

# Olivier Gascuel

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

69

papers

37,275

citations

30

h-index

82

g-index

82

ext. papers

44,963

ext. citations

6.3

avg, IF

7.82

L-index

#	Paper	IF	Citations
69	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal.. <i>Virus Evolution</i> , <b>2022</b> , 8, veac029	3.7	0
68	Gotree/Goalign: toolkit and Go API to facilitate the development of phylogenetic workflows. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab075	3.7	2
67	Cuban history of CRF19 recombinant subtype of HIV-1. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009786	7.6	1
66	Using machine learning and big data to explore the drug resistance landscape in HIV. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008873	5	2
65	Drug resistance mutations in HIV: new bioinformatics approaches and challenges. <i>Current Opinion in Virology</i> , <b>2021</b> , 51, 56-64	7.5	2
64	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 12522-12523	11.5	46
63	A Darwinian Uncertainty Principle. <i>Systematic Biology</i> , <b>2020</b> , 69, 521-529	8.4	7
62	A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 2069-2085	8.3	69
61	NGPhylogeny.fr: new generation phylogenetic services for non-specialists. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W260-W265	20.1	196
60	Distribution and asymptotic behavior of the phylogenetic transfer distance. <i>Journal of Mathematical Biology</i> , <b>2019</b> , 79, 485-508	2	0
59	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , <b>2018</b> , 67, 997-1009	8.4	8
58	Improving pairwise comparison of protein sequences with domain co-occurrence. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005889	5	5
57	SMS: Smart Model Selection in PhyML. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2422-2424	8.3	924
56	The Role of Phylogenetics as a Tool to Predict the Spread of Resistance. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 216, S820-S823	7	6
55	Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005416	5	21
54	The combinatorics of overlapping genes. <i>Journal of Theoretical Biology</i> , <b>2017</b> , 415, 90-101	2.3	20
53	A Stochastic Safety Radius for Distance-Based Tree Reconstruction. <i>Algorithmica</i> , <b>2016</b> , 74, 1386-1403	0.9	1

52	Fast Dating Using Least-Squares Criteria and Algorithms. <i>Systematic Biology</i> , <b>2016</b> , 65, 82-97	8.4	183
51	In-depth analysis of HIV-1 drug resistance mutations in HIV-infected individuals failing first-line regimens in West and Central Africa. <i>Aids</i> , <b>2016</b> , 30, 2577-2589	3.5	17
50	Concomitant emergence of the antisense protein gene of HIV-1 and of the pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 11537-11542	11.5	42
49	FastME 2.0: A Comprehensive, Accurate, and Fast Distance-Based Phylogeny Inference Program. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 2798-800	8.3	505
48	A phylotype-based analysis highlights the role of drug-naive HIV-positive individuals in the transmission of antiretroviral resistance in the UK. <i>Aids</i> , <b>2015</b> , 29, 1917-25	3.5	34
47	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W3-6	20.1	30
46	Mathematical and computational evolutionary biology (2013). <i>Systematic Biology</i> , <b>2015</b> , 64, 1-2	8.4	8
45	Predicting the ancestral character changes in a tree is typically easier than predicting the root state. <i>Systematic Biology</i> , <b>2014</b> , 63, 421-35	8.4	20
44	Deep conservation of human protein tandem repeats within the eukaryotes. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1132-48	8.3	40
43	Identification of divergent protein domains by combining HMM-HMM comparisons and co-occurrence detection. <i>PLoS ONE</i> , <b>2014</b> , 9, e95275	3.7	4
42	Sexually-transmitted/founder HIV-1 cannot be directly predicted from plasma or PBMC-derived viral quasispecies in the transmitting partner. <i>PLoS ONE</i> , <b>2013</b> , 8, e69144	3.7	13
41	The origin and evolutionary history of HIV-1 subtype C in Senegal. <i>PLoS ONE</i> , <b>2012</b> , 7, e33579	3.7	18
40	Branch lengths on birth-death trees and the expected loss of phylogenetic diversity. <i>Systematic Biology</i> , <b>2012</b> , 61, 195-203	8.4	51
39	Modeling protein evolution with several amino acid replacement matrices depending on site rates. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2921-36	8.3	135
38	Combinatorics of distance-based tree inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 16443-8	11.5	9
37	EuPathDomains: the divergent domain database for eukaryotic pathogens. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 698-707	4.5	6
36	Survey of branch support methods demonstrates accuracy, power, and robustness of fast likelihood-based approximation schemes. <i>Systematic Biology</i> , <b>2011</b> , 60, 685-99	8.4	565
35	Accounting for solvent accessibility and secondary structure in protein phylogenetics is clearly beneficial. <i>Systematic Biology</i> , <b>2010</b> , 59, 277-87	8.4	70

