

# Beatriz Mello

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4555306/publications.pdf>

Version: 2024-02-01

24  
papers

618  
citations

933447

10  
h-index

642732

23  
g-index

26  
all docs

26  
docs citations

26  
times ranked

977  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mode and Rate of Evolution of Haemosporidian Mitochondrial Genomes: Timing the Radiation of Avian Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 383-403.	8.9	122
2	Estimating TimeTrees with MEGA and the TimeTree Resource. <i>Molecular Biology and Evolution</i> , 2018, 35, 2334-2342.	8.9	92
3	Phylogenetic analysis and a time tree for a large drosophilid data set (Diptera: Drosophilidae). <i>Zoological Journal of the Linnean Society</i> , 2013, 169, 765-775.	2.3	86
4	Fast and Accurate Estimates of Divergence Times from Big Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 45-50.	8.9	52
5	Comparative evaluation of maximum parsimony and Bayesian phylogenetic reconstruction using empirical morphological data. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1477-1484.	1.7	47
6	Reliable Confidence Intervals for RelTime Estimates of Evolutionary Divergence Times. <i>Molecular Biology and Evolution</i> , 2020, 37, 280-290.	8.9	36
7	Combining fossil and molecular data to date the diversification of New World Primates. <i>Journal of Evolutionary Biology</i> , 2013, 26, 2438-2446.	1.7	35
8	Sigmodontine rodents diversified in South America prior to the complete rise of the Panamanian Isthmus. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2014, 52, 249-256.	1.4	31
9	Assignment of Calibration Information to Deeper Phylogenetic Nodes is More Effective in Obtaining Precise and Accurate Divergence Time Estimates. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13908.	1.2	18
10	Molecular dating for phylogenies containing a mix of populations and species by using Bayesian and RelTime approaches. <i>Molecular Ecology Resources</i> , 2021, 21, 122-136.	4.8	18
11	Conservation phylogenetics and computational species delimitation of Neotropical primates. <i>Biological Conservation</i> , 2018, 217, 397-406.	4.1	11
12	Incorrect handling of calibration information in divergence time inference: an example from volcanic islands. <i>Ecology and Evolution</i> , 2012, 2, 493-500.	1.9	10
13	Employing statistical learning to derive species-level genetic diversity for mammalian species. <i>Mammal Review</i> , 2020, 50, 240-251.	4.8	10
14	Phylogenetic analysis and a time tree for a large drosophilid data set (Diptera: Drosophilidae). <i>Zoological Journal of the Linnean Society</i> , 2013, , .	2.3	8
15	Performance of Hidden Markov Models in Recovering the Standard Classification of Glycoside Hydrolases. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431770340.	1.2	7
16	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1623-1631.	1.7	7
17	Molecular dating of the blood pigment hemocyanin provides new insight into the origin of animals. <i>Geobiology</i> , 2022, 20, 333-345.	2.4	5
18	Analysis of Adaptive Evolution in Lyssavirus Genomes Reveals Pervasive Diversifying Selection during Species Diversification. <i>Viruses</i> , 2014, 6, 4465-4478.	3.3	4

#	ARTICLE	IF	CITATIONS
19	A phylogenomic study of Steganinae fruit flies (Diptera: Drosophilidae): strong gene tree heterogeneity and evidence for monophyly. <i>BMC Evolutionary Biology</i> , 2020, 20, 141.	3.2	4
20	Evolution of a key enzyme of aerobic metabolism reveals Proterozoic functional subunit duplication events and an ancient origin of animals. <i>Scientific Reports</i> , 2021, 11, 15744.	3.3	4
21	The Estimated Pacemaker for Great Apes Supports the Hominoid Slowdown Hypothesis. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431985598.	1.2	3
22	The performance of outgroup-free rooting under evolutionary radiations. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107434.	2.7	3
23	Impact of long-term chromosomal shuffling on the multispecies coalescent analysis of two anthropoid primate lineages. <i>Ecology and Evolution</i> , 2018, 8, 1206-1216.	1.9	2
24	Comparative evaluation of macroevolutionary regimes of Ruminantia and selected mammalian lineages. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 814-824.	1.6	1