

Agnieszka A Golicz

List of Publications by Year in descending order

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Version: 2024-02-01

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	Grain dispersal mechanism in cereals arose from a genome duplication followed by changes in spatial expression of genes involved in pollen development. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1263-1277.	3.6	1
2	Pangenomics in crop improvement—“from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	2.8	33
3	An SCSSGeneLoss-Based Method for Constructing a Gene Presence–Absence Table Using Mosdepth. <i>Methods in Molecular Biology</i> , 2022, , 73-80.	0.9	3
4	On the Role of Transposable Elements in the Regulation of Gene Expression and Subgenomic Interactions in Crop Genomes. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 157-189.	5.7	28
5	A dynamic intron retention program regulates the expression of several hundred genes during pollen meiosis. <i>Plant Reproduction</i> , 2021, 34, 225-242.	2.2	17
6	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.3	44
7	Analysis of the quinoa genome reveals conservation and divergence of the flowering pathways. <i>Functional and Integrative Genomics</i> , 2020, 20, 245-258.	3.5	22
8	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. <i>Trends in Genetics</i> , 2020, 36, 132-145.	6.7	137
9	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020, 25, 148-158.	8.8	177
10	Plant pan-genomes are the new reference. <i>Nature Plants</i> , 2020, 6, 914-920.	9.3	302
11	Global Role of Crop Genomics in the Face of Climate Change. <i>Frontiers in Plant Science</i> , 2020, 11, 922.	3.6	45
12	Rice 3D chromatin structure correlates with sequence variation and meiotic recombination rate. <i>Communications Biology</i> , 2020, 3, 235.	4.4	18
13	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	8.3	79
14	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. <i>Methods in Molecular Biology</i> , 2020, 2107, 35-47.	0.9	7
15	Method for Genome-Wide Association Study: A Soybean Example. <i>Methods in Molecular Biology</i> , 2020, 2107, 147-158.	0.9	2
16	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , 2019, 17, 789-800.	8.3	92
17	Genome-wide analysis of the Hsf gene family in <i>Brassica oleracea</i> and a comparative analysis of the Hsf gene family in <i>B. oleracea</i> , <i>B. rapa</i> and <i>B. napus</i> . <i>Functional and Integrative Genomics</i> , 2019, 19, 515-531.	3.5	44
18	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019, 17, 881-892.	8.3	79

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19	lncRNAs in Plant and Animal Sexual Reproduction. Trends in Plant Science, 2018, 23, 195-205.	8.8	82
20	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. Plant Physiology, 2018, 176, 2133-2147.	4.8	88
21	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. Journal of Experimental Botany, 2018, 69, 3689-3702.	4.8	27
22	MCRiceRepGP: a framework for the identification of genes associated with sexual reproduction in rice. Plant Journal, 2018, 96, 188-202.	5.7	13
23	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . Plant Biotechnology Journal, 2018, 16, 1265-1274.	8.3	217
24	The pangenome of hexaploid bread wheat. Plant Journal, 2017, 90, 1007-1013.	5.7	313
25	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. Plant Biotechnology Journal, 2017, 15, 1602-1610.	8.3	150
26	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). Plant Physiology, 2016, 172, 272-283.	4.8	88
27	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
28	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . Nature Communications, 2016, 7, 13390.	12.8	375
29	An efficient approach to BAC based assembly of complex genomes. Plant Methods, 2016, 12, 2.	4.3	22
30	Towards plant pangenomics. Plant Biotechnology Journal, 2016, 14, 1099-1105.	8.3	203
31	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
32	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. Journal of Experimental Botany, 2015, 66, 1489-1498.	4.8	46
33	Gene loss in the fungal canola pathogen <i>Leptosphaeria maculans</i> . Functional and Integrative Genomics, 2015, 15, 189-196.	3.5	50
34	Skim-Based Genotyping by Sequencing. Methods in Molecular Biology, 2015, 1245, 257-270.	0.9	39
35	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089