

# Jean François Dufayard

## List of Publications by Year in descending order

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papers

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35428  
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#	ARTICLE	IF	CITATIONS
1	Genomicus in 2022: comparative tools for thousands of genomes and reconstructed ancestors. <i>Nucleic Acids Research</i> , 2022, 50, D1025-D1031.	14.0	45
2	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.	4.4	13
3	GreenPhylDB v5: a comparative pangenomic database for plant genomes. <i>Nucleic Acids Research</i> , 2021, 49, D1464-D1471.	14.0	25
4	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
5	Correction to "GreenPhylDB v5: a comparative pangenomic database for plant genomes". <i>Nucleic Acids Research</i> , 2021, 49, 7203-7203.	14.0	2
6	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.	3.8	18
7	Comprehensive classification of the plant non-specific lipid transfer protein superfamily towards its sequence-structure-function analysis. <i>PeerJ</i> , 2019, 7, e7504.	2.0	15
8	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 08, 381.	3.8	57
9	Evolutionary Dynamics of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) Subfamily in Angiosperms. <i>Plant Physiology</i> , 2016, 170, 1595-1610.	5.1	118
10	Impact of recurrent gene duplication on adaptation of plant genomes. <i>BMC Plant Biology</i> , 2014, 14, 151.	3.7	32
11	Identification of the <i>Hevea brasiliensis</i> AP2/ERF superfamily by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 30.	2.9	74
12	The Banana Genome Hub. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat035.	3.2	156
13	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.	3.7	44
14	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. <i>Systematic Biology</i> , 2011, 60, 685-699.	6.0	989
15	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. <i>Systematic Biology</i> , 2010, 59, 307-321.	6.0	15,775
16	Databases of homologous gene families for comparative genomics. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.7	120
17	Estimating Maximum Likelihood Phylogenies with PhyML. <i>Methods in Molecular Biology</i> , 2009, 537, 113-137.	0.0	782
18	Tree pattern matching in phylogenetic trees: automatic search for orthologs or paralogs in homologous gene sequence databases. <i>Bioinformatics</i> , 2005, 21, 2596-2603.	4.2	161