

GAPIT Version 3: Boosting Power and Accuracy for Gen

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genome-wide association mapping of <i>Pyrenophora teres</i> f. <i>maculata</i> and <i>Pyrenophora teres</i> f. <i>teres</i> resistance loci utilizing natural Turkish wild and landrace barley populations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
2	Eagle for better genome-wide association mapping. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
3	Genome-wide association studies of mineral and phytic acid concentrations in pea (<i>Pisum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.8	9
4	Genome-wide analysis reveals demographic and life-history patterns associated with habitat modification in landlocked, deep-spawning sockeye salmon (<i>Oncorhynchus nerka</i>). <i>Ecology and Evolution</i> , 2021, 11, 13186-13205.	0.8	2
5	Interactions of the barley <i>SD1</i> and <i>SD2</i> seed dormancy loci influence preharvest sprouting, seed dormancy, and malting quality. <i>Crop Science</i> , 2022, 62, 120-138.	0.8	5
6	Evaluations of Genomic Prediction and Identification of New Loci for Resistance to Stripe Rust Disease in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 710485.	1.1	9
8	Genome-wide association mapping and genomic prediction for adult stage sclerotinia stem rot resistance in <i>Brassica napus</i> (L) under field environments. <i>Scientific Reports</i> , 2021, 11, 21773.	1.6	21
9	Genomic Regions Associated with Fusarium Wilt Resistance in Flax. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12383.	1.8	10
10	Understanding Heterosis, Genetic Effects, and Genome Wide Associations for Forage Quantity and Quality Traits in Multi-Cut Pearl Millet. <i>Frontiers in Plant Science</i> , 2021, 12, 687859.	1.7	3
11	Genome-wide association study reveals white lupin candidate gene involved in anthracnose resistance. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	1.8	4
12	Genome-wide superior alleles, haplotypes and candidate genes associated with tolerance on sodic-dispersive soils in wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 1113-1128.	1.8	3
13	Genomic footprints of sorghum domestication and breeding selection for multiple end uses. <i>Molecular Plant</i> , 2022, 15, 537-551.	3.9	15
14	Genome-wide association study of cassava starch paste properties. <i>PLoS ONE</i> , 2022, 17, e0262888.	1.1	3
15	Genome Assembly of Alfalfa Cultivar Zhongmu-4 and Identification of SNPs Associated with Agronomic Traits. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 14-28.	3.0	26
16	Unraveling the complex genetic basis of growth in New Zealand silver trevally (<i>Pseudocaranx</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	0.8	8
18	Insights Into the Genetic Architecture of Complex Traits in Napier Grass (<i>Cenchrus purpureus</i>) and QTL Regions Governing Forage Biomass Yield, Water Use Efficiency and Feed Quality Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 678862.	1.7	12
19	Pilot scale genome wide association mapping identified novel loci for grain yield traits in rice. <i>Plant Physiology Reports</i> , 2022, 27, 11-21.	0.7	1
20	Single Nucleotide Polymorphism Detection for Peach Gummosis Disease Resistance by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2021, 12, 763618.	1.7	4

