Bui Quang Minh

List of Publications by Year
in descending order

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	Assessing Confidence in Root Placement on Phylogenies: An Empirical Study Using Nonreversible Models for Mammals. Systematic Biology, 2022, 71, 959-972.	2.7	25
2	nQMaker: Estimating Time Nonreversible Amino Acid Substitution Models. Systematic Biology, 2022, 71, 1110-1123.	2.7	9
3	AliSim: A Fast and Versatile Phylogenetic Sequence Simulator for the Genomic Era. Molecular Biology and Evolution, 2022, 39, .	3.5	28
4	QMaker: Fast and Accurate Method to Estimate Empirical Models of Protein Evolution. Systematic Biology, 2021, 70, 1046-1060.	2.7	39
5	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. Nature, 2021, 591, 30-33.	13.7	92
6	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. Molecular Biology and Evolution, 2021, 38, 2915-2929.	3.5	39
7	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. Systematic Biology, 2020, 69, 249-264.	2.7	75
8	Newly Emerged Serotype 1c of Shigella flexneri: Multiple Origins and Changing Drug Resistance Landscape. Genes, 2020, 11, 1042.	1.0	1
9	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. Nature Communications, 2020, 11, 3939.	5.8	102
10	New Methods to Calculate Concordance Factors for Phylogenomic Datasets. Molecular Biology and Evolution, 2020, 37, 2727-2733.	3.5	354
11	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Molecular Biology and Evolution, 2020, 37, 1530-1534.	3.5	5,960
12	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. PLoS Biology, 2020, 18, e3000954.	2.6	73
13	pQMaker: empirically estimating amino acid substitution models in a parallel environment. , 2020, , .		1
14	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
15	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
16	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
17	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
18	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0

#	Article	IF	Citations
19	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
20	The Prevalence and Impact of Model Violations in Phylogenetic Analysis. Genome Biology and Evolution, 2019, 11, 3341-3352.	1.1	105
21	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. Molecular Biology and Evolution, 2019, 36, 1294-1301.	3.5	27
22	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. ELife, 2019, 8, .	2.8	51
23	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. Nature Communications, 2018, 9, 1517.	5.8	256
24	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. Systematic Biology, 2018, 67, 552-558.	2.7	11
25	UFBoot2: Improving the Ultrafast Bootstrap Approximation. Molecular Biology and Evolution, 2018, 35, 518-522.	3.5	5,798
26	Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. Systematic Biology, 2018, 67, 216-235.	2.7	328
27	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. BMC Evolutionary Biology, 2018, 18, 11.	3.2	129
28	ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods, 2017, 14, 587-589.	9.0	9,486
29	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	0.5	18
30	A new phylogenetic tree sampling method for maximum parsimony bootstrapping and proof-of-concept implementation. , 2016, , .		2
31	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. Systematic Biology, 2016, 65, 997-1008.	2.7	1,453
32	Reversible polymorphism-aware phylogenetic models and their application to tree inference. Journal of Theoretical Biology, 2016, 407, 362-370.	0.8	70
33	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research, 2016, 44, W232-W235.	6.5	3,039
34	Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta and Cryptista. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152802.	1.2	222
35	Split Diversity: Measuring and Optimizing Biodiversity Using Phylogenetic Split Networks. Topics in Biodiversity and Conservation, 2016, , 173-195.	0.3	5
36	Split diversity in constrained conservation prioritization using integer linear programming. Methods in Ecology and Evolution, 2015, 6, 83-91.	2.2	75

#	ARTICLE	IF	CITATIONS
37	Consequences of Common Topological Rearrangements for Partition Trees in Phylogenomic Inference. Journal of Computational Biology, 2015, 22, 1129-1142.	0.8	14
38	Building Population-Specific Reference Genomes: A Case Study of Vietnamese Reference Genome. , 2015, , .		3
39	Whole genome analysis of a Vietnamese trio. Journal of Biosciences, 2015, 40, 113-124.	0.5	4
40	IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. Molecular Biology and Evolution, 2015, 32, 268-274.	3.5	16,610
41	The Phylogenetic Likelihood Library. Systematic Biology, 2015, 64, 356-362.	2.7	118
42	Discovery of the first light‐dependent protochlorophyllide oxidoreductase in anoxygenic phototrophic bacteria. Molecular Microbiology, 2014, 93, 1066-1078.	1.2	44
43	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. Molecular Biology and Evolution, 2014, 31, 239-249.	3.5	127
44	A novel Fibroblast Growth Factor Receptor family member promotes neuronal outgrowth and synaptic plasticity in Aplysia. Amino Acids, 2014, 46, 2477-2488.	1.2	10
45	Ultrafast Approximation for Phylogenetic Bootstrap. Molecular Biology and Evolution, 2013, 30, 1188-1195.	3.5	3,123
46	SDA*: A Simple and Unifying Solution to Recent Bioinformatic Challenges for Conservation Genetics. , 2010, , .		2
47	Quantitative detection and typing of hepatitis D virus in human serum by real-time polymerase chain reaction and melting curve analysis. Diagnostic Microbiology and Infectious Disease, 2010, 67, 172-179.	0.8	21
48	Distribution and Phylogeny of Light-Oxygen-Voltage-Blue-Light-Signaling Proteins in the Three Kingdoms of Life. Journal of Bacteriology, 2009, 191, 7234-7242.	1.0	95
49	Taxon Selection under Split Diversity. Systematic Biology, 2009, 58, 586-594.	2.7	34
50	Budgeted Phylogenetic Diversity on Circular Split Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 22-29.	1.9	8
51	Phylogenetic Diversity within Seconds. Systematic Biology, 2006, 55, 769-773.	2.7	37
52	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. Bioinformatics, 2005, 21, 3794-3796.	1.8	69