

Timothy G Vaughan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/583952/publications.pdf>

Version: 2024-02-01

23
papers

4,190
citations

471371

17
h-index

642610

23
g-index

39
all docs

39
docs citations

39
times ranked

7469
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	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	13.7	363
3	Phylogenetics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 2102-2116.	3.5	131
4	Efficient Bayesian inference under the structured coalescent. <i>Bioinformatics</i> , 2014, 30, 2272-2279.	1.8	118
5	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth-death SIR model. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131106.	1.5	104
6	IcyTree: rapid browser-based visualization for phylogenetic trees and networks. <i>Bioinformatics</i> , 2017, 33, 2392-2394.	1.8	91
7	The origin and early spread of SARS-CoV-2 in Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	83
8	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
9	A Stochastic Simulator of Birth-Death Master Equations with Application to Phylogenetics. <i>Molecular Biology and Evolution</i> , 2013, 30, 1480-1493.	3.5	73
10	Genetic diversity loss in a biodiversity hotspot: ancient <i>scnDNA</i> quantifies genetic decline and former connectivity in a critically endangered marsupial. <i>Molecular Ecology</i> , 2015, 24, 5813-5828.	2.0	48
11	Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. <i>Genetics</i> , 2017, 205, 857-870.	1.2	45
12	A Multitype Birth-Death Model for Bayesian Inference of Lineage-Specific Birth and Death Rates. <i>Systematic Biology</i> , 2020, 69, 973-986.	2.7	44
13	Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.	3.5	39
14	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
15	How well can the exponential-growth coalescent approximate constant-rate birth-death population dynamics?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150420.	1.2	29
16	Molecular Approaches to Understanding Transmission and Source Attribution in Nontyphoidal <i>Salmonella</i> and Their Application in Africa. <i>Clinical Infectious Diseases</i> , 2015, 61, S259-S265.	2.9	26
17	Detection of HIV transmission clusters from phylogenetic trees using a multi-state birth-death model. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180512.	1.5	22
18	Extinction Times in Autocatalytic Systems. <i>Journal of Physical Chemistry A</i> , 2010, 114, 10481-10491.	1.1	21

#	ARTICLE	IF	CITATIONS
19	Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1498-1507.	2.2	14
20	Joint Inference of Migration and Reassortment Patterns for Viruses with Segmented Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
21	Epidemiological inference from pathogen genomes: A review of phylodynamic models and applications. <i>Virus Evolution</i> , 2022, 8, .	2.2	9
22	Within-host demographic fluctuations and correlations in early retroviral infection. <i>Journal of Theoretical Biology</i> , 2012, 295, 86-99.	0.8	6
23	Field validation of phylodynamic analytical methods for inference on epidemiological processes in wildlife. <i>Transboundary and Emerging Diseases</i> , 2021, , .	1.3	1