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22	Identification of the Potential Genes Regulating Seed Germination Speed in Maize. <i>Plants</i> , 2022, 11, 556.	1.6	4
23	Evaluation of Methods for Measuring Fusarium-Damaged Kernels of Wheat. <i>Agronomy</i> , 2022, 12, 532.	1.3	6
24	Epigenomics as a paradigm to understand the nuances of phenotypes. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	7
25	Genome-Wide Association Study for Resistance to <i>Rhynchosporium</i> in a Diverse Collection of Spring Barley Germplasm. <i>Agronomy</i> , 2022, 12, 782.	1.3	2
26	GWAS for Stripe Rust Resistance in Wild Emmer Wheat (<i>Triticum dicoccoides</i>) Population: Obstacles and Solutions. <i>Crops</i> , 2022, 2, 42-61.	0.6	7
27	Genome-wide association study and genomic prediction of white rust resistance in USDA GRIN spinach germplasm. <i>Horticulture Research</i> , 2022, 9, .	2.9	16
28	XSim version 2: simulation of modern breeding programs. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
29	Genome-Wide Association Studies Provide Insight Into the Genetic Determination for Hyperpigmentation of the Visceral Peritoneum in Broilers. <i>Frontiers in Genetics</i> , 2022, 13, 820297.	1.1	1
30	Unraveling the Genetic Basis of Key Agronomic Traits of Wrinkled Vining Pea (<i>Pisum sativum</i> L.) for Sustainable Production. <i>Frontiers in Plant Science</i> , 2022, 13, 844450.	1.7	6
31	GWAS for main effects and epistatic interactions for grain morphology traits in wheat. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 651-668.	1.4	6
33	Detection of Breeding-Relevant Fruit Cracking and Fruit Firmness Quantitative Trait Loci in Sweet Cherry via Pedigree-Based and Genome-Wide Association Approaches. <i>Frontiers in Plant Science</i> , 2022, 13, 823250.	1.7	5
34	Identification of Secreted Protein Gene-Based SNP Markers Associated with Virulence Phenotypes of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Wheat Stripe Rust Pathogen. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4114.	1.8	3
35	Trend, population structure, and trait mapping from 15 years of national varietal trials of UK winter wheat. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
36	Mapping maize chlorotic mottle virus tolerance loci in the Maize 282 Association Panel. <i>Crop Science</i> , 2022, 62, 1497-1510.	0.8	3
37	Genetic mapping and genomic prediction of sclerotinia stem rot resistance to rapeseed/canola (<i>Brassica napus</i> L.) at seedling stage. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2167-2184.	1.8	5
38	Genomic selection applications can improve the environmental performance of aquatics: A case study on the heat tolerance of abalone. <i>Evolutionary Applications</i> , 2022, 15, 992-1001.	1.5	17
39	Genetic analysis of resistance to bean leaf crumple virus identifies a candidate <i>LRR-ERLK</i> gene. <i>Plant Journal</i> , 2023, 114, 23-38.	2.8	4
40	Dissecting the Genetic Architecture of Carbon Partitioning in Sorghum Using Multiscale Phenotypes. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7

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41	Phenotypic variation and genome-wide association studies of main culm panicle node number, maximum node production rate, and degree-days to heading in rice. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
42	ATP-dependent DNA helicase (TaDHL), a Novel Reduced-Height (Rht) Gene in Wheat. <i>Genes</i> , 2022, 13, 979.	1.0	8
43	A genome-wide association study unveils key chromosome regions involved in determining sodium accumulation in wheat under conditions of low potassium supply. <i>Journal of Plant Physiology</i> , 2022, 275, 153739.	1.6	2
45	Genome-wide association mapping of resistance to the sorghum aphid in <i>Sorghum bicolor</i> . <i>Genomics</i> , 2022, 114, 110408.	1.3	7
46	Recombination Landscape Divergence Between Populations is Marked by Larger Low-Recombining Regions in Domesticated Rye. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
48	Genome-wide association analysis of heat tolerance in the northern pike (<i>Esox Lucius</i>). <i>Aquaculture</i> , 2022, 559, 738459.	1.7	4
49	Genome-wide association study identified candidate SNPs and genes associated with hypoxia tolerance in large yellow croaker (<i>Larimichthys crocea</i>). <i>Aquaculture</i> , 2022, 560, 738472.	1.7	7
50	Population Genomics and Haplotype Analysis in Bread Wheat Identify a Gene Regulating Glume Pubescence. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
52	Genetic basis underlying tiller angle in rice (<i>Oryza sativa</i> L.) by genome-wide association study. <i>Plant Cell Reports</i> , 0, , .	2.8	4
53	Genomic Regions Associated With Seed Meal Quality Traits in <i>Brassica napus</i> Germplasm. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
54	Multi-Locus Genome-Wide Association Studies to Characterize Fusarium Head Blight (FHB) Resistance in Hard Winter Wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
55	Genetic dissection of grain iron and zinc, and thousand kernel weight in wheat (<i>Triticum aestivum</i> L.) using genome-wide association study. <i>Scientific Reports</i> , 2022, 12, .	1.6	13
56	Genome-Wide Association Study of Body Weight Trait in Yaks. <i>Animals</i> , 2022, 12, 1855.	1.0	4
57	Genome-Wide Association Study of Leaf Rust and Stem Rust Seedling and Adult Resistances in Tetraploid Wheat Accessions Harvested in Kazakhstan. <i>Plants</i> , 2022, 11, 1904.	1.6	4
60	Genetic dissection of nitrogen induced changes in the shoot and root biomass of spinach. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
62	Whole-genome analysis of hard winter wheat germplasm identifies genomic regions associated with spike and kernel traits. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2953-2967.	1.8	7
63	Genome-wide association study for grain yield and component traits in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	1.1	16
66	Genomic selection with fixed-effect markers improves the prediction accuracy for Capsaicinoid contents in <i>Capsicum annuum</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	6

