Mario dos Reis

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Solving the riddle of codon usage preferences: a test for translational selection. Nucleic Acids Research, 2004, 32, 5036-5044.	14.5	629
2	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 3491-3500.	2.6	449
3	Uncertainty in the Timing of Origin of Animals and the Limits of Precision in Molecular Timescales. Current Biology, 2015, 25, 2939-2950.	3.9	370
4	Approximate Likelihood Calculation on a Phylogeny for Bayesian Estimation of Divergence Times. Molecular Biology and Evolution, 2011, 28, 2161-2172.	8.9	303
5	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. Proceedings of the United States of America, 2019, 116, 22657-22663.	7.1	291
6	Statistical Properties of the Branch-Site Test of Positive Selection. Molecular Biology and Evolution, 2011, 28, 1217-1228.	8.9	289
7	Bayesian molecular clock dating of species divergences in the genomics era. Nature Reviews Genetics, 2016, 17, 71-80.	16.3	244
8	Unexpected correlations between gene expression and codon usage bias from microarray data for the whole Escherichia coli K-12 genome. Nucleic Acids Research, 2003, 31, 6976-6985.	14.5	219
9	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. Genome Biology and Evolution, 2016, 8, 330-344.	2.5	195
10	Churchill, a Zinc Finger Transcriptional Activator, Regulates the Transition between Gastrulation and Neurulation. Cell, 2003, 115, 603-613.	28.9	182
11	Phylogenomic Resolution of the Cetacean Tree of Life Using Target Sequence Capture. Systematic Biology, 2020, 69, 479-501.	5.6	160
12	A biologist's guide to Bayesian phylogenetic analysis. Nature Ecology and Evolution, 2017, 1, 1446-1454.	7.8	154
13	Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. New Phytologist, 2018, 218, 819-834.	7.3	149
14	Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case. Systematic Biology, 2018, 67, 594-615.	5.6	143
15	The unbearable uncertainty of Bayesian divergence time estimation. Journal of Systematics and Evolution, 2013, 51, 30-43.	3.1	130
16	Dating Tips for Divergence-Time Estimation. Trends in Genetics, 2015, 31, 637-650.	6.7	126
17	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Sitewise Mutation-Selection Models. Genetics, 2012, 190, 1101-1115.	2.9	114
18	Identifying Changes in Selective Constraints: Host Shifts in Influenza. PLoS Computational Biology, 2009, 5, e1000564.	3.2	106

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19	A Beginners Guide to Estimating the Non-synonymous to Synonymous Rate Ratio of all Protein-Coding Genes in a Genome. Methods in Molecular Biology, 2015, 1201, 65-90.	0.9	105
20	Estimating Translational Selection in Eukaryotic Genomes. Molecular Biology and Evolution, 2009, 26, 451-461.	8.9	87
21	Neither phylogenomic nor palaeontological data support a Palaeogene origin of placental mammals. Biology Letters, 2014, 10, 20131003.	2.3	87
22	A species-level timeline of mammal evolution integrating phylogenomic data. Nature, 2022, 602, 263-267.	27.8	84
23	Geogenetic patterns in mouse lemurs (genus <i>Microcebus</i>) reveal the ghosts of Madagascar's forests past. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8049-8056.	7.1	81
24	The Impact of the Rate Prior on Bayesian Estimation of Divergence Times with Multiple Loci. Systematic Biology, 2014, 63, 555-565.	5.6	78
25	Molecular Evolutionary Characterization of a V1R Subfamily Unique to Strepsirrhine Primates. Genome Biology and Evolution, 2014, 6, 213-227.	2.5	71
26	Characterization of the Uncertainty of Divergence Time Estimation under Relaxed Molecular Clock Models Using Multiple Loci. Systematic Biology, 2015, 64, 267-280.	5.6	70
27	The impact of ancestral population size and incomplete lineage sorting on Bayesian estimation of species divergence times. Environmental Epigenetics, 2015, 61, 874-885.	1.8	59
28	Analysis of the Albumin/α-Fetoprotein/Afamin/Group specific component gene family in the context of zebrafish liver differentiation. Gene Expression Patterns, 2010, 10, 237-243.	0.8	58
29	A Penalized-Likelihood Method to Estimate the Distribution of Selection Coefficients from Phylogenetic Data. Genetics, 2014, 197, 257-271.	2.9	55
30	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. Molecular Ecology, 2011, 20, no-no.	3.9	48
31	Comparison of different strategies for using fossil calibrations to generate the time prior in Bayesian molecular clock dating. Molecular Phylogenetics and Evolution, 2017, 114, 386-400.	2.7	46
32	Why Do More Divergent Sequences Produce Smaller Nonsynonymous/Synonymous Rate Ratios in Pairwise Sequence Comparisons?. Genetics, 2013, 195, 195-204.	2.9	44
33	Dire wolves were the last of an ancient New World canid lineage. Nature, 2021, 591, 87-91.	27.8	43
34	Archaeology and evolution of transfer RNA genes in the Escherichia coli genome. Rna, 2006, 12, 933-942.	3.5	41
35	How to calculate the non-synonymous to synonymous rate ratio of protein-coding genes under the Fisher–Wright mutation–selection framework. Biology Letters, 2015, 11, 20141031.	2.3	39
36	Using Non-Homogeneous Models of Nucleotide Substitution to Identify Host Shift Events: Application to the Origin of the 1918 â€~Spanish' Influenza Pandemic Virus. Journal of Molecular Evolution, 2009, 69, 333-345.	1.8	36

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37	Bayesian Molecular Clock Dating Using Genome-Scale Datasets. Methods in Molecular Biology, 2019, 1910, 309-330.	0.9	33
38	An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. Systematic Biology, 2018, 67, 61-77.	5.6	32
39	Molecular Clocks without Rocks: New Solutions for Old Problems. Trends in Genetics, 2020, 36, 845-856.	6.7	32
40	Pedigree-based and phylogenetic methods support surprising patterns of mutation rate and spectrum in the gray mouse lemur. Heredity, 2021, 127, 233-244.	2.6	30
41	Rapid morphological evolution in placental mammals post-dates the origin of the crown group. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182418.	2.6	29
42	Charting the Host Adaptation of Influenza Viruses. Molecular Biology and Evolution, 2011, 28, 1755-1767.	8.9	28
43	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. Systematic Biology, 2019, 68, 967-986.	5.6	27
44	RelTime Rates Collapse to a Strict Clock When Estimating the Timeline of Animal Diversification. Genome Biology and Evolution, 2017, 9, 1320-1328.	2.5	25
45	Dietary Diversification and Specialization in Neotropical Bats Facilitated by Early Molecular Evolution. Molecular Biology and Evolution, 2021, 38, 3864-3883.	8.9	24
46	Notes on the birth–death prior with fossil calibrations for Bayesian estimation of species divergence times. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150128.	4.0	16
47	Finding Direction in the Search for Selection. Journal of Molecular Evolution, 2017, 84, 39-50.	1.8	15
48	Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. Molecular Biology and Evolution, 2014, 31, 1902-1913.	8.9	13
49	A Mutation–Selection Model of Protein Evolution under Persistent Positive Selection. Molecular Biology and Evolution, 2022, 39, .	8.9	10
50	Nectar-feeding bats and birds show parallel molecular adaptations in sugar metabolism enzymes. Current Biology, 2021, 31, 4667-4674.e6.	3.9	7
51	Fossil-free dating. Nature Ecology and Evolution, 2018, 2, 771-772.	7.8	3
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52 Bayesian Phylogenomic Dating. , 2020, , 221-249.