

Nicola De Maio

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50 papers	2,356 citations	23 h-index	48 g-index
61 ext. papers	4,057 ext. citations	9.4 avg, IF	5.17 L-index

#	Paper	IF	Citations
50	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019 , 15, e1006650	5	1014
49	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
48	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. <i>PLoS Genetics</i> , 2015 , 11, e1005421	6	133
47	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019 , 5,	4.4	93
46	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. <i>PLoS Computational Biology</i> , 2016 , 12, e1005130	5	64
45	Variation in thermal performance and reaction norms among populations of <i>Drosophila melanogaster</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013 , 67, 3573-87	3.8	58
44	Ultrafast Sample placement on Existing tRees (USHER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. <i>Nature Genetics</i> , 2021 , 53, 809-816	36.3	58
43	Covert dissemination of carbapenemase-producing <i>Klebsiella pneumoniae</i> (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 3025-3034	5.1	48
42	Linking great apes genome evolution across time scales using polymorphism-aware phylogenetic models. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2249-62	8.3	45
41	Estimating empirical codon hidden Markov models. <i>Molecular Biology and Evolution</i> , 2013 , 30, 725-36	8.3	43
40	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020 , 16, e1009175	6	43
39	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2537-2554	8.3	42
38	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism-calling pipelines. <i>GigaScience</i> , 2020 , 9,	7.6	42
37	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. <i>Systematic Biology</i> , 2015 , 64, 1018-31	8.4	41
36	Bayesian reconstruction of transmission within outbreaks using genomic variants. <i>PLoS Computational Biology</i> , 2018 , 14, e1006117	5	37
35	Two Distinct Patterns of <i>Clostridium difficile</i> Diversity Across Europe Indicating Contrasting Routes of Spread. <i>Clinical Infectious Diseases</i> , 2018 , 67, 1035-1044	11.6	36
34	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1608-1613	8.3	36

33	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016 , 407, 362-370	2.3	34
32	Combining genomics and epidemiology to analyse bi-directional transmission of in a multi-host system. <i>ELife</i> , 2019 , 8,	8.9	33
31	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021 , 591, 30-33	50.4	27
30	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	25
29	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. <i>Environmental Microbiomes</i> , 2019 , 14, 7	5.6	24
28	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , 2016 , 2,	4.4	23
27	The Bacterial Sequential Markov Coalescent. <i>Genetics</i> , 2017 , 206, 333-343	4	17
26	Genomic reconstruction of the SARS-CoV-2 epidemic in England. <i>Nature</i> , 2021 ,	50.4	16
25	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
24	Pandemic-Scale Phylogenomics Reveals Elevated Recombination Rates in the SARS-CoV-2 Spike Region		16
23	Ultrafast Sample Placement on Existing Trees (USHER) Empowers Real-Time Phylogenetics for the SARS-CoV-2 Pandemic 2020 ,		14
22	BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis		12
21	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. <i>PLoS Computational Biology</i> , 2021 , 17, e1008561	5	12
20	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5819-5824	8.3	12
19	Genomic reconstruction of the SARS-CoV-2 epidemic in England		9
18	Mutation rates and selection on synonymous mutations in SARS-CoV-2 2021 ,		6
17	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021 , 15, 2322-2335	11.9	4
16	A daily-updated database and tools for comprehensive SARS-CoV-2 mutation-annotated trees 2021 ,		4

15	Short-range template switching in great ape genomes explored using pair hidden Markov models. <i>PLoS Genetics</i> , 2021 , 17, e1009221	6	3
14	Repeated global migrations on different plant hosts by the tropical pathogen <i>Phytophthora palmivora</i>		2
13	VGsim: scalable viral genealogy simulator for global pandemic 2021 ,		2
12	Genetic Variability of the SARS-CoV-2 Pocketome. <i>Journal of Proteome Research</i> , 2021 , 20, 4212-4215	5.6	2
11	The Cumulative Indel Model: Fast and Accurate Statistical Evolutionary Alignment. <i>Systematic Biology</i> , 2021 , 70, 236-257	8.4	2
10	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples		1
9	phastSim: efficient simulation of sequence evolution for pandemic-scale datasets 2021 ,		1
8	The SARS-CoV-2 replication-transcription complex is a priority target for broad-spectrum pan-coronavirus drugs		1
7	A phylogenetic approach for weighting genetic sequences. <i>BMC Bioinformatics</i> , 2021 , 22, 285	3.6	0
6	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010056	5	0
5	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021 , 7, veab065	3.7	
4	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
3	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
2	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
1	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		