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67	Genome-Wide Association Study (GWAS) Reveals an SNP Associated with Waxy Trait and Development of a Functional Marker for Predicting Waxy Maize (<i>Zea mays</i> L. var. <i>ceratina</i>). <i>Agronomy</i> , 2022, 12, 2289.	1.3	1
68	Separation of the effects of two reduced height (<i>Rht</i>) genes and genomic background to select for less Fusarium head blight of short-strawed winter wheat (<i>Triticum aestivum</i> L.) varieties. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4303-4326.	1.8	4
69	Resequencing worldwide spinach germplasm for identification of field resistance QTLs to downy mildew and assessment of genomic selection methods. <i>Horticulture Research</i> , 2022, 9, .	2.9	2
70	Exploring genetic diversity of wild and related tetraploid wheat species <i>Triticum turgidum</i> and <i>Triticum timopheevii</i> . <i>Journal of Advanced Research</i> , 2023, 48, 47-60.	4.4	4
71	How can we breed for phosphate efficiency in maize (<i>Zea mays</i>)?. <i>Plant Breeding</i> , 0, , .	1.0	0
72	Genome-wide association mapping of septoria nodorum blotch resistance in Nordic winter and spring wheat collections. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4169-4182.	1.8	8
75	High-quality chromosome-scale genomes facilitate effective identification of large structural variations in hot and sweet peppers. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
76	Worldwide Selection Footprints for Drought and Heat in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Plants</i> , 2022, 11, 2289.	1.6	4
77	Mapping and selection of downy mildew resistance in spinach cv. whale by low coverage whole genome sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
78	High-resolution genome-wide association study of a large Czech collection of sweet cherry (<i>Prunus avium</i> L.) on fruit maturity and quality traits. <i>Horticulture Research</i> , 2023, 10, .	2.9	3
79	Deep learning-based phenotyping for genome wide association studies of sudden death syndrome in soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
80	Focusing the GWAS <i>Lens</i> on days to flower using latent variable phenotypes derived from global multienvironment trials. <i>Plant Genome</i> , 0, , .	1.6	1
81	A family of methyl esterases converts methyl salicylate to salicylic acid in ripening tomato fruit. <i>Plant Physiology</i> , 2023, 191, 110-124.	2.3	4
83	Determination of traits responding to iron toxicity stress at different stages and genome-wide association analysis for iron toxicity tolerance in rice (<i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
84	Genome-wide association mapping of seed oligosaccharides in chickpea. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
86	N6-methyladenosine RNA modification promotes viral genomic RNA stability and infection. <i>Nature Communications</i> , 2022, 13, .	5.8	18
87	Genomic prediction of tocochromanols in exotic-derived maize. <i>Plant Genome</i> , 2023, 16, .	1.6	3
88	Rice Pangenome Array (<i>RPCA</i>): an efficient genotyping solution for pangenome-based accelerated crop improvement in rice. <i>Plant Journal</i> , 0, , .	2.8	5

