

Gabriel Luz Wallau

List of Publications by Year in descending order

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74
papers

2,637
citations

331670

21
h-index

233421

45
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93
all docs

93
docs citations

93
times ranked

4569
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA virus EVEs in insect genomes. <i>Current Opinion in Insect Science</i> , 2022, 49, 42-47.	4.4	13
2	ViralFlow: A Versatile Automated Workflow for SARS-CoV-2 Genome Assembly, Lineage Assignment, Mutations and Intra-host Variant Detection. <i>Viruses</i> , 2022, 14, 217.	3.3	40
3	Mosquito long non-coding RNAs are enriched with Transposable Elements. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210215.	1.3	0
4	Spread of Gamma (P.1) Sub-Lineages Carrying Spike Mutations Close to the Furin Cleavage Site and Deletions in the N-Terminal Domain Drives Ongoing Transmission of SARS-CoV-2 in Amazonas, Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0236621.	3.0	28
5	Phylogenetic-based inference reveals distinct transmission dynamics of SARS-CoV-2 lineages Gamma and P.2 in Brazil. <i>IScience</i> , 2022, 25, 104156.	4.1	16
6	Unusual SARS-CoV-2 intra-host diversity reveals lineage superinfection. <i>Microbial Genomics</i> , 2022, 8, .	2.0	18
7	An unfolding monkeypox outbreak in Europe and beyond. <i>Military Medical Research</i> , 2022, 9, .	3.4	2
8	Mitogenome of <i>Coprophanæus ensifer</i> and phylogenetic analysis of the Scarabaeidae family (Coleoptera). <i>Genetics and Molecular Biology</i> , 2021, 44, e20200417.	1.3	1
9	Immune evasion of SARS-CoV-2 variants of concern is driven by low affinity to neutralizing antibodies. <i>Chemical Communications</i> , 2021, 57, 6094-6097.	4.1	18
10	A Potential SARS-CoV-2 Variant of Interest (VOI) Harboring Mutation E484K in the Spike Protein Was Identified within Lineage B.1.1.33 Circulating in Brazil. <i>Viruses</i> , 2021, 13, 724.	3.3	38
11	COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence. <i>Nature Medicine</i> , 2021, 27, 1230-1238.	30.7	279
12	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil. <i>Nature Communications</i> , 2021, 12, 2619.	12.8	43
13	<i>In silico</i> predictions of protein interactions between Zika virus and human host. <i>PeerJ</i> , 2021, 9, e11770.	2.0	3
14	Metatranscriptomic analysis identifies different viral-like sequences in two neotropical <i>Mansoniini</i> mosquito species. <i>Virus Research</i> , 2021, 301, 198455.	2.2	4
15	Characterization of Mariner transposons in seven species of <i>Rhus</i> gall aphids. <i>Scientific Reports</i> , 2021, 11, 16349.	3.3	4
16	A Sanger-based approach for scaling up screening of SARS-CoV-2 variants of interest and concern. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104910.	2.3	28
17	The ongoing evolution of variants of concern and interest of SARS-CoV-2 in Brazil revealed by convergent indels in the amino (N)-terminal domain of the spike protein. <i>Virus Evolution</i> , 2021, 7, veab069.	4.9	31
18	Systematic Review of Wolbachia Symbiont Detection in Mosquitoes: An Entangled Topic about Methodological Power and True Symbiosis. <i>Pathogens</i> , 2021, 10, 39.	2.8	25

