

# Louis Du Plessis

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40  
papers

6,511  
citations

23  
h-index

44  
g-index

44  
ext. papers

10,719  
ext. citations

19.1  
avg, IF

6.13  
L-index

#	Paper	IF	Citations
40	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , <b>2020</b> , 368, 493-497	33.3	1373
39	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1403-1407	26.6	1250
38	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006650	5	1014
37	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , <b>2021</b> , 184, 64-75.e11	56.2	518
36	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , <b>2020</b> , 369, 1255-1260	33.3	277
35	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , <b>2015</b> , 16, 76	18.3	229
34	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , <b>2022</b> ,	50.4	205
33	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , <b>2021</b> , 7, veab064	3.7	176
32	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , <b>2020</b> , 181, 997-1003.e9	56.2	175
31	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> , <b>2021</b> , 35, 109292	10.6	172
30	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , <b>2020</b> , 369, 582-587	33.3	162
29	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , <b>2021</b> , 371, 708-712	33.3	159
28	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , <b>2015</b> , 16, 83	18.3	103
27	Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR. <i>EBioMedicine</i> , <b>2020</b> , 59, 102960	8.8	99
26	The what, where, how and why of gene ontology--a primer for bioinformaticians. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 723-35	13.4	97
25	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> , <b>2014</b> , 111, 3496-501	11.5	86
24	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , <b>2018</b> , 23, 855-864.e7	23.4	60

23	Insights into the early epidemic spread of ebola in sierra leone provided by viral sequence data. <i>PLOS Currents</i> , <b>2014</b> , 6,		53
22	Taming the BEAST-A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , <b>2018</b> , 67, 170-174	8.4	43
21	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , <b>2021</b> , 373, 889-895	33.3	41
20	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , <b>2021</b> , 6, 415	26.6	35
19	The effect of human mobility and control measures on the COVID-19 epidemic in China <b>2020</b> ,		26
18	Getting to the root of epidemic spread with phylodynamic analysis of genomic data. <i>Trends in Microbiology</i> , <b>2015</b> , 23, 383-6	12.4	23
17	Ancient Bacterial Genomes Reveal a High Diversity of <i>Treponema pallidum</i> Strains in Early Modern Europe. <i>Current Biology</i> , <b>2020</b> , 30, 3788-3803.e10	6.3	21
16	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 2454-68	8.3	19
15	The genomes of <i>Crithidia bombi</i> and <i>C. expoeki</i> , common parasites of bumblebees. <i>PLoS ONE</i> , <b>2018</b> , 13, e0189738	3.7	16
14	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2414-2429	8.3	10
13	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		9
12	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 751	17.4	7
11	Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China		6
10	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
9	Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza.. <i>Molecular Biology and Evolution</i> , <b>2022</b> ,	8.3	5
8	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , <b>2021</b> , 7, veab053	3.7	4
7	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		3
6	Ancient bacterial genomes reveal a formerly unknown diversity of <i>Treponema pallidum</i> strains in early modern Europe		2

5	Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India		2
4	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 1012	17.4	2
3	The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK		2
2	Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza		1
1	A computationally tractable birth-death model that combines phylogenetic and epidemiological data.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009805	5	0