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90	Genetic Dissection of Phosphorus Use Efficiency and Genotype-by-Environment Interaction in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13943.	1.8	4
91	Identification of Genomic Loci Controlling Grain Macro and Micronutrient Variation in a Wild Barley (<i>Hordeum vulgare</i> spp. <i>spontaneum</i>) Diversity Panel. <i>Agronomy</i> , 2022, 12, 2839.	1.3	2
93	Novel Single-Nucleotide Variants for Morpho-Physiological Traits Involved in Enhancing Drought Stress Tolerance in Barley. <i>Plants</i> , 2022, 11, 3072.	1.6	2
94	Identification of a QTL region for ashy stem blight resistance using genome-wide association and lineage analysis in common bean recombinant inbred lines derived from BAT 477 and NY6020-4. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
95	Genomic basis of the giga-chromosomes and giga-genome of tree peony <i>Paeonia ostii</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	16
96	Genetic Determinants of Fiber-Associated Traits in Flax Identified by Omics Data Integration. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14536.	1.8	2
97	TeaGVD: A comprehensive database of genomic variations for uncovering the genetic architecture of metabolic traits in tea plants. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
98	Genome-wide association study for resistance in bread wheat (<i>Triticum aestivum</i> L.) to stripe rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) races in Argentina. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	4
99	A multi-reference parent nested-association mapping population to dissect the genetics of quantitative traits in durum wheat. <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 1471-1485.	0.8	4
100	Genome wide association studies for acid phosphatase activity at varying phosphorous levels in <i>Brassica juncea</i> L. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
101	Genome-wide association study reveals novel genomic regions governing agronomic and grain quality traits and superior allelic combinations for Basmati rice improvement. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
102	Graph-based pangenomics maximizes genotyping density and reveals structural impacts on fungal resistance in melon. <i>Nature Communications</i> , 2022, 13, .	5.8	7
103	Exome-wide variation in a diverse barley panel reveals genetic associations with ten agronomic traits in Eastern landraces. <i>Journal of Genetics and Genomics</i> , 2023, 50, 241-252.	1.7	2
106	Distinct genomic loci underlie quantitative resistance to <i>Meloidogyne enterolobii</i> galling and reproduction in <i>Citrullus amarus</i> . <i>Plant Disease</i> , 0, , .	0.7	0
107	AgroGenome: Interactive Genomic-Based Web Server Developed Based on Data Collected for Accessions Stored in Polish Genebank. <i>Agriculture (Switzerland)</i> , 2023, 13, 193.	1.4	2
108	An integrated genomic and biochemical approach to investigate the potentiality of heirloom tomatoes: Breeding resources for food quality and sustainable agriculture. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
109	Genetics of spot blotch resistance in bread wheat (<i>Triticum aestivum</i> L.) using five models for GWAS. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
110	Genome-wide association study of yield-related traits in common wheat (<i>Triticum aestivum</i> L.) under normal and drought treatment conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5

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111	Multiomics Based Association Mapping in Wheat Reveals Genetic Architecture of Quality and Allergenic Related Proteins. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1485.	1.8	1
112	Genome-Wide Association Study of Arabinoxylan Content from a 562 Hexaploid Wheat Collection. <i>Plants</i> , 2023, 12, 184.	1.6	3
113	Dissecting the genetic architecture of leaf morphology traits in mungbean (<i>Vigna radiata</i> (L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	1.8	7
116	Wild barley (<i>Hordeum spontaneum</i>) and landraces (<i>Hordeum vulgare</i>) from Turkey contain an abundance of novel <i>Rhynchosporium commune</i> resistance loci. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	0
117	Marker-trait association analyses revealed major novel QTLs for grain yield and related traits in durum wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
118	Genome-wide association and genomic prediction for resistance to southern corn rust in DH and testcross populations. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
119	Genome-wide association analyses of leaf rust resistance in cultivated emmer wheat. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	1
120	Detection of the local adaptive and genome-wide associated loci in southeast Nigerian taro (<i>Colocasia esculenta</i> (L.) Schott) populations. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
121	White Lupin Drought Tolerance: Genetic Variation, Trait Genetic Architecture, and Genome-Enabled Prediction. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2351.	1.8	2
122	Candidate genes affecting stomatal density in rice (<i>Oryza sativa</i> L.) identified by genome-wide association. <i>Plant Science</i> , 2023, 330, 111624.	1.7	3
123	QTL and Candidate Genes for Flax Disease Resistance. <i>Compendium of Plant Genomes</i> , 2023, , 121-148.	0.3	1
124	Genome-wide association study identifies 12 new genetic loci associated with growth traits in pigs. <i>Journal of Integrative Agriculture</i> , 2024, 23, 217-227.	1.7	1
125	White Lupin Adaptation to Moderately Calcareous Soils: Phenotypic Variation and Genome-Enabled Prediction. <i>Plants</i> , 2023, 12, 1139.	1.6	0
128	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. <i>Nature Communications</i> , 2023, 14, .	5.8	10
130	Identification of leaf rust resistance loci in a geographically diverse panel of wheat using genome-wide association analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
131	Association mapping unravels the genetics controlling seedling drought stress tolerance in winter wheat. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
132	Genome-wide association analysis and validation with KASP markers for nut and shell traits in almond (<i>Prunus dulcis</i> [Mill.] D.A.Webb). <i>Tree Genetics and Genomes</i> , 2023, 19, .	0.6	5
133	The broad use of the Pm8 resistance gene in wheat resulted in hypermutation of the AvrPm8 gene in the powdery mildew pathogen. <i>BMC Biology</i> , 2023, 21, .	1.7	11

