

Bui Quang Minh

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

48,610
citations

185998

28
h-index

264894

42
g-index

75
all docs

75
docs citations

75
times ranked

32746
citing authors

#	ARTICLE	IF	CITATIONS
1	IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. <i>Molecular Biology and Evolution</i> , 2015, 32, 268-274.	3.5	16,610
2	ModelFinder: fast model selection for accurate phylogenetic estimates. <i>Nature Methods</i> , 2017, 14, 587-589.	9.0	9,486
3	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	3.5	5,960
4	UFBoot2: Improving the Ultrafast Bootstrap Approximation. <i>Molecular Biology and Evolution</i> , 2018, 35, 518-522.	3.5	5,798
5	Ultrafast Approximation for Phylogenetic Bootstrap. <i>Molecular Biology and Evolution</i> , 2013, 30, 1188-1195.	3.5	3,123
6	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. <i>Nucleic Acids Research</i> , 2016, 44, W232-W235.	6.5	3,039
7	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. <i>Systematic Biology</i> , 2016, 65, 997-1008.	2.7	1,453
8	New Methods to Calculate Concordance Factors for Phylogenomic Datasets. <i>Molecular Biology and Evolution</i> , 2020, 37, 2727-2733.	3.5	354
9	Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. <i>Systematic Biology</i> , 2018, 67, 216-235.	2.7	328
10	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. <i>Nature Communications</i> , 2018, 9, 1517.	5.8	256
11	Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta and Cryptista. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152802.	1.2	222
12	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018, 18, 11.	3.2	129
13	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. <i>Molecular Biology and Evolution</i> , 2014, 31, 239-249.	3.5	127
14	The Phylogenetic Likelihood Library. <i>Systematic Biology</i> , 2015, 64, 356-362.	2.7	118
15	The Prevalence and Impact of Model Violations in Phylogenetic Analysis. <i>Genome Biology and Evolution</i> , 2019, 11, 3341-3352.	1.1	105
16	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. <i>Nature Communications</i> , 2020, 11, 3939.	5.8	102
17	Distribution and Phylogeny of Light-Oxygen-Voltage-Blue-Light-Signaling Proteins in the Three Kingdoms of Life. <i>Journal of Bacteriology</i> , 2009, 191, 7234-7242.	1.0	95
18	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021, 591, 30-33.	13.7	92

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19	Split diversity in constrained conservation prioritization using integer linear programming. <i>Methods in Ecology and Evolution</i> , 2015, 6, 83-91.	2.2	75
20	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. <i>Systematic Biology</i> , 2020, 69, 249-264.	2.7	75
21	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. <i>PLoS Biology</i> , 2020, 18, e3000954.	2.6	73
22	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016, 407, 362-370.	0.8	70
23	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. <i>Bioinformatics</i> , 2005, 21, 3794-3796.	1.8	69
24	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. <i>ELife</i> , 2019, 8, .	2.8	51
25	Discovery of the first light-dependent protochlorophyllide oxidoreductase in anoxygenic phototrophic bacteria. <i>Molecular Microbiology</i> , 2014, 93, 1066-1078.	1.2	44
26	QMaker: Fast and Accurate Method to Estimate Empirical Models of Protein Evolution. <i>Systematic Biology</i> , 2021, 70, 1046-1060.	2.7	39
27	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. <i>Molecular Biology and Evolution</i> , 2021, 38, 2915-2929.	3.5	39
28	Phylogenetic Diversity within Seconds. <i>Systematic Biology</i> , 2006, 55, 769-773.	2.7	37
29	Taxon Selection under Split Diversity. <i>Systematic Biology</i> , 2009, 58, 586-594.	2.7	34
30	AliSim: A Fast and Versatile Phylogenetic Sequence Simulator for the Genomic Era. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	28
31	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. <i>Molecular Biology and Evolution</i> , 2019, 36, 1294-1301.	3.5	27
32	Assessing Confidence in Root Placement on Phylogenies: An Empirical Study Using Nonreversible Models for Mammals. <i>Systematic Biology</i> , 2022, 71, 959-972.	2.7	25
33	Quantitative detection and typing of hepatitis D virus in human serum by real-time polymerase chain reaction and melting curve analysis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2010, 67, 172-179.	0.8	21
34	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
35	Consequences of Common Topological Rearrangements for Partition Trees in Phylogenomic Inference. <i>Journal of Computational Biology</i> , 2015, 22, 1129-1142.	0.8	14
36	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. <i>Systematic Biology</i> , 2018, 67, 552-558.	2.7	11

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37	A novel Fibroblast Growth Factor Receptor family member promotes neuronal outgrowth and synaptic plasticity in <i>Aplysia</i> . <i>Amino Acids</i> , 2014, 46, 2477-2488.	1.2	10
38	nQMaker: Estimating Time Nonreversible Amino Acid Substitution Models. <i>Systematic Biology</i> , 2022, 71, 1110-1123.	2.7	9
39	Budgeted Phylogenetic Diversity on Circular Split Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 22-29.	1.9	8
40	Split Diversity: Measuring and Optimizing Biodiversity Using Phylogenetic Split Networks. <i>Topics in Biodiversity and Conservation</i> , 2016, , 173-195.	0.3	5
41	Whole genome analysis of a Vietnamese trio. <i>Journal of Biosciences</i> , 2015, 40, 113-124.	0.5	4
42	Building Population-Specific Reference Genomes: A Case Study of Vietnamese Reference Genome. , 2015, , .		3
43	SDA*: A Simple and Unifying Solution to Recent Bioinformatic Challenges for Conservation Genetics. , 2010, , .		2
44	A new phylogenetic tree sampling method for maximum parsimony bootstrapping and proof-of-concept implementation. , 2016, , .		2
45	Newly Emerged Serotype 1c of <i>Shigella flexneri</i> : Multiple Origins and Changing Drug Resistance Landscape. <i>Genes</i> , 2020, 11, 1042.	1.0	1
46	pQMaker: empirically estimating amino acid substitution models in a parallel environment. , 2020, , .		1
47	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
48	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
49	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
50	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
51	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
52	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0