

Louis Du Plessis

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

13,444
citations

236925

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395702

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docs citations

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times ranked

21018
citing authors

#	ARTICLE	IF	CITATIONS
1	Purifying Selection Determines the Short-Term Time Dependency of Evolutionary Rates in SARS-CoV-2 and pH1N1 Influenza. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	42
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
3	A computationally tractable birth-death model that combines phylogenetic and epidemiological data. <i>PLoS Computational Biology</i> , 2022, 18, e1009805.	3.2	7
4	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	12.8	27
5	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
6	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. <i>Emerging Infectious Diseases</i> , 2022, 28, 751-758.	4.3	4
7	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	13.3	352
8	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
9	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021, 6, 415-415.	13.3	65
10	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
11	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	4.9	14
12	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
13	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
14	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	4.9	774
15	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	13.3	2,291
16	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
17	Ancient Bacterial Genomes Reveal a High Diversity of <i>Treponema pallidum</i> Strains in Early Modern Europe. <i>Current Biology</i> , 2020, 30, 3788-3803.e10.	3.9	47
18	Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR. <i>EBioMedicine</i> , 2020, 59, 102960.	6.1	149

#	ARTICLE	IF	CITATIONS
19	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
20	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	12.6	253
21	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	12.6	2,168
22	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 2414-2429.	8.9	30
23	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
24	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	5.6	79
25	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	11.0	82
26	The genomes of <i>Crithidia bombi</i> and <i>C. expoeki</i> , common parasites of bumblebees. <i>PLoS ONE</i> , 2018, 13, e0189738.	2.5	26
27	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , 2016, 33, 2454-2468.	8.9	28
28	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , 2015, 16, 83.	8.8	130
29	Getting to the root of epidemic spread with phylodynamic analysis of genomic data. <i>Trends in Microbiology</i> , 2015, 23, 383-386.	7.7	36
30	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
31	Gene expression differences underlying genotype-by-genotype specificity in a host–parasite system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3496-3501.	7.1	109
32	Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. <i>PLOS Currents</i> , 2014, 6, .	1.4	71
33	The what, where, how and why of gene ontology—a primer for bioinformaticians. <i>Briefings in Bioinformatics</i> , 2011, 12, 723-735.	6.5	122