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19	Optimization and Clinical Validation of Colorimetric Reverse Transcription Loop-Mediated Isothermal Amplification, a Fast, Highly Sensitive and Specific COVID-19 Molecular Diagnostic Tool That Is Robust to Detect SARS-CoV-2 Variants of Concern. <i>Frontiers in Microbiology</i> , 2021, 12, 713713.	3.5	22
20	Identification of a novel SARS-CoV-2 P.1 sub-lineage in Brazil provides new insights about the mechanisms of emergence of variants of concern. <i>Virus Evolution</i> , 2021, 7, veab091.	4.9	28
21	Sequencing of ZIKV genomes directly from <i>Ae. aegypti</i> and <i>Cx. quinquefasciatus</i> mosquitoes collected during the 2015–16 epidemics in Recife. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104180.	2.3	4
22	Polymorphisms in GSTE2 is associated with temephos resistance in <i>Aedes aegypti</i> . <i>Pesticide Biochemistry and Physiology</i> , 2020, 165, 104464.	3.6	16
23	Culicidae evolutionary history focusing on the Culicinae subfamily based on mitochondrial phylogenomics. <i>Scientific Reports</i> , 2020, 10, 18823.	3.3	37
24	In and Outs of Chuviridae Endogenous Viral Elements: Origin of a Potentially New Retrovirus and Signature of Ancient and Ongoing Arms Race in Mosquito Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 542437.	2.3	26
25	Multiple Introductions Followed by Ongoing Community Spread of SARS-CoV-2 at One of the Largest Metropolitan Areas of Northeast Brazil. <i>Viruses</i> , 2020, 12, 1414.	3.3	47
26	Comparative Genomics of <i>Acinetobacter baumannii</i> Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 1176.	3.5	24
27	Diverse mobilome of <i>Dichotomius (Luederwaldtinia) schiffleri</i> (Coleoptera: Scarabaeidae) reveals long-range horizontal transfer events of DNA transposons. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1339-1353.	2.1	8
28	The Emergence of Chikungunya ECSA Lineage in a Mayaro Endemic Region on the Southern Border of the Amazon Forest. <i>Tropical Medicine and Infectious Disease</i> , 2020, 5, 105.	2.3	11
29	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
30	Characterization of the mitogenome of <i>Rhammatocerus brasiliensis</i> and phylogenetic analysis of the family Acrididae (Orthoptera). <i>Gene</i> , 2020, 731, 144362.	2.2	2
31	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020, 15, e0226098.	2.5	7
32	Evolutionary Dynamics and Dissemination Pattern of the SARS-CoV-2 Lineage B.1.1.33 During the Early Pandemic Phase in Brazil. <i>Frontiers in Microbiology</i> , 2020, 11, 615280.	3.5	62
33	Mosquito genomes are frequently invaded by transposable elements through horizontal transfer. <i>PLoS Genetics</i> , 2020, 16, e1008946.	3.5	31
34	Beyond diversity loss and climate change: Impacts of Amazon deforestation on infectious diseases and public health. <i>Anais Da Academia Brasileira De Ciencias</i> , 2020, 92, e20191375.	0.8	176
35	A differential transcriptional profile by <i>Culex quinquefasciatus</i> larvae resistant to <i>Lysinibacillus sphaericus</i> IAB59 highlights genes and pathways associated with the resistance phenotype. <i>Parasites and Vectors</i> , 2019, 12, 407.	2.5	12
36	Spread of two Zika virus lineages in Midwest Brazil. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103974.	2.3	4

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37	The mobilome of <i>Drosophila incompta</i> , a flower-breeding species: comparison of transposable element landscapes among generalist and specialist flies. <i>Chromosome Research</i> , 2019, 27, 203-219.	2.2	9
38	Zika virus detection, isolation and genome sequencing through Culicidae sampling during the epidemic in Vitória, Espírito Santo, Brazil. <i>Parasites and Vectors</i> , 2019, 12, 220.	2.5	18
39	Genome sequencing reveals coinfection by multiple chikungunya virus genotypes in a recent outbreak in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007332.	3.0	21
40	Activation of p38MAPK and NRF2 signaling pathways in the toxicity induced by chlorpyrifos in <i>Drosophila melanogaster</i> : Protective effects of <i>Psidium guajava</i> pomifera L. (Myrtaceae) hydroalcoholic extract. <i>Arabian Journal of Chemistry</i> , 2019, 12, 3490-3502.	4.9	12
41	Genetic exchange in eukaryotes through horizontal transfer: connected by the mobilome. <i>Mobile DNA</i> , 2018, 9, 6.	3.6	50
42	HTT-DB: new features and updates. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, .	3.0	16
43	Revisiting Key Entry Routes of Human Epidemic Arboviruses into the Mainland Americas through Large-Scale Phylogenomics. <i>International Journal of Genomics</i> , 2018, 2018, 1-9.	1.6	22
44	<i>Drosophila</i> parasitoid wasps bears a distinct DNA transposon profile. <i>Mobile DNA</i> , 2018, 9, 23.	3.6	7
45	Persistent detection of Zika virus RNA from an infant with severe microcephaly – a case report. <i>BMC Infectious Diseases</i> , 2018, 18, 388.	2.9	17
46	Culicidae fauna (Diptera: Culicidae) survey in urban, ecotonal and forested areas, from the Moreno municipality - Pernambuco State, Brazil.. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2018, 51, 523-527.	0.9	5
47	Phylogenetic positioning of the Antarctic alga <i>Prasiola crisa</i> (Trebouxiophyceae) using organellar genomes and their structural analysis. <i>Journal of Phycology</i> , 2017, 53, 908-915.	2.3	6
48	<i>Senecio brasiliensis</i> impairs eclosion rate and induces apoptotic cell death in larvae of <i>Drosophila melanogaster</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 198, 45-57.	2.6	12
49	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
50	Inferring the phylogenetic position of the <i>Drosophila flavopilosa</i> group: Incongruence within and between mitochondrial and nuclear multilocus datasets. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 208-221.	1.4	7
51	Zika virus replication in the mosquito <i>Culex quinquefasciatus</i> in Brazil. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-11.	6.5	150
52	<i>Dichotomius</i> (Luederwaldtinia) <i>schiffleri</i> (Coleoptera: Scarabaeidae) mitochondrial genome and phylogenetic relationships within the superfamily Scarabaeoidea. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 887-888.	0.4	5
53	Response to: “Lack of evidence for Zika virus transmission by <i>Culex</i> mosquitoes”. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-2.	6.5	4
54	Evolutionary history of the mariner element <i>galluhop</i> in avian genomes. <i>Mobile DNA</i> , 2017, 8, 11.	3.6	4

