

Mario dos Reis

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

5,724
citations

126708

33
h-index

182168

51
g-index

57
all docs

57
docs citations

57
times ranked

7365
citing authors

#	ARTICLE	IF	CITATIONS
1	A Mutation-Selection Model of Protein Evolution under Persistent Positive Selection. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
2	A species-level timeline of mammal evolution integrating phylogenomic data. <i>Nature</i> , 2022, 602, 263-267.	13.7	84
3	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021, 591, 87-91.	13.7	43
4	Dietary Diversification and Specialization in Neotropical Bats Facilitated by Early Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 3864-3883.	3.5	24
5	Pedigree-based and phylogenetic methods support surprising patterns of mutation rate and spectrum in the gray mouse lemur. <i>Heredity</i> , 2021, 127, 233-244.	1.2	30
6	Nectar-feeding bats and birds show parallel molecular adaptations in sugar metabolism enzymes. <i>Current Biology</i> , 2021, 31, 4667-4674.e6.	1.8	7
7	Phylogenomic Resolution of the Cetacean Tree of Life Using Target Sequence Capture. <i>Systematic Biology</i> , 2020, 69, 479-501.	2.7	160
8	Molecular Clocks without Rocks: New Solutions for Old Problems. <i>Trends in Genetics</i> , 2020, 36, 845-856.	2.9	32
9	Bayesian Phylogenomic Dating. , 2020, , 221-249.		2
10	Bayesian Molecular Clock Dating Using Genome-Scale Datasets. <i>Methods in Molecular Biology</i> , 2019, 1910, 309-330.	0.4	33
11	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22657-22663.	3.3	291
12	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
13	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. <i>Systematic Biology</i> , 2019, 68, 967-986.	2.7	27
14	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
15	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
16	Fossil-free dating. <i>Nature Ecology and Evolution</i> , 2018, 2, 771-772.	3.4	3
17	An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. <i>Systematic Biology</i> , 2018, 67, 61-77.	2.7	32
18	Finding Direction in the Search for Selection. <i>Journal of Molecular Evolution</i> , 2017, 84, 39-50.	0.8	15

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19	RelTime Rates Collapse to a Strict Clock When Estimating the Timeline of Animal Diversification. <i>Genome Biology and Evolution</i> , 2017, 9, 1320-1328.	1.1	25
20	A biologist's guide to Bayesian phylogenetic analysis. <i>Nature Ecology and Evolution</i> , 2017, 1, 1446-1454.	3.4	154
21	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
22	Geogenetic patterns in mouse lemurs (genus <i>Microcebus</i>) reveal the ghosts of Madagascar's forests past. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8049-8056.	3.3	81
23	Notes on the birth-death prior with fossil calibrations for Bayesian estimation of species divergence times. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150128.	1.8	16
24	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	1.1	195
25	Bayesian molecular clock dating of species divergences in the genomics era. <i>Nature Reviews Genetics</i> , 2016, 17, 71-80.	7.7	244
26	The impact of ancestral population size and incomplete lineage sorting on Bayesian estimation of species divergence times. <i>Environmental Epigenetics</i> , 2015, 61, 874-885.	0.9	59
27	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
28	How to calculate the non-synonymous to synonymous rate ratio of protein-coding genes under the Fisher-Wright mutation-selection framework. <i>Biology Letters</i> , 2015, 11, 20141031.	1.0	39
29	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
30	Dating Tips for Divergence-Time Estimation. <i>Trends in Genetics</i> , 2015, 31, 637-650.	2.9	126
31	A Beginners Guide to Estimating the Non-synonymous to Synonymous Rate Ratio of all Protein-Coding Genes in a Genome. <i>Methods in Molecular Biology</i> , 2015, 1201, 65-90.	0.4	105
32	A Penalized-Likelihood Method to Estimate the Distribution of Selection Coefficients from Phylogenetic Data. <i>Genetics</i> , 2014, 197, 257-271.	1.2	55
33	Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. <i>Molecular Biology and Evolution</i> , 2014, 31, 1902-1913.	3.5	13
34	Molecular Evolutionary Characterization of a V1R Subfamily Unique to Strepsirrhine Primates. <i>Genome Biology and Evolution</i> , 2014, 6, 213-227.	1.1	71
35	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
36	Neither phylogenomic nor palaeontological data support a Palaeogene origin of placental mammals. <i>Biology Letters</i> , 2014, 10, 20131003.	1.0	87

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37	Why Do More Divergent Sequences Produce Smaller Nonsynonymous/Synonymous Rate Ratios in Pairwise Sequence Comparisons?. <i>Genetics</i> , 2013, 195, 195-204.	1.2	44
38	The unbearable uncertainty of Bayesian divergence time estimation. <i>Journal of Systematics and Evolution</i> , 2013, 51, 30-43.	1.6	130
39	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
40	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Site-wise Mutation-Selection Models. <i>Genetics</i> , 2012, 190, 1101-1115.	1.2	114
41	Statistical Properties of the Branch-Site Test of Positive Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 1217-1228.	3.5	289
42	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. <i>Molecular Ecology</i> , 2011, 20, no-no.	2.0	48
43	Charting the Host Adaptation of Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2011, 28, 1755-1767.	3.5	28
44	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
45	Analysis of the Albumin/Î±-Fetoprotein/Afamin/Group specific component gene family in the context of zebrafish liver differentiation. <i>Gene Expression Patterns</i> , 2010, 10, 237-243.	0.3	58
46	Estimating Translational Selection in Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2009, 26, 451-461.	3.5	87
47	Identifying Changes in Selective Constraints: Host Shifts in Influenza. <i>PLoS Computational Biology</i> , 2009, 5, e1000564.	1.5	106
48	Using Non-Homogeneous Models of Nucleotide Substitution to Identify Host Shift Events: Application to the Origin of the 1918 "Spanish" Influenza Pandemic Virus. <i>Journal of Molecular Evolution</i> , 2009, 69, 333-345.	0.8	36
49	Archaeology and evolution of transfer RNA genes in the <i>Escherichia coli</i> genome. <i>Rna</i> , 2006, 12, 933-942.	1.6	41
50	Solving the riddle of codon usage preferences: a test for translational selection. <i>Nucleic Acids Research</i> , 2004, 32, 5036-5044.	6.5	629
51	Churchill, a Zinc Finger Transcriptional Activator, Regulates the Transition between Gastrulation and Neurulation. <i>Cell</i> , 2003, 115, 603-613.	13.5	182
52	Unexpected correlations between gene expression and codon usage bias from microarray data for the whole <i>Escherichia coli</i> K-12 genome. <i>Nucleic Acids Research</i> , 2003, 31, 6976-6985.	6.5	219