

Leonardo de Oliveira Martins

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

935
citations

758635

12
h-index

552369

26
g-index

41
all docs

41
docs citations

41
times ranked

1607
citing authors

#	ARTICLE	IF	CITATIONS
1	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
2	<i>SimPhy</i> : Phylogenomic Simulation of Gene, Locus, and Species Trees. <i>Systematic Biology</i> , 2016, 65, 334-344.	2.7	122
3	Nanoneedle-Mediated Stimulation of Cell Mechanotransduction Machinery. <i>ACS Nano</i> , 2019, 13, 2913-2926.	7.3	101
4	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021, 13, 21.	3.6	94
5	Evolutionary Process of Deep-Sea Bathymodiolus Mussels. <i>PLoS ONE</i> , 2010, 5, e10363.	1.1	81
6	Exposure of Salmonella biofilms to antibiotic concentrations rapidly selects resistance with collateral tradeoffs. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 3.	2.9	42
7	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. <i>Systematic Biology</i> , 2016, 65, 397-416.	2.7	40
8	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. <i>Microbial Genomics</i> , 2021, 7, .	1.0	31
9	Phylogenetic Detection of Recombination with a Bayesian Prior on the Distance between Trees. <i>PLoS ONE</i> , 2008, 3, e2651.	1.1	27
10	Evolutionary relationships of deep-sea mussels inferred by mitochondrial DNA sequences. <i>Marine Biology</i> , 2006, 149, 1111-1122.	0.7	26
11	Phylogeography of Loaches of the Genus <i>Lefua</i> (Balitoridae, Cypriniformes) Inferred from Mitochondrial DNA Sequences. <i>Zoological Science</i> , 2005, 22, 157-168.	0.3	25
12	Lineage-specific positive selection at the merozoite surface protein 1 (<i>mSP1</i>) locus of <i>Plasmodium vivax</i> and related simian malaria parasites. <i>BMC Evolutionary Biology</i> , 2010, 10, 52.	3.2	24
13	Genomic epidemiology and the role of international and regional travel in the SARS-CoV-2 epidemic in Zimbabwe: a retrospective study of routinely collected surveillance data. <i>The Lancet Global Health</i> , 2021, 9, e1658-e1666.	2.9	19
14	Species Tree Estimation from Genome-Wide Data with <i>guenomu</i> . <i>Methods in Molecular Biology</i> , 2017, 1525, 461-478.	0.4	14
15	Taxonomic resolution of the ribosomal RNA operon in bacteria: implications for its use with long-read sequencing. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz016.	1.5	14
16	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. <i>Lancet Microbe</i> , The, 2021, 2, e177.	3.4	13
17	Testing for Universal Common Ancestry. <i>Systematic Biology</i> , 2014, 63, 838-842.	2.7	10
18	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9

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19	Codon pairs of the HIV-1 vif gene correlate with CD4+ T cell count. BMC Infectious Diseases, 2013, 13, 173.	1.3	8
20	Unsorted Homology within Locus and Species Trees. Systematic Biology, 2014, 63, 988-992.	2.7	8
21	A Likelihood-based Index of Protein Protein Binding Affinities with Application to Influenza HA Escape from Antibodies. Molecular Biology and Evolution, 2007, 24, 1627-1638.	3.5	6
22	Proving universal common ancestry with similar sequences. Trends in Evolutionary Biology, 2012, 4, 5.	0.4	5
23	Infinitely long branches and an informal test of common ancestry. Biology Direct, 2016, 11, 19.	1.9	4
24	Datasets for benchmarking antimicrobial resistance genes in bacterial metagenomic and whole genome sequencing. Scientific Data, 2022, 9, .	2.4	4
25	Distribution of distances between topologies and its effect on detection of phylogenetic recombination. Annals of the Institute of Statistical Mathematics, 2010, 62, 145-159.	0.5	3
26	Tatajuba: exploring the distribution of homopolymer tracts. NAR Genomics and Bioinformatics, 2022, 4, lqac003.	1.5	1