> , 2014, 209, 126-135.	1.0	11
22	Patterns of Transmitted HIV Drug Resistance in Europe Vary by Risk Group. <i>PLoS ONE</i> , 2014, 9, e94495.	1.1	32
23	Limited cross-border infections in patients newly diagnosed with HIV in Europe. <i>Retrovirology</i> , 2013, 10, 36.	0.9	52
24	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics. <i>Retrovirology</i> , 2013, 10, 7.	0.9	129
25	HIV-1 fitness landscape models for indinavir treatment pressure using observed evolution in longitudinal sequence data are predictive for treatment failure. <i>Infection, Genetics and Evolution</i> , 2013, 19, 349-360.	1.0	4
26	Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools. <i>Infection, Genetics and Evolution</i> , 2013, 19, 337-348.	1.0	313
27	HIV-2EU: Supporting Standardized HIV-2 Drug Resistance Interpretation in Europe. <i>Clinical Infectious Diseases</i> , 2013, 56, 1654-1658.	2.9	31
28	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013, 29, 1477-1480.	1.8	29
29	Declining Prevalence of HIV-1 Drug Resistance in Antiretroviral Treatment-exposed Individuals in Western Europe. <i>Journal of Infectious Diseases</i> , 2013, 207, 1216-1220.	1.9	53
30	Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response. <i>PLoS ONE</i> , 2013, 8, e61436.	1.1	17
31	Predictors of Attrition and Immunological Failure in HIV-1 Patients on Highly Active Antiretroviral Therapy from Different Healthcare Settings in Mozambique. <i>PLoS ONE</i> , 2013, 8, e82718.	1.1	21
32	Effect of Natural Polymorphisms in the HIV-1 CRF02_AG Protease on Protease Inhibitor Hypersusceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2719-2725.	1.4	11
33	Treatment-associated polymorphisms in protease are significantly associated with higher viral load and lower CD4 count in newly diagnosed drug-naive HIV-1 infected patients. <i>Retrovirology</i> , 2012, 9, 81.	0.9	23
34	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , 2012, 93, 889-899.	1.3	56
35	Phylodynamics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012, 12, 453-460.	1.0	52
36	Appearance of a Single Amino Acid Insertion at Position 33 in HIV Type 1 Protease Under a Lopinavir-Containing Regimen, Associated with Reduced Protease Inhibitor Susceptibility. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 1223-1229.	0.5	0

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37	Origin and Epidemiological History of HIV-1 CRF14_BG. <i>PLoS ONE</i> , 2011, 6, e24130.	1.1	28
38	Molecular Epidemiological Analysis of Paired pol/env Sequences from Portuguese HIV Type 1 Patients. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 803-805.	0.5	15
39	Antiretroviral therapy in treatment-naïve patients with HIV infection. <i>Current Opinion in HIV and AIDS</i> , 2011, 6, S3-S11.	1.5	23
40	Cell-Associated Viral Burden Provides Evidence of Ongoing Viral Replication in Aviremic HIV-2-Infected Patients. <i>Journal of Virology</i> , 2011, 85, 2429-2438.	1.5	50
41	Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1886-1896.	1.3	56
42	European recommendations for the clinical use of HIV drug resistance testing: 2011 update. <i>AIDS Reviews</i> , 2011, 13, 77-108.	0.5	106
43	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010, 11, 409.	1.2	12
44	Effect of human immunodeficiency virus type 1 protease inhibitor therapy and subtype on development of resistance in subtypes B and G. <i>Infection, Genetics and Evolution</i> , 2010, 10, 373-379.	1.0	9
45	Comparative performance of the REGA subtyping tool version 2 versus version 1. <i>Infection, Genetics and Evolution</i> , 2010, 10, 380-385.	1.0	13
46	Resistance pathways of human immunodeficiency virus type 1 against the combination of zidovudine and lamivudine. <i>Journal of General Virology</i> , 2010, 91, 1898-1908.	1.3	16
47	Genetic Subtypes of HIV Type 1 Circulating in Slovakia. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1103-1107.	0.5	7
48	Drug Resistance Mutations for Surveillance of Transmitted HIV-1 Drug-Resistance: 2009 Update. <i>PLoS ONE</i> , 2009, 4, e4724.	1.1	823
49	Rapid clinical progression to AIDS and death in a persistently seronegative HIV-1 infected heterosexual young man. <i>Aids</i> , 2009, 23, 2359-2362.	1.0	12
50	Antiretroviral Drug Resistance in Human Immunodeficiency Virus Type 2. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3611-3619.	1.4	70
51	Discordant genotypic interpretation and phenotypic role of protease mutations in HIV-1 subtypes B and G. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 63, 593-599.	1.3	18
52	Transmission of Drug-Resistant HIV-1 Is Stabilizing in Europe. <i>Journal of Infectious Diseases</i> , 2009, 200, 1503-1508.	1.9	213
53	Full genome sequence of three isolates of hepatitis C virus subtype 4b from Portugal. <i>Archives of Virology</i> , 2009, 154, 127-132.	0.9	9
54	The rise and fall of K65R in a Portuguese HIV-1 Drug Resistance database, despite continuously increasing use of tenofovir†. <i>Infection, Genetics and Evolution</i> , 2009, 9, 683-688.	1.0	8