34	New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. <i>Systematic Biology</i> , <b>2010</b> , 59, 307-21	8.4	10954
33	SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 221-4	8.3	4001
32	Inferring ancestral sequences in taxon-rich phylogenies. <i>Mathematical Biosciences</i> , <b>2010</b> , 227, 125-35	3.9	14
31	Robustness of phylogenetic inference based on minimum evolution. <i>Bulletin of Mathematical Biology</i> , <b>2010</b> , 72, 1820-39	2.1	8
30	Consistency of topological moves based on the balanced minimum evolution principle of phylogenetic inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2009</b> , 6, 110-7	3	18
29	An improved general amino acid replacement matrix. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 1307-208.3	8.3	1959
28	Phylogenetic mixture models for proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2008</b> , 363, 3965-76	5.8	132
27	Empirical profile mixture models for phylogenetic reconstruction. <i>Bioinformatics</i> , <b>2008</b> , 24, 2317-23	7.2	189
26	Duplication and inversion history of a tandemly repeated genes family. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 462-78	1.7	24
25	Genomics, biogeography, and the diversification of placental mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 14395-400	11.5	135
24	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. <i>Genome Research</i> , <b>2007</b> , 17, 320-7	9.7	170
23	Neighbor-joining revealed. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 1997-2000	8.3	168
22	Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. <i>Systematic Biology</i> , <b>2006</b> , 55, 539-52	8.4	1908
21	SDM: a fast distance-based approach for (super) tree building in phylogenomics. <i>Systematic Biology</i> , <b>2006</b> , 55, 740-55	8.4	60
20	An exact and polynomial distance-based algorithm to reconstruct single copy tandem duplication trees. <i>Journal of Discrete Algorithms</i> , <b>2005</b> , 3, 362-374		3
19	Topological rearrangements and local search method for tandem duplication trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2005</b> , 2, 15-28	3	15
18	Performance Analysis of Hierarchical Clustering Algorithms. <i>Journal of Classification</i> , <b>2004</b> , 21, 3-18	1.2	11
17	Theoretical foundation of the balanced minimum evolution method of phylogenetic inference and its relationship to weighted least-squares tree fitting. <i>Molecular Biology and Evolution</i> , <b>2004</b> , 21, 587-98	8.3	147

16	On the consistency of the minimum evolution principle of phylogenetic inference. <i>Discrete Applied Mathematics</i> , <b>2003</b> , 127, 63-77	1	14
15	A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. <i>Systematic Biology</i> , <b>2003</b> , 52, 696-704	8.4	13613
14	The combinatorics of tandem duplication trees. <i>Systematic Biology</i> , <b>2003</b> , 52, 110-8	8.4	20
13	Improvement of distance-based phylogenetic methods by a local maximum likelihood approach using triplets. <i>Molecular Biology and Evolution</i> , <b>2002</b> , 19, 1952-63	8.3	29
12	Reconstructing the duplication history of tandemly repeated genes. <i>Molecular Biology and Evolution</i> , <b>2002</b> , 19, 278-88	8.3	61
11	Efficient biased estimation of evolutionary distances when substitution rates vary across sites. <i>Molecular Biology and Evolution</i> , <b>2002</b> , 19, 534-43	8.3	34
10	Fast and accurate phylogeny reconstruction algorithms based on the minimum-evolution principle. <i>Journal of Computational Biology</i> , <b>2002</b> , 9, 687-705	1.7	315
9	Quartet-based phylogenetic inference: improvements and limits. <i>Molecular Biology and Evolution</i> , <b>2001</b> , 18, 1103-16	8.3	73
8	Strengths and limitations of the minimum evolution principle. <i>Systematic Biology</i> , <b>2001</b> , 50, 621-7	8.4	22
7	Data Model and Classification by Trees: The Minimum Variance Reduction (MVR) Method. <i>Journal of Classification</i> , <b>2000</b> , 17, 67-99	1.2	16
6	On the optimization principle in phylogenetic analysis and the minimum-evolution criterion. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 401-5	8.3	30
5	Twelve Numerical, Symbolic and Hybrid Supervised Classification Methods. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , <b>1998</b> , 12, 517-571	1.1	7
4	A reduction algorithm for approximating a (nonmetric) dissimilarity by a tree distance. <i>Journal of Classification</i> , <b>1996</b> , 13, 129-155	1.2	12
3	Distribution-free performance bounds with the resubstitution error estimate. <i>Pattern Recognition Letters</i> , <b>1992</b> , 13, 757-764	4.7	10
2	Protein export in prokaryotes and eukaryotes: indications of a difference in the mechanism of exportation. <i>Journal of Molecular Evolution</i> , <b>1986</b> , 24, 130-42	3.1	38
1	Gotree/Goalign : Toolkit and Go API to facilitate the development of phylogenetic workflows		1