

Bastien Boussau

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7552443/publications.pdf>

Version: 2024-02-01

18
papers

3,682
citations

567281

15
h-index

839539

18
g-index

28
all docs

28
docs citations

28
times ranked

5185
citing authors

#	ARTICLE	IF	CITATIONS
1	Nucleotide Usage Biases Distort Inferences of the Species Tree. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	7
2	Detecting adaptive convergent amino acid evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180234.	4.0	15
3	Gene transfers can date the tree of life. <i>Nature Ecology and Evolution</i> , 2018, 2, 904-909.	7.8	52
4	Accurate Detection of Convergent Amino-Acid Evolution with PCOC. <i>Molecular Biology and Evolution</i> , 2018, 35, 2296-2306.	8.9	50
5	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4602-E4611.	7.1	232
6	RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. <i>Systematic Biology</i> , 2016, 65, 726-736.	5.6	538
7	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	5.6	226
8	Genome-scale phylogenetic analysis finds extensive gene transfer among fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140335.	4.0	77
9	Assessing Approaches for Inferring Species Trees from Multi-Copy Genes. <i>Systematic Biology</i> , 2015, 64, 325-339.	5.6	17
10	Strepsiptera, Phylogenomics and the Long Branch Attraction Problem. <i>PLoS ONE</i> , 2014, 9, e107709.	2.5	51
11	Evidence for GC-biased gene conversion as a driver of between-lineage differences in avian base composition. <i>Genome Biology</i> , 2014, 15, 549.	8.8	76
12	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
13	Probabilistic Graphical Model Representation in Phylogenetics. <i>Systematic Biology</i> , 2014, 63, 753-771.	5.6	96
14	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1745-1750.	8.9	163
15	Efficient Exploration of the Space of Reconciled Gene Trees. <i>Systematic Biology</i> , 2013, 62, 901-912.	5.6	176
16	Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17513-17518.	7.1	150
17	What genomes have to say about the evolution of the Earth. <i>Gondwana Research</i> , 2012, 21, 483-494.	6.0	18
18	Non-homogeneous models of sequence evolution in the Bio++ suite of libraries and programs. <i>BMC Evolutionary Biology</i> , 2008, 8, 255.	3.2	122