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55	De novo Assembly and Annotation of the Antarctic Alga <i>Prasiola crispa</i> Transcriptome. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 89.	3.5	5
56	High-Fat Diet Induces Oxidative Stress and MPK2 and HSP83 Gene Expression in <i>Drosophila melanogaster</i> . <i>Oxidative Medicine and Cellular Longevity</i> , 2016, 2016, 1-12.	4.0	38
57	<i>Wolbachia</i> from <i>Drosophila incompta</i> : just a hitchhiker shared b <i>etween</i> <i>Drosophila</i> in the New and Old World?. <i>Insect Molecular Biology</i> , 2016, 25, 487-499.	2.0	10
58	Risks of <i>Wolbachia</i> mosquito control. <i>Science</i> , 2016, 351, 1273-1273.	12.6	13
59	VHICA, a New Method to Discriminate between Vertical and Horizontal Transposon Transfer: Application to the <i>Mariner</i> Family within <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 1094-1109.	8.9	62
60	Assessment of Water Pollution Signs in the Brazilian Pampa Biome Using Stress Biomarkers in Fish (<i>Astyanax</i> sp.). <i>Journal of Ecosystems</i> , 2015, 2015, 1-7.	0.7	8
61	Oxidative stress markers in fish (<i>Astyanax</i> sp. and <i>Danio rerio</i>) exposed to urban and agricultural effluents in the Brazilian Pampa biome. <i>Environmental Science and Pollution Research</i> , 2015, 22, 15526-15535.	5.3	21
62	<i>Eugenia uniflora</i> leaves essential oil induces toxicity in <i>Drosophila melanogaster</i> : involvement of oxidative stress mechanisms. <i>Toxicology Research</i> , 2015, 4, 634-644.	2.1	47
63	HTT-DB: Horizontally transferred transposable elements database. <i>Bioinformatics</i> , 2015, 31, 2915-2917.	4.1	50
64	Draft Plastid and Mitochondrial Genome Sequences from Antarctic Alga <i>Prasiola crispa</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	8
65	An evaluation of the ecological relationship between <i>Drosophila</i> species and their parasitoid wasps as an opportunity for horizontal transposon transfer. <i>Molecular Genetics and Genomics</i> , 2015, 290, 67-78.	2.1	18
66	Fumigant Activity of the <i>Psidium guajava</i> Var. <i>Pomifera</i> (Myrtaceae) Essential Oil in <i>Drosophila melanogaster</i> by Means of Oxidative Stress. <i>Oxidative Medicine and Cellular Longevity</i> , 2014, 2014, 1-8.	4.0	26
67	Characterization of the complete mitochondrial genome of flower-breeding <i>Drosophila incompta</i> (Diptera, Drosophilidae). <i>Genetica</i> , 2014, 142, 525-535.	1.1	19
68	Genomic landscape and evolutionary dynamics of mariner transposable elements within the <i>Drosophila</i> genus. <i>BMC Genomics</i> , 2014, 15, 727.	2.8	31
69	Horizontal Transposon Transfer in Eukarya: Detection, Bias, and Perspectives. <i>Genome Biology and Evolution</i> , 2012, 4, 801-811.	2.5	103
70	The role of vertical and horizontal transfer in the evolution of Paris-like elements in drosophilid species. <i>Genetica</i> , 2011, 139, 1487-1497.	1.1	3
71	The evolutionary history of mariner-like elements in Neotropical drosophilids. <i>Genetica</i> , 2011, 139, 327-338.	1.1	8
72	Behaviour of the Common Moorhen in Rio Grande do Sul, Brazil. <i>Acta Ethologica</i> , 2010, 13, 127-135.	0.9	7

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73	Isolation of high quality DNA: a protocol combining <i>â€œ</i> erennet <i>â€™</i> and glass milk. Electronic Journal of Biotechnology, 2009, 12, 0-0.	2.2	14
74	The mariner transposable element in natural populations of <i>Drosophila simulans</i> . Heredity, 2008, 101, 53-59.	2.6	19