

Ziheng Yang

List of Publications by Year in descending order

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126
papers

48,114
citations

12303

69
h-index

17546

121
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145
all docs

145
docs citations

145
times ranked

34419
citing authors

#	ARTICLE	IF	CITATIONS
1	PAML 4: Phylogenetic Analysis by Maximum Likelihood. <i>Molecular Biology and Evolution</i> , 2007, 24, 1586-1591.	3.5	11,130
2	PAML: a program package for phylogenetic analysis by maximum likelihood. <i>Bioinformatics</i> , 1997, 13, 555-556.	1.8	3,510
3	Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: Approximate methods. <i>Journal of Molecular Evolution</i> , 1994, 39, 306-314.	0.8	2,657
4	Bayes Empirical Bayes Inference of Amino Acid Sites Under Positive Selection. <i>Molecular Biology and Evolution</i> , 2005, 22, 1107-1118.	3.5	2,095
5	Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. <i>Genetics</i> , 2000, 155, 431-449.	1.2	2,064
6	Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. <i>Journal of Molecular Evolution</i> , 1996, 43, 304-311.	0.8	1,486
7	Likelihood Models for Detecting Positively Selected Amino Acid Sites and Applications to the HIV-1 Envelope Gene. <i>Genetics</i> , 1998, 148, 929-936.	1.2	1,419
8	Codon-Substitution Models for Detecting Molecular Adaptation at Individual Sites Along Specific Lineages. <i>Molecular Biology and Evolution</i> , 2002, 19, 908-917.	3.5	1,238
9	Bayesian species delimitation using multilocus sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9264-9269.	3.3	1,154
10	Among-site rate variation and its impact on phylogenetic analyses. <i>Trends in Ecology and Evolution</i> , 1996, 11, 367-372.	4.2	1,091
11	Bayes Estimation of Species Divergence Times and Ancestral Population Sizes Using DNA Sequences From Multiple Loci. <i>Genetics</i> , 2003, 164, 1645-1656.	1.2	946
12	Estimating the pattern of nucleotide substitution. <i>Journal of Molecular Evolution</i> , 1994, 39, 105-111.	0.8	939
13	Bayesian Estimation of Species Divergence Times Under a Molecular Clock Using Multiple Fossil Calibrations with Soft Bounds. <i>Molecular Biology and Evolution</i> , 2006, 23, 212-226.	3.5	742
14	Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 1585-1592.	3.5	658
15	The timescale of early land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2274-E2283.	3.3	654
16	Synonymous and nonsynonymous rate variation in nuclear genes of mammals. <i>Journal of Molecular Evolution</i> , 1998, 46, 409-418.	0.8	619
17	Best Practices for Justifying Fossil Calibrations. <i>Systematic Biology</i> , 2012, 61, 346-359.	2.7	616
18	Molecular phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2012, 13, 303-314.	7.7	572

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19	The BPP program for species tree estimation and species delimitation. <i>Environmental Epigenetics</i> , 2015, 61, 854-865.	0.9	568
20	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3491-3500.	1.2	449
21	Unguided Species Delimitation Using DNA Sequence Data from Multiple Loci. <i>Molecular Biology and Evolution</i> , 2014, 31, 3125-3135.	3.5	449
22	Estimation of Primate Speciation Dates Using Local Molecular Clocks. <i>Molecular Biology and Evolution</i> , 2000, 17, 1081-1090.	3.5	441
23	Inferring Speciation Times under an Episodic Molecular Clock. <i>Systematic Biology</i> , 2007, 56, 453-466.	2.7	388
24	Maximum-likelihood models for combined analyses of multiple sequence data. <i>Journal of Molecular Evolution</i> , 1996, 42, 587-596.	0.8	387
25	Uncertainty in the Timing of Origin of Animals and the Limits of Precision in Molecular Timescales. <i>Current Biology</i> , 2015, 25, 2939-2950.	1.8	370
26	Codon-Substitution Models to Detect Adaptive Evolution that Account for Heterogeneous Selective Pressures Among Site Classes. <i>Molecular Biology and Evolution</i> , 2002, 19, 49-57.	3.5	343
27	Comparison of Likelihood and Bayesian Methods for Estimating Divergence Times Using Multiple Gene Loci and Calibration Points, with Application to a Radiation of Cute-Looking Mouse Lemur Species. <i>Systematic Biology</i> , 2003, 52, 705-716.	2.7	327
28	The Influence of Gene Flow on Species Tree Estimation: A Simulation Study. <i>Systematic Biology</i> , 2014, 63, 17-30.	2.7	308
29	Mutation-Selection Models of Codon Substitution and Their Use to Estimate Selective Strengths on Codon Usage. <i>Molecular Biology and Evolution</i> , 2008, 25, 568-579.	3.5	304
30	Approximate Likelihood Calculation on a Phylogeny for Bayesian Estimation of Divergence Times. <i>Molecular Biology and Evolution</i> , 2011, 28, 2161-2172.	3.5	303
31	Statistical Properties of the Branch-Site Test of Positive Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 1217-1228.	3.5	289
32	Phylogenetic analysis using parsimony and likelihood methods. <i>Journal of Molecular Evolution</i> , 1996, 42, 294-307.	0.8	277
33	Species Tree Inference with BPP Using Genomic Sequences and the Multispecies Coalescent. <i>Molecular Biology and Evolution</i> , 2018, 35, 2585-2593.	3.5	265
34	On the Best Evolutionary Rate for Phylogenetic Analysis. <i>Systematic Biology</i> , 1998, 47, 125-133.	2.7	259
35	Improved Reversible Jump Algorithms for Bayesian Species Delimitation. <i>Genetics</i> , 2013, 194, 245-253.	1.2	251
36	The Effect of Insertions, Deletions, and Alignment Errors on the Branch-Site Test of Positive Selection. <i>Molecular Biology and Evolution</i> , 2010, 27, 2257-2267.	3.5	249