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134	Effects of genetic components of plant development on yield-related traits in wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742	1.7	0
135	Development and characterization of a sorghum multi-parent advanced generation intercross (MAGIC) population for capturing diversity among seed parent gene pool. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
136	Multiple-model GWAS identifies optimal allelic combinations of quantitative trait loci for malic acid in tomato. <i>Horticulture Research</i> , 2023, 10, .	2.9	2
137	Identification of candidate genes for LepR1 resistance against <i>Leptosphaeria maculans</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
138	The genetic architecture of soybean photothermal adaptation to high latitudes. <i>Journal of Experimental Botany</i> , 2023, 74, 2987-3002.	2.4	2
141	QTL Mapping: Strategy, Progress, and Prospects in Flax. <i>Compendium of Plant Genomes</i> , 2023, , 69-99.	0.3	0
142	Heritability and gene functions associated with sclerotia formation of <i>Rhizoctonia solani</i> AG-7 using whole genome sequencing and genome-wide association study. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
143	Genome-Wide Association Study for Grain Protein, Thousand Kernel Weight, and Normalized Difference Vegetation Index in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Genes</i> , 2023, 14, 637.	1.0	2
144	A Genome-Wide Association Study to Identify Novel Candidate Genes Related to Low-Nitrogen Tolerance in Cucumber (<i>Cucumis sativus</i> L.). <i>Genes</i> , 2023, 14, 662.	1.0	0
145	Genome-Wide Association Analysis of Grain Hardness in Common Wheat. <i>Genes</i> , 2023, 14, 672.	1.0	1
146	The Allele Catalog Tool: a web-based interactive tool for allele discovery and analysis. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
147	Genetic architecture of rust resistance in a wheat (<i>Triticum turgidum</i>) diversity panel. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
149	Genomics-driven breeding for local adaptation of durum wheat is enhanced by farmersâ€™ traditional knowledge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
150	Preselection of QTL markers enhances accuracy of genomic selection in Norway spruce. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
151	A translome-transcriptome multi-omics gene regulatory network reveals the complicated functional landscape of maize. <i>Genome Biology</i> , 2023, 24, .	3.8	8
153	Genome-wide association study in two-row spring barley landraces identifies QTL associated with plantlets root system architecture traits in well-watered and osmotic stress conditions. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
154	Genome-Wide Association Study on Reproductive Traits Using Imputation-Based Whole-Genome Sequence Data in Yorkshire Pigs. <i>Genes</i> , 2023, 14, 861.	1.0	3
155	CT-Based Phenotyping and Genome-Wide Association Analysis of the Internal Structure and Components of Maize Kernels. <i>Agronomy</i> , 2023, 13, 1078.	1.3	0

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156	Skim resequencing finely maps the downy mildew resistance loci in spinach cultivars Whale and Lazio. Horticulture Research, 0, , .	2.9	0
158	Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. Theoretical and Applied Genetics, 2023, 136, .	1.8	4
159	Re-sequencing and transcriptomic analysis reveal differential expression patterns and sequence variation in glucosyltransferase gene related to anthocyanin biosynthesis in walnut (Juglans regia) Tj ETQq0 0 0 rgBT/Overlook 10 Tf 50		