

# Qiqing Tao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1129955/publications.pdf>

Version: 2024-02-01

16  
papers

518  
citations

933447

10  
h-index

996975

15  
g-index

21  
all docs

21  
docs citations

21  
times ranked

701  
citing authors

#	ARTICLE	IF	CITATIONS
1	TopHap: rapid inference of key phylogenetic structures from common haplotypes in large genome collections with limited diversity. <i>Bioinformatics</i> , 2022, 38, 2719-2726.	4.1	7
2	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
3	An Evolutionary Portrait of the Progenitor SARS-CoV-2 and Its Dominant Offshoots in COVID-19 Pandemic. <i>Molecular Biology and Evolution</i> , 2021, 38, 3046-3059.	8.9	54
4	Molecular and morphological clocks for estimating evolutionary divergence times. <i>Bmc Ecology and Evolution</i> , 2021, 21, 83.	1.6	7
5	Data-driven speciation tree prior for better species divergence times in calibration-poor molecular phylogenies. <i>Bioinformatics</i> , 2021, 37, i102-i110.	4.1	8
6	Assessing Rapid Relaxed-Clock Methods for Phylogenomic Dating. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	7
7	Reliable Confidence Intervals for RelTime Estimates of Evolutionary Divergence Times. <i>Molecular Biology and Evolution</i> , 2020, 37, 280-290.	8.9	36
8	Relative Efficiencies of Simple and Complex Substitution Models in Estimating Divergence Times in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2020, 37, 1819-1831.	8.9	16
9	A new method for inferring timetrees from temporally sampled molecular sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007046.	3.2	19
10	Efficient Methods for Dating Evolutionary Divergences. , 2020, , 197-219.		14
11	Using a GTR+ $\hat{\Gamma}$ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated. <i>Bioinformatics</i> , 2020, 36, i884-i894.	4.1	6
12	A Machine Learning Method for Detecting Autocorrelation of Evolutionary Rates in Large Phylogenies. <i>Molecular Biology and Evolution</i> , 2019, 36, 811-824.	8.9	45
13	Theoretical Foundation of the RelTime Method for Estimating Divergence Times from Variable Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2018, 35, 1770-1782.	8.9	164
14	Accurate timetrees require accurate calibrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9510-E9511.	7.1	22
15	RelTime Relaxes the Strict Molecular Clock throughout the Phylogeny. <i>Genome Biology and Evolution</i> , 2018, 10, 1631-1636.	2.5	25
16	Fast and Accurate Estimates of Divergence Times from Big Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 45-50.	8.9	52