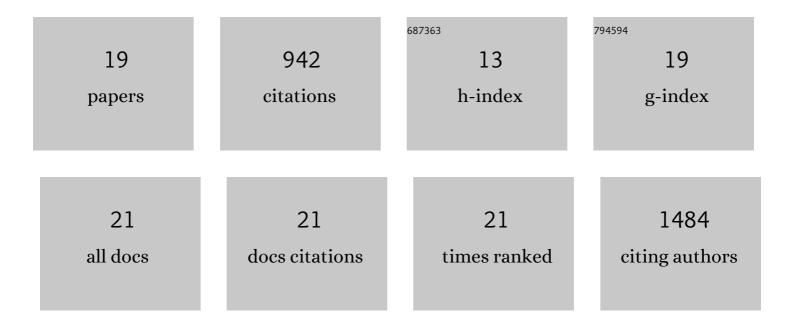
Jean-Michel Michno

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8963562/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	CRISPR/Cas mutagenesis of soybean and Medicago truncatula using a new web-tool and a modified Cas9 enzyme. GM Crops and Food, 2015, 6, 243-252.	3.8	162
2	<scp>CRISPR</scp> /Cas9 and <scp>TALEN</scp> s generate heritable mutations for genes involved in small <scp>RNA</scp> processing of <i>Glycine max</i> and <i>Medicago truncatula</i> . Plant Biotechnology Journal, 2018, 16, 1125-1137.	8.3	147
3	Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. Plant Cell, 2018, 30, 2922-2942.	6.6	137
4	Genetic Architecture of Soybean Yield and Agronomic Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3367-3375.	1.8	98
5	Identical Substitutions in Magnesium Chelatase Paralogs Result in Chlorophyll-Deficient Soybean Mutants. G3: Genes, Genomes, Genetics, 2015, 5, 123-131.	1.8	57
6	Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. BMC Biotechnology, 2016, 16, 41.	3.3	54
7	Genome Resilience and Prevalence of Segmental Duplications Following Fast Neutron Irradiation of Soybean. Genetics, 2014, 198, 967-981.	2.9	53
8	Unraveling gene function in agricultural species using gene co-expression networks. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 53-63.	1.9	47
9	An Induced Chromosomal Translocation in Soybean Disrupts a <i>KASI</i> Ortholog and Is Associated with a High-Sucrose and Low-Oil Seed Phenotype. G3: Genes, Genomes, Genetics, 2017, 7, 1215-1223.	1.8	42
10	Genome Editing in Soybean with CRISPR/Cas9. Methods in Molecular Biology, 2019, 1917, 217-234.	0.9	27
11	MicroRNA Maturation and MicroRNA Target Gene Expression Regulation Are Severely Disrupted in Soybean dicer-like1 Double Mutants. G3: Genes, Genomes, Genetics, 2016, 6, 423-433.	1.8	23
12	Evaluating an interspecific Helianthus annuus×Helianthus tuberosus population for use in a perennial sunflower breeding program. Field Crops Research, 2014, 155, 254-264.	5.1	21
13	Integration, abundance, and transmission of mutations and transgenes in a series of CRISPR/Cas9 soybean lines. BMC Biotechnology, 2020, 20, 10.	3.3	21
14	Identification and Fineâ€Mapping of a Soybean Quantitative Trait Locus on Chromosome 5 Conferring Tolerance to Iron Deficiency Chlorosis. Plant Genome, 2019, 12, 190007.	2.8	14
15	Using multiple reference genomes to identify and resolve annotation inconsistencies. BMC Genomics, 2020, 21, 281.	2.8	10
16	Identification of Candidate Susceptibility Genes to Puccinia graminis f. sp. tritici in Wheat. Frontiers in Plant Science, 2021, 12, 657796.	3.6	10
17	The importance of genotype identity, genetic heterogeneity, and bioinformatic handling for properly assessing genomic variation in transgenic plants. BMC Biotechnology, 2018, 18, 38.	3.3	9
18	A bacterial gene codA encoding cytosine deaminase is an effective conditional negative selectable marker in Glycine max. Plant Cell Reports, 2015, 34, 1707-1716.	5.6	5

#	Article	IF	CITATIONS
19	Identification of nodulationâ€related genes in <i>Medicago truncatula</i> using genomeâ€wide association studies and coâ€expression networks. Plant Direct, 2020, 4, e00220.	1.9	4