Agnieszka A Golicz

List of Publications by Year
in descending order

35 papers	5,019 citations	257450 24 h-index	345221 36 g-index
38 all docs	38 docs citations	38 times ranked	4771 citing authors

#	Article	IF	Citations
1	Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
2	The pangenome of an agronomically important crop plant Brassica oleracea. Nature Communications, 2016, 7, 13390.	12.8	375
3	The pangenome of hexaploid bread wheat. Plant Journal, 2017, 90, 1007-1013.	5.7	313
4	Plant pan-genomes are the new reference. Nature Plants, 2020, 6, 914-920.	9.3	302
5	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus. Plant Biotechnology Journal, 2018, 16, 1265-1274.	8.3	217
6	Towards plant pangenomics. Plant Biotechnology Journal, 2016, 14, 1099-1105.	8.3	203
7	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. Trends in Plant Science, 2020, 25, 148-158.	8.8	177
8	Assembly and comparison of two closely related Brassica napus genomes. Plant Biotechnology Journal, 2017, 15, 1602-1610.	8.3	150
9	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. Trends in Genetics, 2020, 36, 132-145.	6.7	137
10	Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome. Plant Biotechnology Journal, 2019, 17, 789-800.	8.3	92
11	The Genome of a Southern Hemisphere Seagrass Species (Zostera muelleri). Plant Physiology, 2016, 172, 272-283.	4.8	88
12	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. Plant Physiology, 2018, 176, 2133-2147.	4.8	88
13	lncRNAs in Plant and Animal Sexual Reproduction. Trends in Plant Science, 2018, 23, 195-205.	8.8	82
14	Insight into the evolution and functional characteristics of the panâ€genome assembly from sesame landraces and modern cultivars. Plant Biotechnology Journal, 2019, 17, 881-892.	8.3	79
15	Trait associations in the pangenome of pigeon pea (Cajanus cajan). Plant Biotechnology Journal, 2020, 18, 1946-1954.	8.3	79
16	Gene loss in the fungal canola pathogen Leptosphaeria maculans. Functional and Integrative Genomics, 2015, 15, 189-196.	3.5	50
17	Genome-wide survey of the seagrass Zostera muelleri suggests modification of the ethylene signalling network. Journal of Experimental Botany, 2015, 66, 1489-1498.	4.8	46
18	Global Role of Crop Genomics in the Face of Climate Change. Frontiers in Plant Science, 2020, 11, 922.	3.6	45

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19	Genome-wide analysis of the Hsf gene family in Brassica oleracea and a comparative analysis of the Hsf gene family in B. oleracea, B. rapa and B. napus. Functional and Integrative Genomics, 2019, 19, 515-531.	3.5	44
20	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. Plant Biotechnology Journal, 2021, 19, 2488-2500.	8.3	44
21	An investigation of causes of false positive single nucleotide polymorphisms using simulated reads from a small eukaryote genome. BMC Bioinformatics, 2015, 16, 382.	2.6	42
22	The emergence of molecular profiling and omics techniques in seagrass biology; furthering our understanding of seagrasses. Functional and Integrative Genomics, 2016, 16, 465-480.	3.5	41
23	Skim-Based Genotyping by Sequencing. Methods in Molecular Biology, 2015, 1245, 257-270.	0.9	39
24	Pangenomics in crop improvementâ€"from coding structural variations to finding regulatory variants with pangenome graphs. Plant Genome, 2022, 15, e20177.	2.8	33
25	On the Role of Transposable Elements in the Regulation of Gene Expression and Subgenomic Interactions in Crop Genomes. Critical Reviews in Plant Sciences, 2021, 40, 157-189.	5.7	28
26	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. Journal of Experimental Botany, 2018, 69, 3689-3702.	4.8	27
27	An efficient approach to BAC based assembly of complex genomes. Plant Methods, 2016, 12, 2.	4.3	22
28	Analysis of the quinoa genome reveals conservation and divergence of the flowering pathways. Functional and Integrative Genomics, 2020, 20, 245-258.	3.5	22
29	Rice 3D chromatin structure correlates with sequence variation and meiotic recombination rate. Communications Biology, 2020, 3, 235.	4.4	18
30	A dynamic intron retention program regulates the expression of several hundred genes during pollen meiosis. Plant Reproduction, 2021, 34, 225-242.	2.2	17
31	MCRiceRepGP: a framework for the identification of genes associated with sexual reproduction in rice. Plant Journal, 2018, 96, 188-202.	5.7	13
32	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. Methods in Molecular Biology, 2020, 2107, 35-47.	0.9	7
33	An SGSGeneloss-Based Method for Constructing a Gene Presenceâ€"Absence Table Using Mosdepth. Methods in Molecular Biology, 2022, , 73-80.	0.9	3
34	Method for Genome-Wide Association Study: A Soybean Example. Methods in Molecular Biology, 2020, 2107, 147-158.	0.9	2
35	Grain dispersal mechanism in cereals arose from a genome duplication followed by changes in spatial expression of genes involved in pollen development. Theoretical and Applied Genetics, 2022, 135, 1263-1277.	3.6	1