

# Jean-François Dufayard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5950015/publications.pdf>

Version: 2024-02-01

18  
papers

18,132  
citations

623734

14  
h-index

713466

21  
g-index

21  
all docs

21  
docs citations

21  
times ranked

30764  
citing authors

#	ARTICLE	IF	CITATIONS
1	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. <i>Systematic Biology</i> , 2010, 59, 307-321.	5.6	15,166
2	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. <i>Systematic Biology</i> , 2011, 60, 685-699.	5.6	912
3	Estimating Maximum Likelihood Phylogenies with PhyML. <i>Methods in Molecular Biology</i> , 2009, 537, 113-137.	0.9	771
4	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	21.4	413
5	Tree pattern matching in phylogenetic trees: automatic search for orthologs or paralogs in homologous gene sequence databases. <i>Bioinformatics</i> , 2005, 21, 2596-2603.	4.1	161
6	The Banana Genome Hub. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat035.	3.0	151
7	Databases of homologous gene families for comparative genomics. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	118
8	Evolutionary Dynamics of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) Subfamily in Angiosperms. <i>Plant Physiology</i> , 2016, 170, 1595-1610.	4.8	114
9	Identification of the <i>Hevea brasiliensis</i> AP2/ERF superfamily by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 30.	2.8	73
10	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 08, 381.	3.6	54
11	Some ethylene biosynthesis and AP2/ERF genes reveal a specific pattern of expression during somatic embryogenesis in <i>Hevea brasiliensis</i> . <i>BMC Plant Biology</i> , 2012, 12, 244.	3.6	43
12	Genomicus in 2022: comparative tools for thousands of genomes and reconstructed ancestors. <i>Nucleic Acids Research</i> , 2022, 50, D1025-D1031.	14.5	39
13	Impact of recurrent gene duplication on adaptation of plant genomes. <i>BMC Plant Biology</i> , 2014, 14, 151.	3.6	32
14	GreenPhylDB v5: a comparative pangenomic database for plant genomes. <i>Nucleic Acids Research</i> , 2021, 49, D1464-D1471.	14.5	22
15	Transcriptional Regulation of Sorghum Stem Composition: Key Players Identified Through Co-expression Gene Network and Comparative Genomics Analyses. <i>Frontiers in Plant Science</i> , 2020, 11, 224.	3.6	17
16	Comprehensive classification of the plant non-specific lipid transfer protein superfamily towards its sequenceâ€“structureâ€“function analysis. <i>PeerJ</i> , 2019, 7, e7504.	2.0	15
17	Badnaviruses and banana genomes: a long association sheds light on <i>Musa</i> phylogeny and origin. <i>Molecular Plant Pathology</i> , 2021, 22, 216-230.	4.2	12
18	RapGreen, an interactive software and web package to explore and analyze phylogenetic trees. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab088.	3.2	2