Nicola De Maio

List of Publications by Year
in descending order

39 papers	5,223 citations	236612 25 h-index	377514 34 g-index
61 all docs	61 docs citations	61 times ranked	8708 citing authors

#	Article	IF	Citations
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	1.5	2,484
2	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	1.8	289
3	Ultrafast Sample placement on Existing tRees (UShER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. Nature Genetics, 2021, 53, 809-816.	9.4	264
4	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. PLoS Genetics, 2015, 11, e1005421.	1.5	216
5	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. Microbial Genomics, 2019, 5, .	1.0	171
6	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. PLoS Computational Biology, 2016, 12, e1005130.	1.5	104
7	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphismâ€"calling pipelines. GigaScience, 2020, 9, .	3.3	92
8	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. Nature, 2021, 591, 30-33.	13.7	92
9	Stability of SARS-CoV-2 phylogenies. PLoS Genetics, 2020, 16, e1009175.	1.5	92
10	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. Genome Biology and Evolution, 2021, 13, .	1.1	83
11	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	13.7	80
12	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. Molecular Biology and Evolution, 2021, 38, 1608-1613.	3.5	79
13	Linking Great Apes Genome Evolution across Time Scales Using Polymorphism-Aware Phylogenetic Models. Molecular Biology and Evolution, 2013, 30, 2249-2262.	3.5	73
14	Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. Journal of Antimicrobial Chemotherapy, 2017, 72, 3025-3034.	1.3	73
15	VARIATION IN THERMAL PERFORMANCE AND REACTION NORMS AMONG POPULATIONS OF<i>DROSOPHILA MELANOGASTER</i>. Evolution; International Journal of Organic Evolution, 2013, 67, 3573-3587.	1.1	72
16	Reversible polymorphism-aware phylogenetic models and their application to tree inference. Journal of Theoretical Biology, 2016, 407, 362-370.	0.8	70
17	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	1.5	69
18	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. Environmental Microbiomes, 2019, 14, 7.	2.2	69

#	ARTICLE	IF	CITATIONS
19	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. Molecular Biology and Evolution, 2021, 38, 5819-5824.	3.5	69
20	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. Systematic Biology, 2015, 64, 1018-1031.	2.7	66
21	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. Molecular Biology and Evolution, 2017, 34, 2537-2554.	3.5	65
22	Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. ELife, 2019, 8, .	2.8	63
23	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. Clinical Infectious Diseases, 2018, 67, 1035-1044.	2.9	60
24	Estimating Empirical Codon Hidden Markov Models. Molecular Biology and Evolution, 2013, 30, 725-736.	3.5	51
25	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. PLoS Computational Biology, 2021, 17, e1008561.	1.5	48
26	SimBac: simulation of whole bacterial genomes with homologous recombination. Microbial Genomics, 2016, 2, .	1.0	33
27	The Bacterial Sequential Markov Coalescent. Genetics, 2017, 206, 333-343.	1.2	28
28	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	4.4	24
29	Genetic Variability of the SARS-CoV-2 Pocketome. Journal of Proteome Research, 2021, 20, 4212-4215.	1.8	23
30	Accounting for spatial sampling patterns in Bayesian phylogeography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
31	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets. PLoS Computational Biology, 2022, 18, e1010056.	1.5	13
32	Short-range template switching in great ape genomes explored using pair hidden Markov models. PLoS Genetics, 2021, 17, e1009221.	1.5	11
33	The Cumulative Indel Model: Fast and Accurate Statistical Evolutionary Alignment. Systematic Biology, 2021, 70, 236-257.	2.7	8
34	A phylogenetic approach for weighting genetic sequences. BMC Bioinformatics, 2021, 22, 285.	1.2	3
35	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. Virus Evolution, 2021, 7, veab065.	2.2	0
36	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0

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37	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0
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39	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0