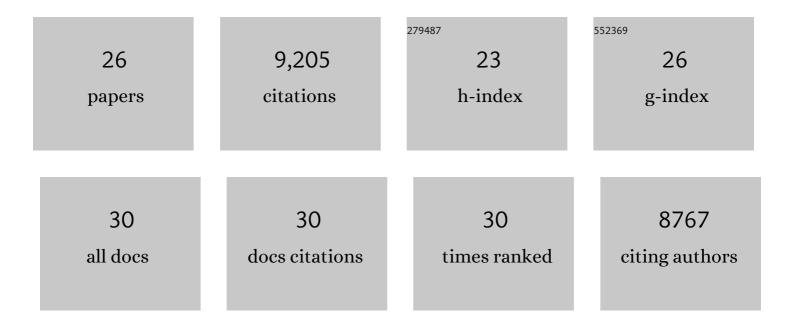
Hervé Philippe

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Tunicates and not cephalochordates are the closest living relatives of vertebrates. Nature, 2006, 439, 965-968.	13.7	1,488
2	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
3	Phylogenomics and the reconstruction of the tree of life. Nature Reviews Genetics, 2005, 6, 361-375.	7.7	1,038
4	Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough. PLoS Biology, 2011, 9, e1000602.	2.6	932
5	MUST, a computer package of Management Utilities for Sequences and Trees. Nucleic Acids Research, 1993, 21, 5264-5272.	6.5	585
6	Suppression of long-branch attraction artefacts in the animal phylogeny using a site-heterogeneous model. BMC Evolutionary Biology, 2007, 7, S4.	3.2	551
7	A General Comparison of Relaxed Molecular Clock Models. Molecular Biology and Evolution, 2007, 24, 2669-2680.	3.5	454
8	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. Current Biology, 2017, 27, 958-967.	1.8	423
9	Acoelomorph flatworms are deuterostomes related to Xenoturbella. Nature, 2011, 470, 255-258.	13.7	400
10	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. Science, 2010, 330, 1381-1385.	6.0	251
11	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. Molecular Biology and Evolution, 2010, 27, 1698-1709.	3.5	248
12	Phylotranscriptomic consolidation of the jawed vertebrate timetree. Nature Ecology and Evolution, 2017, 1, 1370-1378.	3.4	247
13	Additional molecular support for the new chordate phylogeny. Genesis, 2008, 46, 592-604.	0.8	207
14	SCaFoS: a tool for Selection, Concatenation and Fusion of Sequences for phylogenomics. BMC Evolutionary Biology, 2007, 7, S2.	3.2	158
15	Phylogenomic Insights into Animal Evolution. Current Biology, 2015, 25, R876-R887.	1.8	154
16	Mutation-selection models of coding sequence evolution with site-heterogeneous amino acid fitness profiles. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4629-4634.	3.3	152
17	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. Current Biology, 2019, 29, 1818-1826.e6.	1.8	120
18	Critical Analysis of Eukaryotic Phylogeny: A Case Study Based on the HSP70 Family. Journal of Eukaryotic Microbiology, 1999, 46, 116-124.	0.8	96

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#	Article	IF	CITATIONS
19	Environmental temperatures shape thermal physiology as well as diversification and genome-wide substitution rates in lizards. Nature Communications, 2019, 10, 4077.	5.8	89
20	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
21	Difficult phylogenetic questions: more data, maybe; better methods, certainly. BMC Biology, 2011, 9, 91.	1.7	66
22	Site-specific time heterogeneity of the substitution process and its impact on phylogenetic inference. BMC Evolutionary Biology, 2011, 11, 17.	3.2	54
23	Inferring the shallow phylogeny of true salamanders (Salamandra) by multiple phylogenomic approaches. Molecular Phylogenetics and Evolution, 2017, 115, 16-26.	1.2	44
24	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. Molecular Phylogenetics and Evolution, 2021, 155, 106967.	1.2	22
25	Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage. Molecular Biology and Evolution, 2018, 35, 1463-1472.	3.5	10
26	Conditional Approximate Bayesian Computation: A New Approach for Across-Site Dependency in High-Dimensional Mutation–Selection Models. Molecular Biology and Evolution, 2018, 35, 2819-2834.	3.5	5