

HervÃ© Philippe

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

9,205
citations

279487

23
h-index

552369

26
g-index

30
all docs

30
docs citations

30
times ranked

8767
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106967.	1.2	22
2	Environmental temperatures shape thermal physiology as well as diversification and genome-wide substitution rates in lizards. <i>Nature Communications</i> , 2019, 10, 4077.	5.8	89
3	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. <i>Current Biology</i> , 2019, 29, 1818-1826.e6.	1.8	120
4	Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage. <i>Molecular Biology and Evolution</i> , 2018, 35, 1463-1472.	3.5	10
5	Conditional Approximate Bayesian Computation: A New Approach for Across-Site Dependency in High-Dimensional Mutation-Selection Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2819-2834.	3.5	5
6	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. <i>Current Biology</i> , 2017, 27, 958-967.	1.8	423
7	Inferring the shallow phylogeny of true salamanders (<i>Salamandra</i>) by multiple phylogenomic approaches. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 16-26.	1.2	44
8	Phylotranscriptomic consolidation of the jawed vertebrate timetree. <i>Nature Ecology and Evolution</i> , 2017, 1, 1370-1378.	3.4	247
9	Phylogenomic Insights into Animal Evolution. <i>Current Biology</i> , 2015, 25, R876-R887.	1.8	154
10	Acoelomorph flatworms are deuterostomes related to Xenoturbella. <i>Nature</i> , 2011, 470, 255-258.	13.7	400
11	Difficult phylogenetic questions: more data, maybe; better methods, certainly. <i>BMC Biology</i> , 2011, 9, 91.	1.7	66
12	Site-specific time heterogeneity of the substitution process and its impact on phylogenetic inference. <i>BMC Evolutionary Biology</i> , 2011, 11, 17.	3.2	54
13	Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough. <i>PLoS Biology</i> , 2011, 9, e1000602.	2.6	932
14	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. <i>Molecular Biology and Evolution</i> , 2010, 27, 1698-1709.	3.5	248
15	Mutation-selection models of coding sequence evolution with site-heterogeneous amino acid fitness profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4629-4634.	3.3	152
16	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	6.0	251
17	Additional molecular support for the new chordate phylogeny. <i>Genesis</i> , 2008, 46, 592-604.	0.8	207
18	A General Comparison of Relaxed Molecular Clock Models. <i>Molecular Biology and Evolution</i> , 2007, 24, 2669-2680.	3.5	454

#	ARTICLE	IF	CITATIONS
19	SCaFoS: a tool for Selection, Concatenation and Fusion of Sequences for phylogenomics. BMC Evolutionary Biology, 2007, 7, S2.	3.2	158
20	Suppression of long-branch attraction artefacts in the animal phylogeny using a site-heterogeneous model. BMC Evolutionary Biology, 2007, 7, S4.	3.2	551
21	Tunicates and not cephalochordates are the closest living relatives of vertebrates. Nature, 2006, 439, 965-968.	13.7	1,488
22	Phylogenomics and the reconstruction of the tree of life. Nature Reviews Genetics, 2005, 6, 361-375.	7.7	1,038
23	A Bayesian Mixture Model for Across-Site Heterogeneities in the Amino-Acid Replacement Process. Molecular Biology and Evolution, 2004, 21, 1095-1109.	3.5	1,329
24	Critical Analysis of Eukaryotic Phylogeny: A Case Study Based on the HSP70 Family. Journal of Eukaryotic Microbiology, 1999, 46, 116-124.	0.8	96
25	How Many Nucleotides Are Required to Resolve a Phylogenetic Problem? The Use of a New Statistical Method Applicable to Available Sequences. Molecular Phylogenetics and Evolution, 1994, 3, 292-309.	1.2	71
26	MUST, a computer package of Management Utilities for Sequences and Trees. Nucleic Acids Research, 1993, 21, 5264-5272.	6.5	585