

Alexandra Gerber

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,863
citations

331670

21
h-index

302126

39
g-index

51
all docs

51
docs citations

51
times ranked

6020
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Surveillance Tracks the First Community Outbreak of the SARS-CoV-2 Delta (B.1.617.2) Variant in Brazil. <i>Journal of Virology</i> , 2022, 96, JVI0122821.	3.4	21
2	Seroprevalence, Prevalence, and Genomic Surveillance: Monitoring the Initial Phases of the SARS-CoV-2 Pandemic in Betim, Brazil. <i>Frontiers in Microbiology</i> , 2022, 13, 799713.	3.5	4
3	Emergence of Within-Host SARS-CoV-2 Recombinant Genome After Coinfection by Gamma and Delta Variants: A Case Report. <i>Frontiers in Public Health</i> , 2022, 10, 849978.	2.7	14
4	Zika virus disrupts gene expression in human myoblasts and myotubes: Relationship with susceptibility to infection. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010166.	3.0	3
5	Zrg1, a cryptococcal protein associated with regulation of growth in nutrient deprivation conditions. <i>Genomics</i> , 2021, 113, 805-814.	2.9	0
6	Exome-Wide Search for Genes Associated With Central Nervous System Inflammatory Demyelinating Diseases Following CHIKV Infection: The Tip of the Iceberg. <i>Frontiers in Genetics</i> , 2021, 12, 639364.	2.3	8
7	Common Dysregulation of Innate Immunity Pathways in Human Primary Astrocytes Infected With Chikungunya, Mayaro, Oropouche, and Zika Viruses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 641261.	3.9	7
8	Genomic Characterization of a Novel SARS-CoV-2 Lineage from Rio de Janeiro, Brazil. <i>Journal of Virology</i> , 2021, 95, .	3.4	302
9	Pervasive transmission of E484K and emergence of VUI-NP13L with evidence of SARS-CoV-2 co-infection events by two different lineages in Rio Grande do Sul, Brazil. <i>Virus Research</i> , 2021, 296, 198345.	2.2	105
10	Intra-host evolution during SARS-CoV-2 prolonged infection. <i>Virus Evolution</i> , 2021, 7, veab078.	4.9	68
11	Genomic surveillance of SARS-CoV-2 tracks early interstate transmission of P.1 lineage and diversification within P.2 clade in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009835.	3.0	23
12	Turnover of SARS-CoV-2 Lineages Shaped the Pandemic and Enabled the Emergence of New Variants in the State of Rio de Janeiro, Brazil. <i>Viruses</i> , 2021, 13, 2013.	3.3	13
13	Maternal SARS-CoV-2 Infection Associated to Systemic Inflammatory Response and Pericardial Effusion in the Newborn: A Case Report. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, 536-539.	1.3	19
14	Genome and plasmid context of two rmtG-carrying <i>Enterobacter hormaechei</i> isolated from urinary tract infections in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 36-40.	2.2	10
15	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
16	Transcriptomic Analysis of the Early Strobilar Development of <i>Echinococcus granulosus</i> . <i>Pathogens</i> , 2020, 9, 465.	2.8	7
17	Molecular alterations in the extracellular matrix in the brains of newborns with congenital Zika syndrome. <i>Science Signaling</i> , 2020, 13, .	3.6	39
18	Zika virus targets the human thymic epithelium. <i>Scientific Reports</i> , 2020, 10, 1378.	3.3	16

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19	Genome-wide DNA methylation analysis of <i>Metarhizium anisopliae</i> during tick mimicked infection condition. <i>BMC Genomics</i> , 2019, 20, 836.	2.8	14
20	A comparative in silico linear B-cell epitope prediction and characterization for South American and African <i>Trypanosoma vivax</i> strains. <i>Genomics</i> , 2019, 111, 407-417.	2.9	16
21	Cryptococcal dissemination to the central nervous system requires the vacuolar calcium transporter Pmc1. <i>Cellular Microbiology</i> , 2018, 20, e12803.	2.1	21
22	Genome-wide diversity and differentiation in New World populations of the human malaria parasite <i>Plasmodium vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005824.	3.0	47
23	Metagenomic analysis of sediments under seaports influence in the Equatorial Atlantic Ocean. <i>Science of the Total Environment</i> , 2016, 557-558, 888-900.	8.0	11
24	Isolation of Infective Zika Virus from Urine and Saliva of Patients in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004816.	3.0	173
25	<i>Trypanosoma cruzi</i> Clone Dm28c Draft Genome Sequence. <i>Genome Announcements</i> , 2014, 2, .	0.8	39
26	Comparative genome analysis of entomopathogenic fungi reveals a complex set of secreted proteins. <i>BMC Genomics</i> , 2014, 15, 822.	2.8	49
27	Genome of the Avirulent Human-Infective Trypanosome "Trypanosoma rangeli". <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3176.	3.0	72
28	Draft Genome Sequence of the <i>Xylose-Fermenting Yeast Spathaspora arborariae</i> UFMG-HM19.1A. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
29	Taxonomic and functional profiles of soil samples from Atlantic forest and Caatinga biomes in northeastern Brazil. <i>MicrobiologyOpen</i> , 2014, 3, 299-315.	3.0	48
30	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: <i>Sporothrix schenckii</i> and <i>Sporothrix brasiliensis</i> . <i>BMC Genomics</i> , 2014, 15, 943.	2.8	121
31	De novo transcriptome analysis of <i>Hevea brasiliensis</i> tissues by RNA-seq and screening for molecular markers. <i>BMC Genomics</i> , 2014, 15, 236.	2.8	82
32	Unravelling the Transcriptome Profile of the Swine Respiratory Tract Mycoplasmas. <i>PLoS ONE</i> , 2014, 9, e110327.	2.5	34
33	Pyrosequencing-based analysis reveals a novel capsular gene cluster in a KPC-producing <i>Klebsiella pneumoniae</i> clinical isolate identified in Brazil. <i>BMC Microbiology</i> , 2012, 12, 173.	3.3	25
34	Soil bacterial community abundance and diversity in ice-free areas of Keller Peninsula, Antarctica. <i>Applied Soil Ecology</i> , 2012, 61, 7-15.	4.3	36
35	Metagenomic Analysis of the Microbiota from the Crop of an Invasive Snail Reveals a Rich Reservoir of Novel Genes. <i>PLoS ONE</i> , 2012, 7, e48505.	2.5	62
36	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. <i>Nucleic Acids Research</i> , 2011, 39, 6056-6068.	14.5	19

#	ARTICLE	IF	CITATIONS
37	The fatty acid amide hydrolase C385A (P129T) missense variant in cannabis users: Studies of drug use and dependence in caucasians. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 660-666.	1.7	97
38	The fatty acid amide hydrolase 385 A/A (P129T) variant: haplotype analysis of an ancient missense mutation and validation of risk for drug addiction. Human Genetics, 2006, 120, 581-588.	3.8	76
39	Reduced cellular expression and activity of the P129T mutant of human fatty acid amide hydrolase: evidence for a link between defects in the endocannabinoid system and problem drug use. Human Molecular Genetics, 2004, 13, 2113-2119.	2.9	239
40	A missense mutation in human fatty acid amide hydrolase associated with problem drug use. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8394-8399.	7.1	322