

Mathieu Fourment

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

4,878
citations

331670

21
h-index

414414

32
g-index

40
all docs

40
docs citations

40
times ranked

9223
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.	3.2	2,484
2	A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3033-3043.	8.9	383
3	<i>Yersinia pestis</i> and the Plague of Justinian 541–543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , 2014, 14, 319-326.	9.1	358
4	PATRISTIC: a program for calculating patristic distances and graphically comparing the components of genetic change. <i>BMC Evolutionary Biology</i> , 2006, 6, 1.	3.2	309
5	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	2.0	224
6	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	6.0	166
7	African apes as reservoirs of <i>Plasmodium falciparum</i> and the origin and diversification of the <i>Laverania</i> subgenus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10561-10566.	7.1	135
8	A comparison of common programming languages used in bioinformatics. <i>BMC Bioinformatics</i> , 2008, 9, 82.	2.6	88
9	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	4.7	83
10	Inconsistencies in Estimating the Age of HIV-1 Subtypes Due to Heterotachy. <i>Molecular Biology and Evolution</i> , 2012, 29, 451-456.	8.9	65
11	Chimpanzee Malaria Parasites Related to <i>Plasmodium ovale</i> in Africa. <i>PLoS ONE</i> , 2009, 4, e5520.	2.5	62
12	Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution. <i>Journal of General Virology</i> , 2012, 93, 1996-2007.	2.9	57
13	Seqotron: a user-friendly sequence editor for Mac OS X. <i>BMC Research Notes</i> , 2016, 9, 106.	1.4	47
14	The impact of migratory flyways on the spread of avian influenza virus in North America. <i>BMC Evolutionary Biology</i> , 2017, 17, 118.	3.2	45
15	Accumulating Variation at Conserved Sites in Potyvirus Genomes Is Driven by Species Discovery and Affects Degenerate Primer Design. <i>PLoS ONE</i> , 2008, 3, e1586.	2.5	44
16	19 Dubious Ways to Compute the Marginal Likelihood of a Phylogenetic Tree Topology. <i>Systematic Biology</i> , 2020, 69, 209-220.	5.6	40
17	The Recent Establishment of North American H10 Lineage Influenza Viruses in Australian Wild Waterfowl and the Evolution of Australian Avian Influenza Viruses. <i>Journal of Virology</i> , 2013, 87, 10182-10189.	3.4	39
18	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. <i>Systematic Biology</i> , 2018, 67, 490-502.	5.6	29

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19	SWeBLAST: A Sliding Window Web-based BLAST tool for recombinant analysis. <i>Journal of Virological Methods</i> , 2008, 152, 98-101.	2.1	28
20	Avian influenza virus exhibits distinct evolutionary dynamics in wild birds and poultry. <i>BMC Evolutionary Biology</i> , 2015, 15, 120.	3.2	28
21	Molecular Epidemiology of Clade 1 Influenza A Viruses (H5N1), Southern Indochina Peninsula, 2004–2007. <i>Emerging Infectious Diseases</i> , 2009, 15, 1641-1644.	4.3	26
22	Novel non-parametric models to estimate evolutionary rates and divergence times from heterochronous sequence data. <i>BMC Evolutionary Biology</i> , 2014, 14, 163.	3.2	23
23	Evaluating probabilistic programming and fast variational Bayesian inference in phylogenetics. <i>PeerJ</i> , 2019, 7, e8272.	2.0	18
24	Local and relaxed clocks: the best of both worlds. <i>PeerJ</i> , 2018, 6, e5140.	2.0	17
25	Evolutionary dynamics of the N1 neuraminidases of the main lineages of influenza A viruses. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 526-535.	2.7	11
26	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	3.4	10
27	Evidence for Persistence of and Antiviral Resistance and Reassortment Events in Seasonal Influenza Virus Strains Circulating in Cambodia. <i>Journal of Clinical Microbiology</i> , 2010, 48, 295-297.	3.9	9
28	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. <i>Plasmid</i> , 2019, 102, 56-61.	1.4	6
29	Systematic Exploration of the High Likelihood Set of Phylogenetic Tree Topologies. <i>Systematic Biology</i> , 2020, 69, 280-293.	5.6	5
30	A Surrogate Function for One-Dimensional Phylogenetic Likelihoods. <i>Molecular Biology and Evolution</i> , 2018, 35, 242-246.	8.9	4
31	<i>Escherichia coli</i> ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. <i>Emerging Microbes and Infections</i> , 2020, 9, 1780-1792.	6.5	3
32	The VirusBanker database uses a Java program to allow flexible searching through Bunyaviridae sequences. <i>BMC Bioinformatics</i> , 2008, 9, 83.	2.6	2