

Gytis Dudas

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

5,654
citations

257357

24
h-index

315616

38
g-index

56
all docs

56
docs citations

56
times ranked

9480
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	13.7	1,179
2	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	6.0	1,083
3	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
4	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014, 3, e01914.	2.8	299
5	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
6	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	13.5	275
7	Temporal and spatial analysis of the 2014â€“2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	13.7	272
8	The evolution of Ebola virus: Insights from the 2013â€“2016 epidemic. <i>Nature</i> , 2016, 538, 193-200.	13.7	264
9	MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018, 7, .	2.8	172
10	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	2.8	146
11	MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3144-3149.	3.3	142
12	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
13	Evolution and Spread of Ebola Virus in Liberia, 2014â€“2015. <i>Cell Host and Microbe</i> , 2015, 18, 659-669.	5.1	87
14	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	2.1	78
15	Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. <i>ELife</i> , 2021, 10, .	2.8	69
16	Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1â€“PB2â€“HA Gene Complex. <i>Molecular Biology and Evolution</i> , 2015, 32, 162-172.	3.5	63
17	Phylogenetic Analysis of Guinea 2014 EBOV Ebolavirus Outbreak. <i>PLOS Currents</i> , 2014, 6, .	1.4	62
18	MERS-CoV recombination: implications about the reservoir and potential for adaptation. <i>Virus Evolution</i> , 2016, 2, vev023.	2.2	60

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19	Phyldynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	5.8	59
20	Global genome analysis reveals a vast and dynamic anellovirus landscape within the human virome. <i>Cell Host and Microbe</i> , 2021, 29, 1305-1315.e6.	5.1	59
21	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. <i>Nature Communications</i> , 2021, 12, 5769.	5.8	51
22	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018, 22, 1159-1168.	2.9	37
23	The genetics of host-virus coevolution in invertebrates. <i>Current Opinion in Virology</i> , 2014, 8, 73-78.	2.6	35
24	The ability of single genes vs full genomes to resolve time and space in outbreak analysis. <i>BMC Evolutionary Biology</i> , 2019, 19, 232.	3.2	35
25	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17104-17111.	3.3	35
26	Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. <i>Nature Communications</i> , 2021, 12, 5717.	5.8	33
27	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
28	Are arthropods at the heart of virus evolution?. <i>ELife</i> , 2015, 4, .	2.8	26
29	Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics. <i>Lancet Microbe</i> , The, 2022, 3, e284-e293.	3.4	24
30	Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. <i>Virus Evolution</i> , 2019, 5, vez030.	2.2	20
31	Antibody escape and global spread of SARS-CoV-2 lineage A.27. <i>Nature Communications</i> , 2022, 13, 1152.	5.8	20
32	Estimating effective population size changes from preferentially sampled genetic sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007774.	1.5	14
33	Preliminary Evaluation of the Effect of Investigational Ebola Virus Disease Treatments on Viral Genome Sequences. <i>Journal of Infectious Diseases</i> , 2016, 214, S333-S341.	1.9	11
34	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences". <i>Science</i> , 2016, 353, 658-658.	6.0	6
35	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021, 13, 1359.	1.5	6
36	Polymorphism of genetic ambigrams. <i>Virus Evolution</i> , 2021, 7, veab038.	2.2	5

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37	Bulk Milk Tank Samples Are Suitable to Assess Circulation of Tick-Borne Encephalitis Virus in High Endemic Areas. <i>Viruses</i> , 2021, 13, 1772.	1.5	5
38	E-104 Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2018, 77, 43-43.	0.9	0