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37	The Impact of the Representation of Fossil Calibrations on Bayesian Estimation of Species Divergence Times. <i>Systematic Biology</i> , 2010, 59, 74-89.	2.7	247
38	Bayesian molecular clock dating of species divergences in the genomics era. <i>Nature Reviews Genetics</i> , 2016, 17, 71-80.	7.7	244
39	Evaluation of a Bayesian Coalescent Method of Species Delimitation. <i>Systematic Biology</i> , 2011, 60, 747-761.	2.7	242
40	Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. <i>Systematic Biology</i> , 1995, 44, 384-399.	2.7	239
41	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
42	Exploring uncertainty in the calibration of the molecular clock. <i>Biology Letters</i> , 2012, 8, 156-159.	1.0	206
43	Maximum Likelihood Estimation on Large Phylogenies and Analysis of Adaptive Evolution in Human Influenza Virus A. <i>Journal of Molecular Evolution</i> , 2000, 51, 423-432.	0.8	202
44	Branch-Length Prior Influences Bayesian Posterior Probability of Phylogeny. <i>Systematic Biology</i> , 2005, 54, 455-470.	2.7	196
45	Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. <i>Systematic Biology</i> , 2011, 60, 16-31.	2.7	195
46	The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019, 68, 168-181.	2.7	189
47	Estimation of the Transition/Transversion Rate Bias and Species Sampling. <i>Journal of Molecular Evolution</i> , 1999, 48, 274-283.	0.8	186
48	Likelihood and Bayes Estimation of Ancestral Population Sizes in Hominoids Using Data From Multiple Loci. <i>Genetics</i> , 2002, 162, 1811-1823.	1.2	186
49	Inference of selection from multiple species alignments. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 688-694.	1.5	183
50	Estimation of Hominoid Ancestral Population Sizes under Bayesian Coalescent Models Incorporating Mutation Rate Variation and Sequencing Errors. <i>Molecular Biology and Evolution</i> , 2008, 25, 1979-1994.	3.5	177
51	Phylogenetic Inference Using Whole Genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2008, 9, 217-231.	2.5	159
52	A biologist's guide to Bayesian phylogenetic analysis. <i>Nature Ecology and Evolution</i> , 2017, 1, 1446-1454.	3.4	154
53	Maximum likelihood methods for detecting adaptive evolution after gene duplication. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 201-212.	1.2	152
54	Efficient Bayesian Species Tree Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2017, 66, 823-842.	2.7	151

