

Louis Du Plessis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10976043/publications.pdf>

Version: 2024-02-01

33
papers

13,444
citations

236612

25
h-index

395343

33
g-index

44
all docs

44
docs citations

44
times ranked

21018
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
2	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	5.9	2,291
3	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	6.0	2,168
4	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
5	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
6	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	2.2	774
7	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	6.0	454
8	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.	2.9	375
9	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	5.9	352
10	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
11	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
12	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
13	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	13.5	236
14	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.	2.7	149
15	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	6.0	142
16	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , 2015, 16, 83.	3.8	130
17	The what, where, how and why of gene ontology—a primer for bioinformaticians. <i>Briefings in Bioinformatics</i> , 2011, 12, 723-735.	3.2	122
18	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.	3.3	109

#	ARTICLE	IF	CITATIONS
19	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.	5.1	82
20	Taming the BEAST – A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
21	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
22	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021, 6, 415-415.	5.9	65
23	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.	1.8	47
24	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, .	3.5	42
25	Getting to the root of epidemic spread with phylodynamic analysis of genomic data. <i>Trends in Microbiology</i> , 2015, 23, 383-386.	3.5	36
26	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 2414-2429.	3.5	30
27	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , 2016, 33, 2454-2468.	3.5	28
28	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	5.8	27
29	The genomes of <i>Crithidia bombi</i> and <i>C. expoeki</i> , common parasites of bumblebees. <i>PLoS ONE</i> , 2018, 13, e0189738.	1.1	26
30	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	2.2	14
31	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
32	A computationally tractable birth-death model that combines phylogenetic and epidemiological data. <i>PLoS Computational Biology</i> , 2022, 18, e1009805.	1.5	7
33	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. <i>Emerging Infectious Diseases</i> , 2022, 28, 751-758.	2.0	4