

JÃ©rÃ©my Just

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7584615/publications.pdf>

Version: 2024-02-01

21
papers

5,813
citations

516710

16
h-index

752698

20
g-index

25
all docs

25
docs citations

25
times ranked

5484
citing authors

#	ARTICLE	IF	CITATIONS
1	The molecular signatures of compatible and incompatible pollination in Arabidopsis. BMC Genomics, 2021, 22, 268.	2.8	9
2	Rosa spp.. Trends in Genetics, 2020, 36, 146-147.	6.7	2
3	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. Plant Cell, 2020, 32, 833-852.	6.6	60
4	Single and multiple gene knockouts by CRISPR-Cas9 in maize. Plant Cell Reports, 2019, 38, 487-501.	5.6	54
5	The development of a high-density genetic map significantly improves the quality of reference genome assemblies for rose. Scientific Reports, 2019, 9, 5985.	3.3	14
6	The Rosa genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	21.4	344
7	A miR172 target-deficient AP2-like gene correlates with the double flower phenotype in roses. Scientific Reports, 2018, 8, 12912.	3.3	51
8	The Rosa chinensis cv. Viridiflora Phyllody Phenotype Is Associated with Misexpression of Flower Organ Identity Genes. Frontiers in Plant Science, 2016, 7, 996.	3.6	17
9	Sixteen cytosolic glutamine synthetase genes identified in the Brassica napus L. genome are differentially regulated depending on nitrogen regimes and leaf senescence. Journal of Experimental Botany, 2014, 65, 3927-3947.	4.8	43
10	Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
11	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. Genome Biology, 2014, 15, R77.	9.6	456
12	A Dominant Point Mutation in a RING E3 Ubiquitin Ligase Homoeologous Gene Leads to Cleistogamy in Brassica napus. Plant Cell, 2013, 24, 4875-4891.	6.6	21
13	Prevalence of gene expression additivity in genetically stable wheat allohexaploids. New Phytologist, 2013, 197, 730-736.	7.3	36
14	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	21.4	1,893
15	Duplication and partitioning in evolution and function of homoeologous Q loci governing domestication characters in polyploid wheat. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18737-18742.	7.1	168
16	Multilevel regulation and signalling processes associated with adaptation to terminal drought in wild emmer wheat. Functional and Integrative Genomics, 2010, 10, 167-186.	3.5	67
17	Impact of transposable elements on the organization and function of allopolyploid genomes. New Phytologist, 2010, 186, 37-45.	7.3	233
18	Genome-wide gene expression changes in genetically stable synthetic and natural wheat allohexaploids. New Phytologist, 2010, 187, 1181-1194.	7.3	100

#	ARTICLE	IF	CITATIONS
19	Dynamics and Differential Proliferation of Transposable Elements During the Evolution of the B and A Genomes of <i>Wheat</i> . <i>Genetics</i> , 2008, 180, 1071-1086.	2.9	123
20	GenoPlante-Info (GPI): a collection of databases and bioinformatics resources for plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 179-182.	14.5	29
21	Production of homozygous rose line derived from heterozygous genotype. <i>Protocol Exchange</i> , 0, , .	0.3	0