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55	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009, 6, 49.	0.9	114
56	The incidence of multidrug and full class resistance in HIV-1 infected patients is decreasing over time (2001–2006) in Portugal. <i>Retrovirology</i> , 2008, 5, 12.	0.9	43
57	Impact of HIV-1 protease mutations A71V/T and T74S on M89I/V-mediated protease inhibitor resistance in subtype G isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 1201-1204.	1.3	18
58	Bayesian network analyses of resistance pathways against efavirenz and nevirapine. <i>Aids</i> , 2008, 22, 2107-2115.	1.0	21
59	Estimation of an <i>in vivo</i> fitness landscape experienced by HIV-1 under drug selective pressure useful for prediction of drug resistance evolution during treatment. <i>Bioinformatics</i> , 2008, 24, 34-41.	1.8	28
60	Modelled <i>in vivo</i> HIV fitness under drug selective pressure and estimated genetic barrier towards resistance are predictive for virological response. <i>Antiviral Therapy</i> , 2008, 13, 399-407.	0.6	7
61	Modelled <i>in vivo</i> HIV Fitness under drug Selective Pressure and Estimated Genetic Barrier Towards Resistance are Predictive for Virological Response. <i>Antiviral Therapy</i> , 2008, 13, 399-408.	0.6	17
62	Estimating the Relative Contribution of dNTP Pool Imbalance and APOBEC3G/3F Editing to HIV Evolution <i>In Vivo</i> . <i>Journal of Computational Biology</i> , 2007, 14, 1105-1114.	0.8	26
63	Recombination Confounds the Early Evolutionary History of Human Immunodeficiency Virus Type 1: Subtype G Is a Circulating Recombinant Form. <i>Journal of Virology</i> , 2007, 81, 8543-8551.	1.5	84
64	Antiretroviral resistance in different HIV-1 subtypes: impact on therapy outcomes and resistance testing interpretation. <i>Current Opinion in HIV and AIDS</i> , 2007, 2, 123-129.	1.5	23
65	Impact of genetic variation of HIV-1 on drug resistance development. <i>Future Virology</i> , 2007, 2, 303-310.	0.9	0
66	Bayesian network analysis of resistance pathways against HIV-1 protease inhibitors. <i>Infection, Genetics and Evolution</i> , 2007, 7, 382-390.	1.0	30
67	Molecular epidemiology and prevalence of drug resistance-associated mutations in newly diagnosed HIV-1 patients in Portugal. <i>Infection, Genetics and Evolution</i> , 2007, 7, 391-398.	1.0	71
68	Use of a New Dual-Antigen Enzyme-Linked Immunosorbent Assay To Detect and Characterize the Human Antibody Response to the Human Immunodeficiency Virus Type 2 Envelope gp125 and gp36 Glycoproteins. <i>Journal of Clinical Microbiology</i> , 2006, 44, 607-611.	1.8	17
69	HIV-1 pol mutation frequency by subtype and treatment experience: extension of the HIVseq program to seven non-B subtypes. <i>Aids</i> , 2006, 20, 643-651.	1.0	78
70	The Calculated Genetic Barrier for Antiretroviral Drug Resistance Substitutions Is Largely Similar for Different HIV-1 Subtypes. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2006, 41, 352-360.	0.9	90
71	Comparison of the COBAS TAQMAN, HIV-1 HPS with VERSANT HIV-1 RNA 3.0 Assay (bDNA) for plasma RNA quantitation in different HIV-1 subtypes. <i>Journal of Virological Methods</i> , 2006, 135, 223-228.	1.0	14
72	Protease mutation M89I/V is linked to therapy failure in patients infected with the HIV-1 non-B subtypes C, F or G. <i>Aids</i> , 2006, 20, 1789.	1.0	0

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73	Analysis of HIV-1 pol sequences using Bayesian Networks: implications for drug resistance. <i>Bioinformatics</i> , 2006, 22, 2975-2979.	1.8	60
74	Discordances between Interpretation Algorithms for Genotypic Resistance to Protease and Reverse Transcriptase Inhibitors of Human Immunodeficiency Virus Are Subtype Dependent. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 694-701.	1.4	78
75	Protease mutation M89I/V is linked to therapy failure in patients infected with the HIV-1 non-B subtypes C, F or G. <i>Aids</i> , 2005, 19, 1799-1806.	1.0	76
76	Impact of HIV-1 Subtype and Antiretroviral Therapy on Protease and Reverse Transcriptase Genotype: Results of a Global Collaboration. <i>PLoS Medicine</i> , 2005, 2, e112.	3.9	262
77	Prevalence of Drug-Resistant HIV-1 Variants in Untreated Individuals in Europe: Implications for Clinical Management. <i>Journal of Infectious Diseases</i> , 2005, 192, 958-966.	1.9	385
78	An automated genotyping system for analysis of HIV-1 and other microbial sequences. <i>Bioinformatics</i> , 2005, 21, 3797-3800.	1.8	468
79	Transmission of HIV-2. <i>Lancet Infectious Diseases</i> , The, 2003, 3, 683-684.	4.6	23
80	Multicenter evaluation of a new rapid automated human immunodeficiency virus antigen detection assay. <i>Journal of Virological Methods</i> , 1999, 78, 61-70.	1.0	20