

Gonzalo Yebra

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,024
citations

516710

16
h-index

526287

27
g-index

30
all docs

30
docs citations

30
times ranked

1343
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	13.3	352
2	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
3	Increase of Non-B Subtypes and Recombinants Among Newly Diagnosed HIV-1 Native Spaniards and Immigrants in Spain. <i>Current HIV Research</i> , 2008, 6, 327-334.	0.5	58
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	Most HIV Type 1 Non-B Infections in the Spanish Cohort of Antiretroviral Treatment-Naïve HIV-Infected Patients (CoRIS) Are Due to Recombinant Viruses. <i>Journal of Clinical Microbiology</i> , 2012, 50, 407-413.	3.9	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	High Drug Resistance Prevalence among Vertically HIV-Infected Patients Transferred from Pediatric Care to Adult Units in Spain. <i>PLoS ONE</i> , 2012, 7, e52155.	2.5	31
8	Increase of Transmitted Drug Resistance among HIV-Infected Sub-Saharan Africans Residing in Spain in Contrast to the Native Population. <i>PLoS ONE</i> , 2011, 6, e26757.	2.5	29
9	Phylogenetic and demographic characterization of HIV-1 transmission in Madrid, Spain. <i>Infection, Genetics and Evolution</i> , 2013, 14, 232-239.	2.3	25
10	A high HIV-1 strain variability in London, UK, revealed by full-genome analysis: Results from the ICONIC project. <i>PLoS ONE</i> , 2018, 13, e0192081.	2.5	25
11	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016, 6, 39489.	3.3	23
12	Sensitivity of seven HIV subtyping tools differs among subtypes/recombinants in the Spanish cohort of naïve HIV-infected patients (CoRIS). <i>Antiviral Research</i> , 2011, 89, 19-25.	4.1	20
13	Drug resistance prevalence and HIV-1 variant characterization in the naive and pretreated HIV-1-infected paediatric population in Madrid, Spain. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 2362-2371.	3.0	17
14	Different trends of transmitted HIV-1 drug resistance in Madrid, Spain, among risk groups in the last decade. <i>Archives of Virology</i> , 2014, 159, 1079-1087.	2.1	17
15	Clinical Differences and Viral Diversity between Newly HIV Type 1-Diagnosed African and Non-African Patients in Spain (2005–2007). <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 37-44.	1.1	16
16	Trends in Drug Resistance Prevalence in HIV-1-infected Children in Madrid. <i>Pediatric Infectious Disease Journal</i> , 2012, 31, e213-e221.	2.0	16
17	Description of HIV-1 Group M Molecular Epidemiology and Drug Resistance Prevalence in Equatorial Guinea from Migrants in Spain. <i>PLoS ONE</i> , 2013, 8, e64293.	2.5	12
18	Drug Resistance Prevalence in Human Immunodeficiency Virus Type 1 Infected Pediatric Populations in Honduras and El Salvador During 1989–2009. <i>Pediatric Infectious Disease Journal</i> , 2011, 30, e82-e87.	2.0	10

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19	The Maturation Inhibitor Bevirimat (PA-457) can be Active in Patients Carrying HIV type-1 non-B Subtypes and Recombinants. <i>Antiviral Therapy</i> , 2008, 13, 1083-1085.	1.0	10
20	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	4.9	9
21	Radical genome remodelling accompanied the emergence of a novel host-restricted bacterial pathogen. <i>PLoS Pathogens</i> , 2021, 17, e1009606.	4.7	9
22	Acapsular <i>Staphylococcus aureus</i> with a non-functional agr regains capsule expression after passage through the bloodstream in a bacteremia mouse model. <i>Scientific Reports</i> , 2020, 10, 14108.	3.3	8
23	High prevalence and diversity of HIV-1 non-B genetic forms due to immigration in southern Spain: A phylogeographic approach. <i>PLoS ONE</i> , 2017, 12, e0186928.	2.5	7
24	Phylogenetic and Phylogeographic Profiles of Subtype B HIV-1 Epidemics in South Spain. <i>PLoS ONE</i> , 2016, 11, e0168099.	2.5	7
25	Reconstructing the HIV-1 CRF02_AG and CRF06_cpx epidemics in Burkina Faso and West Africa using early samples. <i>Infection, Genetics and Evolution</i> , 2016, 46, 209-218.	2.3	6
26	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
27	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