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55	Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. <i>New Phytologist</i> , 2018, 218, 819-834.	3.5	149
56	Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case. <i>Systematic Biology</i> , 2018, 67, 594-615.	2.7	143
57	An Empirical Examination of the Utility of Codon-Substitution Models in Phylogeny Reconstruction. <i>Systematic Biology</i> , 2005, 54, 808-818.	2.7	142
58	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	2.0	141
59	Challenges in Species Tree Estimation Under the Multispecies Coalescent Model. <i>Genetics</i> , 2016, 204, 1353-1368.	1.2	137
60	The unbearable uncertainty of Bayesian divergence time estimation. <i>Journal of Systematics and Evolution</i> , 2013, 51, 30-43.	1.6	130
61	A Bayesian Implementation of the Multispecies Coalescent Model with Introgression for Phylogenomic Analysis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1211-1223.	3.5	109
62	MtZoa: A general mitochondrial amino acid substitutions model for animal evolutionary studies. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 268-272.	1.2	105
63	Tail Paradox, Partial Identifiability, and Influential Priors in Bayesian Branch Length Inference. <i>Molecular Biology and Evolution</i> , 2012, 29, 325-335.	3.5	92
64	The power of phylogenetic comparison in revealing protein function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3179-3180.	3.3	89
65	Neither phylogenomic nor palaeontological data support a Palaeogene origin of placental mammals. <i>Biology Letters</i> , 2014, 10, 20131003.	1.0	87
66	Probability Distribution of Molecular Evolutionary Trees: A New Method of Phylogenetic Inference. <i>Journal of Molecular Evolution</i> , 1996, 43, 304-311.	0.8	84
67	A species-level timeline of mammal evolution integrating phylogenomic data. <i>Nature</i> , 2022, 602, 263-267.	13.7	84
68	Complexity of the simplest phylogenetic estimation problem. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 109-116.	1.2	81
69	Maximum Likelihood Implementation of an Isolation-with-Migration Model with Three Species for Testing Speciation with Gene Flow. <i>Molecular Biology and Evolution</i> , 2012, 29, 3131-3142.	3.5	81
70	Dating Phylogenies with Sequentially Sampled Tips. <i>Systematic Biology</i> , 2013, 62, 674-688.	2.7	79
71	The evolution of methods for establishing evolutionary timescales. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160020.	1.8	79
72	The Impact of the Rate Prior on Bayesian Estimation of Divergence Times with Multiple Loci. <i>Systematic Biology</i> , 2014, 63, 555-565.	2.7	78

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73	Molecular evolution of the hepatitis B virus genome. <i>Journal of Molecular Evolution</i> , 1995, 41, 587-96.	0.8	77
74	Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the <i>Anopheles gambiae</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2018, 35, 2512-2527.	3.5	76
75	Rates of Nucleotide Substitution and Mammalian Nuclear Gene Evolution: Approximate and Maximum-Likelihood Methods Lead to Different Conclusions. <i>Genetics</i> , 2000, 156, 1299-1308.	1.2	75
76	Substitution Rates in <i>Drosophila</i> Nuclear Genes: Implications for Translational Selection. <i>Genetics</i> , 2001, 157, 295-305.	1.2	74
77	Bayesian species identification under the multispecies coalescent provides significant improvements to <i>scp</i> DNA <i>scp</i> barcoding analyses. <i>Molecular Ecology</i> , 2017, 26, 3028-3036.	2.0	73
78	Characterization of the Uncertainty of Divergence Time Estimation under Relaxed Molecular Clock Models Using Multiple Loci. <i>Systematic Biology</i> , 2015, 64, 267-280.	2.7	70
79	A Likelihood Ratio Test of Speciation with Gene Flow Using Genomic Sequence Data. <i>Genome Biology and Evolution</i> , 2010, 2, 200-211.	1.1	69
80	Coalescent-Based Analyses of Genomic Sequence Data Provide a Robust Resolution of Phylogenetic Relationships among Major Groups of Gibbons. <i>Molecular Biology and Evolution</i> , 2018, 35, 159-179.	3.5	69
81	STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 410-419.	1.1	67
82	Fair-Balance Paradox, Star-tree Paradox, and Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2007, 24, 1639-1655.	3.5	66
83	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824.	4.6	65
84	Searching for efficient Markov chain Monte Carlo proposal kernels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19307-19312.	3.3	64
85	Bayesian selection of misspecified models is overconfident and may cause spurious posterior probabilities for phylogenetic trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1854-1859.	3.3	61
86	On the estimation of ancestral population sizes of modern humans. <i>Genetical Research</i> , 1997, 69, 111-116.	0.3	54
87	Bayesian Species Delimitation Can Be Robust to Guide-Tree Inference Errors. <i>Systematic Biology</i> , 2014, 63, 993-1004.	2.7	52
88	Testing the molecular clock using mechanistic models of fossil preservation and molecular evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170227.	1.2	51
89	Comparison of different strategies for using fossil calibrations to generate the time prior in Bayesian molecular clock dating. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 386-400.	1.2	46
90	Molecular and morphological evidence on the phylogeny of the Elephantidae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 2493-2500.	1.2	45

