

Bernardo Gutierrez

List of Publications by Citations

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Version: 2024-04-19

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

3,407
citations

17
h-index

58
g-index

62
ext. papers

4,839
ext. citations

13.4
avg, IF

5.65
L-index

#	Paper	IF	Citations
47	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020 , 368, 493-497	33.3	1373
46	Preparedness and vulnerability of African countries against importations of COVID-19: a modelling study. <i>Lancet, The</i> , 2020 , 395, 871-877	40	640
45	Epidemiological data from the COVID-19 outbreak, real-time case information. <i>Scientific Data</i> , 2020 , 7, 106	8.2	194
44	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33.3	159
43	Open access epidemiological data from the COVID-19 outbreak. <i>Lancet Infectious Diseases, The</i> , 2020 , 20, 534	25.5	157
42	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020 , 4, 856-865	12.8	151
41	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health, The</i> , 2021 , 6, e335-e345	22.4	146
40	Crowding and the shape of COVID-19 epidemics. <i>Nature Medicine</i> , 2020 , 26, 1829-1834	50.5	97
39	Modelling COVID-19. <i>Nature Reviews Physics</i> , 2020 , 1-3	23.6	91
38	A60 Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
37	A case of SARS-CoV-2 reinfection in Ecuador. <i>Lancet Infectious Diseases, The</i> , 2021 , 21, e142	25.5	44
36	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
35	RcsB is required for inducible acid resistance in <i>Escherichia coli</i> and acts at <i>gadE</i> -dependent and -independent promoters. <i>Journal of Bacteriology</i> , 2011 , 193, 3653-6	3.5	30
34	The effect of human mobility and control measures on the COVID-19 epidemic in China 2020 ,		26
33	Crowding and the epidemic intensity of COVID-19 transmission		25
32	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25057-25067	11.5	25
31	Parallel molecular evolution and adaptation in viruses. <i>Current Opinion in Virology</i> , 2019 , 34, 90-96	7.5	18

30	Psidium guajava in the Galapagos Islands: Population genetics and history of an invasive species. <i>PLoS ONE</i> , 2019 , 14, e0203737	3.7	14
29	Genome sequencing of the first SARS-CoV-2 reported from patients with COVID-19 in Ecuador 2020 ,		9
28	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020 , 11, 5511	17.4	8
27	Preliminary analysis of the genetic diversity and population structure of mortiñ (Vaccinium floribundum Kunth). <i>Biochemical Systematics and Ecology</i> , 2016 , 64, 14-21	1.4	8
26	Molecular characterization of Ecuadorian quinoa (Chenopodium quinoa Willd.) diversity: implications for conservation and breeding. <i>Euphytica</i> , 2019 , 215, 1	2.1	7
25	Dynamics of conflict during the Ebola outbreak in the Democratic Republic of the Congo 2018-2019. <i>BMC Medicine</i> , 2020 , 18, 113	11.4	6
24	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020 , 94,	6.6	5
23	Regeneration of mortiñ (Vaccinium floribundum Kunth) plants through axillary bud culture. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2018 , 54, 112-116	2.3	5
22	Mitochondrial DNA reveals low genetic diversity in Ecuadorian Andean bears. <i>Ursus</i> , 2018 , 29, 43	1.4	5
21	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0007897	4.8	4
20	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021 , 7, veab0513.7	3.7	4
19	Report 46: Factors driving extensive spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals 2021 ,		3
18	Emergence and widespread circulation of a recombinant SARS-CoV-2 lineage in North America		3
17	Genetic diversity and distribution patterns of Ecuadorian capuli (Prunus serotina). <i>Biochemical Systematics and Ecology</i> , 2015 , 60, 67-73	1.4	2
16	A Preliminary Assessment of the Genetic Diversity and Population Structure of Guava, Psidium guajava, in San Cristobal. <i>Social and Ecological Interactions in the Galapagos Islands</i> , 2018 , 3-17	0.2	2
15	Characterizing the genetic diversity of the Andean blueberry (Vaccinium floribundum Kunth.) across the Ecuadorian Highlands. <i>PLoS ONE</i> , 2020 , 15, e0243420	3.7	2
14	Parallel Evolution in the Emergence of Highly Pathogenic Avian Influenza A Viruses		2
13	"Kankasha" in Kassala: A prospective observational cohort study of the clinical characteristics, epidemiology, genetic origin, and chronic impact of the 2018 epidemic of Chikungunya virus infection in Kassala, Sudan. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009387	4.8	2

12	Identification of site-specific evolutionary trajectories shared across human betacoronaviruses 2021 ,		2
11	Data Sharing in Southeast Asia During the First Wave of the COVID-19 Pandemic. <i>Frontiers in Public Health</i> , 2021 , 9, 662842	6	2
10	Understanding the genetic diversity of the guayabillo (<i>Psidium galapageium</i>), an endemic plant of the Galapagos Islands. <i>Global Ecology and Conservation</i> , 2020 , 24, e01350	2.8	1
9	The evolutionary dynamics of Oropouche Virus (OROV) in South America		1
8	Oropouche virus cases identified in Ecuador using an optimised rRT-PCR informed by metagenomic sequencing.		
7	Mycotic pseudoaneurysm of the extracranial carotid artery, a severe and rare disease, a case report. <i>International Journal of Surgery Case Reports</i> , 2020 , 71, 382-385	0.8	0
6	Employing molecular markers to identify <i>Monilinia fructicola</i> in Ecuadorian peach orchards. <i>Australasian Plant Disease Notes</i> , 2013 , 8, 149-152	0.8	0
5	Origin and dispersion pathways of guava in the Galapagos Islands inferred through genetics and historical records. <i>Ecology and Evolution</i> , 2021 , 11, 15111-15131	2.8	0
4	Micropropagation of var. by apical bud, petiole and hypocotyl culture. <i>Plant Biotechnology</i> , 2019 , 36, 91-97	1.3	
3	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897		
2	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897		
1	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897		