Jean-FranÃ§ois Dufayard

List of Publications by Year
in descending order

18	18,132	623734	713466
papers	citations	14	21
		h-index	g-index

21	21	21	30764
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomicus in 2022: comparative tools for thousands of genomes and reconstructed ancestors. Nucleic Acids Research, 2022, 50, D1025-D1031.	14.5	39
2	Badnaviruses and banana genomes: a long association sheds light on Musa phylogeny and origin. Molecular Plant Pathology, 2021, 22, 216-230.	4.2	12
3	GreenPhylDB v5: a comparative pangenomic database for plant genomes. Nucleic Acids Research, 2021, 49, D1464-D1471.	14.5	22
4	RapGreen, an interactive software and web package to explore and analyze phylogenetic trees. NAR Genomics and Bioinformatics, 2021, 3, lqab088.	3.2	2
5	Transcriptional Regulation of Sorghum Stem Composition: Key Players Identified Through Co-expression Gene Network and Comparative Genomics Analyses. Frontiers in Plant Science, 2020, 11, 224.	3.6	17
6	Comprehensive classification of the plant non-specific lipid transfer protein superfamily towards its sequence–structure–function analysis. PeerJ, 2019, 7, e7504.	2.0	15
7	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. Frontiers in Plant Science, 2017, 08, 381.	3.6	54
8	Evolutionary Dynamics of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) Subfamily in Angiosperms. Plant Physiology, 2016, 170, 1595-1610.	4.8	114
9	The genome sequence of the orchid Phalaenopsis equestris. Nature Genetics, 2015, 47, 65-72.	21.4	413
10	Impact of recurrent gene duplication on adaptation of plant genomes. BMC Plant Biology, 2014, 14, 151.	3.6	32
11	Identification of the Hevea brasiliensisAP2/ERF superfamily by RNA sequencing. BMC Genomics, 2013, 14, 30.	2.8	73
12	The Banana Genome Hub. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat035.	3.0	151
13	Some ethylene biosynthesis and AP2/ERF genes reveal a specific pattern of expression during somatic embryogenesis in Hevea brasiliensis. BMC Plant Biology, 2012, 12, 244.	3.6	43
14	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. Systematic Biology, 2011, 60, 685-699.	5.6	912
15	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Systematic Biology, 2010, 59, 307-321.	5.6	15,166
16	Databases of homologous gene families for comparative genomics. BMC Bioinformatics, 2009, 10, S3.	2.6	118
17	Estimating Maximum Likelihood Phylogenies with PhyML. Methods in Molecular Biology, 2009, 537, 113-137.	0.9	771
18	Tree pattern matching in phylogenetic trees: automatic search for orthologs or paralogs in homologous gene sequence databases. Bioinformatics, 2005, 21, 2596-2603.	4.1	161