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91	Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. <i>Systematic Biology</i> , 2017, 66, syw063.	2.7	45
92	Prevalence of cryptic species in morphologically uniform taxa – Fast speciation and evolutionary radiation in Asian frogs. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 723-731.	1.2	45
93	Multilocus estimation of divergence times and ancestral effective population sizes of <i>Oryza</i> species and implications for the rapid diversification of the genus. <i>New Phytologist</i> , 2013, 198, 1155-1164.	3.5	43
94	Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. <i>Systematic Biology</i> , 1995, 44, 384.	2.7	41
95	Evaluation of Ancestral Sequence Reconstruction Methods to Infer Nonstationary Patterns of Nucleotide Substitution. <i>Genetics</i> , 2015, 200, 873-890.	1.2	37
96	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020, 69, 830-847.	2.7	37
97	Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow. <i>National Science Review</i> , 2021, 8, nwab127.	4.6	36
98	Empirical evaluation of a prior for Bayesian phylogenetic inference. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 4031-4039.	1.8	35
99	Bayesian Molecular Clock Dating Using Genome-Scale Datasets. <i>Methods in Molecular Biology</i> , 2019, 1910, 309-330.	0.4	33
100	An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. <i>Systematic Biology</i> , 2018, 67, 61-77.	2.7	32
101	Molecular Clocks without Rocks: New Solutions for Old Problems. <i>Trends in Genetics</i> , 2020, 36, 845-856.	2.9	32
102	Rapid morphological evolution in placental mammals post-dates the origin of the crown group. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182418.	1.2	29
103	Defining Species When There is Gene Flow. <i>Systematic Biology</i> , 2021, 70, 108-119.	2.7	29
104	On the general reversible Markov process model of nucleotide substitution: A reply to Saccone et al.. <i>Journal of Molecular Evolution</i> , 1995, 41, 254.	0.8	27
105	Phylogeny and species delimitation of the <i>Oryza</i> genome diploid species in <i>Oryza</i> . <i>Journal of Systematics and Evolution</i> , 2011, 49, 386-395.	1.6	27
106	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. <i>Systematic Biology</i> , 2019, 68, 967-986.	2.7	27
107	Complexity of the simplest species tree problem. <i>Molecular Biology and Evolution</i> , 2021, 38, 3993-4009.	3.5	22
108	A Simulation Study to Examine the Information Content in Phylogenomic Data Sets under the Multispecies Coalescent Model. <i>Molecular Biology and Evolution</i> , 2020, 37, 3211-3224.	3.5	20

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109	A simulation study to examine the impact of recombination on phylogenomic inferences under the multispecies coalescent model. <i>Molecular Ecology</i> , 2022, 31, 2814-2829.	2.0	20
110	Full-Likelihood Genomic Analysis Clarifies a Complex History of Species Divergence and Introgression: The Example of the <i>erato-sara</i> Group of <i>Heliconius</i> Butterflies. <i>Systematic Biology</i> , 2022, 71, 1159-1177.	2.7	16
111	Reply to Hedges et al.: Accurate timetrees do indeed require accurate calibrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9512-E9513.	3.3	15
112	MAXIMUM LIKELIHOOD ANALYSIS OF ADAPTIVE EVOLUTION IN HIV-1 GP120 ENV GENE. , 2000, , .		15
113	Genome-Scale Data Reveal Deep Lineage Divergence and a Complex Demographic History in the Texas Horned Lizard (<i>Phrynosoma cornutum</i>) throughout the Southwestern and Central United States. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
114	Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. <i>Molecular Biology and Evolution</i> , 2014, 31, 1902-1913.	3.5	13
115	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. , 2012, , .		12
116	Phase Resolution of Heterozygous Sites in Diploid Genomes is Important to Phylogenomic Analysis under the Multispecies Coalescent Model. <i>Systematic Biology</i> , 2022, 71, 334-352.	2.7	11
117	Estimation of Cross-Species Introgression Rates Using Genomic Data Despite Model Unidentifiability. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
118	On the Varied Pattern of Evolution of 2 Fungal Genomes: A Critique of Hughes and Friedman. <i>Molecular Biology and Evolution</i> , 2006, 23, 2279-2282.	3.5	8
119	Dating species divergences using rocks and clocks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150126.	1.8	8
120	Functional and Adaptive Significance of Promoter Mutations That Affect Divergent Myocardial Expressions of <i>TRIM72</i> in Primates. <i>Molecular Biology and Evolution</i> , 2021, 38, 2930-2945.	3.5	6
121	The Asymptotic Behavior of Bootstrap Support Values in Molecular Phylogenetics. <i>Systematic Biology</i> , 2021, 70, 774-785.	2.7	6
122	RELATING PHYSICO-CHEMICAL PROPERTIES OF AMINO ACIDS TO VARIABLE NUCLEOTIDE SUBSTITUTION PATTERNS AMONG SITES. , 1999, , .		3
123	A discrete-beta model for testing gene flow after speciation. <i>Methods in Ecology and Evolution</i> , 2015, 6, 715-724.	2.2	2
124	Ambiguity Coding Allows Accurate Inference of Evolutionary Parameters from Alignments in an Aggregated State-Space. <i>Systematic Biology</i> , 2021, 70, 21-32.	2.7	1
125	A. W. F. Edwards and the Origin of Bayesian Phylogenetics. , 0, , 352-362.		0
126	Proteins: Structure, Function and Evolution. , 2001, , .		0