

Diego Darriba

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/230582/publications.pdf>

Version: 2024-02-01

18
papers

20,055
citations

758635

12
h-index

1058022

14
g-index

21
all docs

21
docs citations

21
times ranked

28446
citing authors

#	ARTICLE	IF	CITATIONS
1	The wall lizards of the Balkan peninsula: Tackling questions at the interface of phylogenomics and population genomics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107121.	1.2	6
2	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 291-294.	3.5	1,021
3	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. <i>Systematic Biology</i> , 2019, 68, 365-369.	2.7	400
4	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. <i>Bioinformatics</i> , 2019, 35, 4453-4455.	1.8	2,287
5	The State of Software for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2018, 35, 1037-1046.	3.5	36
6	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 100-115.	1.2	29
7	Does the choice of nucleotide substitution models matter topologically?. <i>BMC Bioinformatics</i> , 2016, 17, 143.	1.2	32
8	Prediction of missing sequences and branch lengths in phylogenomic data. <i>Bioinformatics</i> , 2016, 32, 1331-1337.	1.8	23
9	Adapting Reproducible Research Capabilities to Resilient Distributed Calculations. <i>International Journal of Grid and High Performance Computing</i> , 2016, 8, 58-69.	0.7	0
10	The Phylogenetic Likelihood Library. <i>Systematic Biology</i> , 2015, 64, 356-362.	2.7	118
11	jmodeltest.org : selection of nucleotide substitution models on the cloud. <i>Bioinformatics</i> , 2014, 30, 1310-1311.	1.8	79
12	A Fault Tolerant Workflow for Reproducible Research. , 2014, , .		1
13	High-performance computing selection of models of DNA substitution for multicore clusters. <i>International Journal of High Performance Computing Applications</i> , 2014, 28, 112-125.	2.4	6
14	Boosting the Performance of Bayesian Divergence Time Estimation with the Phylogenetic Likelihood Library. , 2013, , .		6
15	jModelTest 2: more models, new heuristics and parallel computing. <i>Nature Methods</i> , 2012, 9, 772-772.	9.0	13,416
16	HPC selection of models of DNA substitution. , 2011, , .		2
17	ProtTest 3: fast selection of best-fit models of protein evolution. <i>Bioinformatics</i> , 2011, 27, 1164-1165.	1.8	2,432
18	ProtTest-HPC: Fast Selection of Best-Fit Models of Protein Evolution. <i>Lecture Notes in Computer Science</i> , 2011, , 177-184.	1.0	41