Gilberto Betancor Quintana

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7443491/publications.pdf

Version: 2024-02-01

23 papers

4,360 citations

16 h-index 23 g-index

29 all docs

29 docs citations

times ranked

29

11684 citing authors

#	Article	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. Clinical Microbiology and Infection, 2022, 28, 93-100.	2.8	21
2	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. Lancet Infectious Diseases, The, 2022, 22, 35-42.	4.6	612
3	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	13.5	843
4	SARS-CoV-2 evolution during treatment of chronic infection. Nature, 2021, 592, 277-282.	13.7	802
5	Clinical utility of targeted SARS-CoV-2 serology testing to aid the diagnosis and management of suspected missed, late or post-COVID-19 infection syndromes: Results from a pilot service implemented during the first pandemic wave. PLoS ONE, 2021, 16, e0249791.	1.1	6
6	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. Lancet Public Health, The, 2021, 6, e335-e345.	4.7	269
7	MX2-mediated innate immunity against HIV-1 is regulated by serine phosphorylation. Nature Microbiology, 2021, 6, 1031-1042.	5.9	18
8	Resilient SARS-CoV-2 diagnostics workflows including viral heat inactivation. PLoS ONE, 2021, 16, e0256813.	1.1	23
9	Longitudinal observation and decline of neutralizing antibody responses in the three months following SARS-CoV-2 infection in humans. Nature Microbiology, 2020, 5, 1598-1607.	5.9	1,115
10	Comparative assessment of multiple COVID-19 serological technologies supports continued evaluation of point-of-care lateral flow assays in hospital and community healthcare settings. PLoS Pathogens, 2020, 16, e1008817.	2.1	105
11	Real-world evaluation of a novel technology for quantitative simultaneous antibody detection against multiple SARS-CoV-2 antigens in a cohort of patients presenting with COVID-19 syndrome. Analyst, The, 2020, 145, 5638-5646.	1.7	26
12	The GTPase Domain of MX2 Interacts with the HIV-1 Capsid, Enabling Its Short Isoform to Moderate Antiviral Restriction. Cell Reports, 2019, 29, 1923-1933.e3.	2.9	27
13	Immunoproteasome activation enables human TRIM5α restriction of HIV-1. Nature Microbiology, 2019, 4, 933-940.	5.9	54
14	Multiple components of the nuclear pore complex interact with the amino-terminus of MX2 to facilitate HIV-1 restriction. PLoS Pathogens, 2018, 14, e1007408.	2.1	43
15	Effects of Inner Nuclear Membrane Proteins SUN1/UNC-84A and SUN2/UNC-84B on the Early Steps of HIV-1 Infection. Journal of Virology, 2017, 91, .	1.5	18
16	Oligomerization Requirements for MX2-Mediated Suppression of HIV-1 Infection. Journal of Virology, 2016, 90, 22-32.	1.5	41
17	Effects of HIV-1 reverse transcriptase connection subdomain mutations on polypurine tract removal and initiation of (+)-strand DNA synthesis. Nucleic Acids Research, 2015, 43, 2259-2270.	6.5	22
18	Molecular basis of the association of H208Y and thymidine analogue resistance mutations M41L, L210W and T215Y in the HIV-1 reverse transcriptase of treated patients. Antiviral Research, 2014, 106, 42-52.	1.9	3

#	Article	IF	CITATIONS
19	Clinical, virological and biochemical evidence supporting the association of HIV-1 reverse transcriptase polymorphism R284K and thymidine analogue resistance mutations M41L, L210W and T215Y in patients failing tenofovir/emtricitabine therapy. Retrovirology, 2012, 9, 68.	0.9	7
20	HIV-1 reverse transcriptase connection subdomain mutations involved in resistance to approved non-nucleoside inhibitors. Antiviral Research, 2011, 92, 139-149.	1.9	38
21	A376S in the Connection Subdomain of HIV-1 Reverse Transcriptase Confers Increased Risk of Virological Failure to Nevirapine Therapy. Journal of Infectious Diseases, 2011, 204, 741-752.	1.9	19
22	Mechanisms Involved in the Selection of HIV-1 Reverse Transcriptase Thumb Subdomain Polymorphisms Associated with Nucleoside Analogue Therapy Failure. Antimicrobial Agents and Chemotherapy, 2010, 54, 4799-4811.	1.4	29
23	The GTPase Domain of MX2 Interacts with HIV-1 Capsid Enabling Its Short Isoform to Moderate Antiviral Restriction. SSRN Electronic Journal, 0, , .	0.4	0