Marina Muoz

List of Publications by Year in Descending Order

35 papers	278 citations	9 h-index	14 g-index
43 ext. papers	461 ext. citations	5.5 avg, IF	3.88 L-index

#	Paper	IF	Citations
35	Epidemiological Dynamics of SARS-CoV-2 Variants During Social Protests in Cali, Colombia.. *Frontiers in Medicine*, **2022**, 9, 863911	4.9	0
34	First report and genome sequencing of SARS-CoV-2 in a cat (Felis catus) in Colombia.. *Memorias Do Instituto Oswaldo Cruz*, **2022**, 117, e210375	2.6	
33	Gut microbiota profiles in diarrheic patients with co-occurrence of Clostridioides difficile and Blastocystis. *PLoS ONE*, **2021**, 16, e0248185	3.7	5
32	Phylogenomic Evidence of Reinfection and Persistence of SARS-CoV-2: First Report from Colombia. *Vaccines*, **2021**, 9,	5.3	7
31	Deciphering the introduction and transmission of SARS-CoV-2 in the Colombian Amazon Basin. *PLoS Neglected Tropical Diseases*, **2021**, 15, e0009327	4.8	4
30	Characterizing SARS-CoV-2 genome diversity circulating in South American countries: Signatures of potentially emergent lineages?. *International Journal of Infectious Diseases*, **2021**, 105, 329-332	10.5	11
29	Gut microbiota composition in health-care facility-and community-onset diarrheic patients with Clostridioides difficile infection. *Scientific Reports*, **2021**, 11, 10849	4.9	1
28	Co-Circulation of Bovine Leukemia Virus Haplotypes among Humans, Animals, and Food Products: New Insights of Its Zoonotic Potential. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	4
27	The arrival and spread of SARS-CoV-2 in Colombia. *Journal of Medical Virology*, **2021**, 93, 1158-1163	19.7	22
26	Microbial CommunitiesW Characterization in Urban Recreational Surface Waters Using Next Generation Sequencing. *Microbial Ecology*, **2021**, 81, 847-863	4.4	2
25	Updating changes in human gut microbial communities associated with infection. *Gut Microbes*, **2021**, 13, 1966277	8.8	1
24	Will the emergent SARS-CoV2 B.1.1.7 lineage affect molecular diagnosis of COVID-19?. *Journal of Medical Virology*, **2021**, 93, 2566-2568	19.7	20
23	Evolution and Epidemic Spread of SARS-CoV-2 in Colombia: A Year into the Pandemic. *Vaccines*, **2021**, 9,	5.3	1
22	Describing the intestinal microbiota of Holstein Fasciola-positive and -negative cattle from a hyperendemic area of fascioliasis in central Colombia. *PLoS Neglected Tropical Diseases*, **2021**, 15, e0009658	4.8	2
21	Revisiting the heterogeneous global genomic population structure of. *Microbial Genomics*, **2021**, 7,	4.4	1
20	SARS-CoV-2 in Transit: Characterization of SARS-CoV-2 Genomes From Venezuelan Migrants in Colombia. *International Journal of Infectious Diseases*, **2021**, 110, 410-416	10.5	1
19	SARS-CoV-2 spread across the Colombian-Venezuelan border. *Infection, Genetics and Evolution*, **2020**, 86, 104616	4.5	8

18	Intraspecific Genomic Divergence and Minor Structural Variations in. *Genes*, **2020**, 11,	4.2	6
17	Occurrence of in Patients with Infection. *Pathogens*, **2020**, 9,	4.5	6
16	Comprehensive genome analyses of , a potential biomarker of homeostasis gut recovery. *Microbial Genomics*, **2020**, 6,	4.4	6
15	Genomic analyses reveal moderate levels of ploidy, high heterozygosity and structural variations in a Colombian isolate of Leishmania (Leishmania) amazonensis. *Acta Tropica*, **2020**, 203, 105296	3.2	4
14	Microbiota characterization in Blastocystis-colonized and Blastocystis-free school-age children from Colombia. *Parasites and Vectors*, **2020**, 13, 521	4	4
13	Genetic Diversity Among SARS-CoV2 Strains in South America may Impact Performance of Molecular Detection. *Pathogens*, **2020**, 9,	4.5	16
12	Genomic Diversification, Structural Plasticity, and Hybridization in. *Frontiers in Cellular and Infection Microbiology*, **2020**, 10, 582192	5.9	10
11	High frequency of toxigenic and coinfection among diarrheic patients at health care facility-onset (HCFO) and community-onset (CO) centers in Bogot□Colombia. *Gut Pathogens*, **2019**, 11, 27	5.4	3
10	Integrated genomic epidemiology and phenotypic profiling of Clostridium difficile across intra-hospital and community populations in Colombia. *Scientific Reports*, **2019**, 9, 11293	4.9	5
9	Comparative genomics identifies potential virulence factors in and. *Virulence*, **2019**, 10, 657-676	4.7	7
8	Dissecting the Heterogeneous Population Genetic Structure of : Limitations and Constraints of the Multilocus Sequence Typing Scheme. *Frontiers in Microbiology*, **2019**, 10, 1052	5.7	4
7	Estimating the Intra-taxa Diversity, Population Genetic Structure, and Evolutionary Pathways of and. *Frontiers in Genetics*, **2018**, 9, 148	4.5	12
6	New Insights into (CD) Infection in Latin America: Novel Description of Toxigenic Profiles of Diarrhea-Associated to CD in Bogot□Colombia. *Frontiers in Microbiology*, **2018**, 9, 74	5.7	10
5	Unveiling the Multilocus Sequence Typing (MLST) Schemes and Core Genome Phylogenies for Genotyping. *Frontiers in Microbiology*, **2018**, 9, 1854	5.7	13
4	Community-acquired infection with hypervirulent isolates that carry different toxin and antibiotic resistance loci: a case report. *Gut Pathogens*, **2017**, 9, 63	5.4	3
3	Molecular Epidemiology of and among Indigenous Children from the Colombian Amazon Basin. *Frontiers in Microbiology*, **2017**, 8, 248	5.7	63
2	Mycobacterium tuberculosis PE9 protein has high activity binding peptides which inhibit target cell invasion. *International Journal of Biological Macromolecules*, **2016**, 86, 646-55	7.9	5
1	The role of Mycobacterium tuberculosis Rv3166c protein-derived high-activity binding peptides in inhibiting invasion of human cell lines. *Protein Engineering, Design and Selection*, **2012**, 25, 235-42	1.9	7