

# Leonardo de Oliveira Martins

## List of Publications by Citations

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33  
papers

515  
citations

11  
h-index

22  
g-index

41  
ext. papers

776  
ext. citations

7.8  
avg, IF

3.78  
L-index

#	Paper	IF	Citations
33	SimPhy: Phylogenomic Simulation of Gene, Locus, and Species Trees. <i>Systematic Biology</i> , <b>2016</b> , 65, 334-448	4.4	76
32	Nanoneedle-Mediated Stimulation of Cell Mechanotransduction Machinery. <i>ACS Nano</i> , <b>2019</b> , 13, 2913-2926	12.7	65
31	Evolutionary process of deep-sea bathymodiolus mussels. <i>PLoS ONE</i> , <b>2010</b> , 5, e10363	3.7	62
30	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , <b>2021</b> , 13, 21	14.4	40
29	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , <b>2021</b> , 374, 423-431	33.3	35
28	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. <i>Systematic Biology</i> , <b>2016</b> , 65, 397-416	8.4	27
27	Evolutionary relationships of deep-sea mussels inferred by mitochondrial DNA sequences. <i>Marine Biology</i> , <b>2006</b> , 149, 1111-1122	2.5	25
26	Phylogeography of loaches of the genus <i>Ileua</i> (balitoridae, cypriniformes) inferred from mitochondrial DNA sequences. <i>Zoological Science</i> , <b>2005</b> , 22, 157-68	0.8	21
25	Phylogenetic detection of recombination with a Bayesian prior on the distance between trees. <i>PLoS ONE</i> , <b>2008</b> , 3, e2651	3.7	19
24	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> , <b>2010</b> , 10, 52	3	18
23	Exposure of <i>Salmonella</i> biofilms to antibiotic concentrations rapidly selects resistance with collateral tradeoffs. <i>Npj Biofilms and Microbiomes</i> , <b>2021</b> , 7, 3	8.2	15
22	Species Tree Estimation from Genome-Wide Data with <i>guenomu</i> . <i>Methods in Molecular Biology</i> , <b>2017</b> , 1525, 461-478	1.4	11
21	CoronaHiT: High throughput sequencing of SARS-CoV-2 genomes		11
20	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	11
19	Large scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management		9
18	Taxonomic resolution of the ribosomal RNA operon in bacteria: implications for its use with long-read sequencing. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqz016	3.7	8
17	Testing for universal common ancestry. <i>Systematic Biology</i> , <b>2014</b> , 63, 838-42	8.4	7

16	Antibiotics select for novel pathways of resistance in biofilms		7
15	Unsorted homology within locus and species trees. <i>Systematic Biology</i> , <b>2014</b> , 63, 988-92	8.4	6
14	Codon pairs of the HIV-1 vif gene correlate with CD4+ T cell count. <i>BMC Infectious Diseases</i> , <b>2013</b> , 13, 173	4	6
13	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. <i>Lancet Microbe, The</i> , <b>2021</b> , 2, e177	22.2	6
12	A likelihood-based index of protein protein binding affinities with application to influenza HA escape from antibodies. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 1627-38	8.3	5
11	Infinitely long branches and an informal test of common ancestry. <i>Biology Direct</i> , <b>2016</b> , 11, 19	7.2	4
10	Proving universal common ancestry with similar sequences. <i>Trends in Evolutionary Biology</i> , <b>2012</b> , 4,		3
9	Distribution of distances between topologies and its effect on detection of phylogenetic recombination. <i>Annals of the Institute of Statistical Mathematics</i> , <b>2010</b> , 62, 145-159	1	3
8	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	3
7	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> , <b>2021</b> , 9, e1658-e1666	13.6	3
6	SimPhy: Phylogenomic Simulation of Gene, Locus and Species Trees		2
5	Tatajuba [Exploring the distribution of homopolymer tracts		2
4	Genomic epidemiology of the SARS-CoV-2 epidemic in Zimbabwe: Role of international travel and regional migration in spread		1
3	Replacement of the Alpha variant of SARS-CoV-2 by the Delta variant in Lebanon between April and June 2021		1
2	Estimation of Species Trees		1
1	Tatajuba: exploring the distribution of homopolymer tracts.. <i>NAR Genomics and Bioinformatics</i> , <b>2022</b> , 4, lqac003	3.7	0