

# GAPIT Version 2: An Enhanced Integrated Tool for Genomics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw064.	3.2	15
2	Association mapping utilizing diverse barley lines reveals net form net blotch seedling resistance/susceptibility loci. <i>Theoretical and Applied Genetics</i> , 2017, 130, 915-927.	1.8	37
3	A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. <i>Horticulture Research</i> , 2017, 4, 17017.	2.9	41
4	From Hype to Hope: Genome-Wide Association Studies in Soybean. <i>Compendium of Plant Genomes</i> , 2017, , 95-109.	0.3	0
5	Characterization of Insect Resistance Loci in the USDA Soybean Germplasm Collection Using Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2017, 8, 670.	1.7	53
6	Genome-Wide Association Study Reveals Novel Genes Associated with Culm Cellulose Content in Bread Wheat ( <i>Triticum aestivum</i> , L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1913.	1.7	19
7	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	3.8	363
8	Genetic variation and population structure of maize inbred lines adapted to the mid-altitude sub-humid maize agro-ecology of Ethiopia using single nucleotide polymorphic (SNP) markers. <i>BMC Genomics</i> , 2017, 18, 777.	1.2	36
9	Exploring the potential and limitations of genotyping-by-sequencing for SNP discovery and genotyping in tetraploid potato. <i>Genome</i> , 2018, 61, 449-456.	0.9	31
10	Genome-wide association study of rice grain width variation. <i>Genome</i> , 2018, 61, 233-240.	0.9	7
11	Genome-wide association study and candidate gene analysis of rice cadmium accumulation in grain in a diverse rice collection. <i>Rice</i> , 2018, 11, 61.	1.7	74
12	TRCMGene: A two-step referential compression method for the efficient storage of genetic data. <i>PLoS ONE</i> , 2018, 13, e0206521.	1.1	2
13	Biotechnological and Digital Revolution for Climate-Smart Plant Breeding. <i>Agronomy</i> , 2018, 8, 277.	1.3	58
14	Four Parent Maize (FPM) Population: Effects of Mating Designs on Linkage Disequilibrium and Mapping Quantitative Traits. <i>Plant Genome</i> , 2018, 11, 170102.	1.6	21
15	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018, 121, 648-662.	1.2	53
16	Association mapping in rice: basic concepts and perspectives for molecular breeding. <i>Plant Production Science</i> , 2018, 21, 159-176.	0.9	28
17	Evaluation of the Potential for Genomic Selection to Improve Spring Wheat Resistance to Fusarium Head Blight in the Pacific Northwest. <i>Frontiers in Plant Science</i> , 2018, 9, 911.	1.7	50
18	A Genome-Wide Association Study of Field and Seedling Response to Individual Stem Rust Pathogen Races Reveals Combinations of Race-Specific Genes in North American Spring Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 52.	1.7	66

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19	Genome-Wide Association Mapping for Tolerance to Preharvest Sprouting and Low Falling Numbers in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 141.	1.7	62
20	Investigating Drought Tolerance in Chickpea Using Genome-Wide Association Mapping and Genomic Selection Based on Whole-Genome Resequencing Data. <i>Frontiers in Plant Science</i> , 2018, 9, 190.	1.7	111
21	Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 271.	1.7	43
22	Genotyping of Soybean Cultivars With Medium-Density Array Reveals the Population Structure and QTNs Underlying Maturity and Seed Traits. <i>Frontiers in Plant Science</i> , 2018, 9, 610.	1.7	34
23	Genome-wide Association Study of Agronomic Traits in a Spring-planted North American Elite Hard Red Spring Wheat Panel. <i>Crop Science</i> , 2018, 58, 1838-1852.	0.8	29
24	Genome-Wide Association Study for Spot Blotch Resistance in Hard Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 926.	1.7	77
25	Genetic characterization of inbred lines from Shaan A and B groups for identifying loci associated with maize grain yield. <i>BMC Genetics</i> , 2018, 19, 63.	2.7	28
26	Genome-Wide Association Studies for Dynamic Plant Height and Number of Nodes on the Main Stem in Summer Sowing Soybeans. <i>Frontiers in Plant Science</i> , 2018, 9, 1184.	1.7	67
27	Genome-wide association across <i>Saccharomyces cerevisiae</i> strains reveals substantial variation in underlying gene requirements for toxin tolerance. <i>PLoS Genetics</i> , 2018, 14, e1007217.	1.5	48
28	Genome resequencing of the orange-spotted grouper ( <i>Epinephelus coioides</i> ) for a genome-wide association study on ammonia tolerance. <i>Aquaculture</i> , 2019, 512, 734332.	1.7	24
29	Genome-wide association study and genomic prediction analyses of drought stress tolerance in China in a collection of off-PVP maize inbred lines. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	17
30	Local adaptation drives the diversification of effectors in the fungal wheat pathogen <i>Parastagonospora nodorum</i> in the United States. <i>PLoS Genetics</i> , 2019, 15, e1008223.	1.5	66
31	Last-Generation Genome-Environment Associations Reveal the Genetic Basis of Heat Tolerance in Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Frontiers in Genetics</i> , 2019, 10, 954.	1.1	73
32	CWAS-Assisted Genomic Prediction to Predict Resistance to <i>Septoria tritici</i> Blotch in Nordic Winter Wheat at Seedling Stage. <i>Frontiers in Genetics</i> , 2019, 10, 1224.	1.1	41
33	A Study of Genomic Prediction of 12 Important Traits in the Domesticated Yak ( <i>Bos grunniens</i> ). <i>Animals</i> , 2019, 9, 927.	1.0	3
34	Mining and genomic characterization of resistance to tan spot, <i>Stagonospora nodorum</i> blotch (SNB), and <i>Fusarium</i> head blight in Watkins core collection of wheat landraces. <i>BMC Plant Biology</i> , 2019, 19, 480.	1.6	23
35	Evaluation of a global spring wheat panel for stripe rust: Resistance loci validation and novel resources identification. <i>PLoS ONE</i> , 2019, 14, e0222755.	1.1	21
36	Genomics of Plant Disease Resistance in Legumes. <i>Frontiers in Plant Science</i> , 2019, 10, 1345.	1.7	27

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37	Unraveling the genetic architecture for carbon and nitrogen related traits and leaf hydraulic conductance in soybean using genome-wide association analyses. <i>BMC Genomics</i> , 2019, 20, 811.	1.2	10
38	Genome Wide Association Study and Genomic Selection of Amino Acid Concentrations in Soybean Seeds. <i>Frontiers in Plant Science</i> , 2019, 10, 1445.	1.7	31
39	Deciphering of the Genetic Control of Phenology, Yield, and Pellicle Color in Persian Walnut ( <i>Juglans</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	34
40	Genetic loci and candidate genes of symbiotic nitrogen fixation-related characteristics revealed by a genome-wide association study in soybean. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
41	Training population selection and use of fixed effects to optimize genomic predictions in a historical USA winter wheat panel. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1247-1261.	1.8	78
42	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	1.7	66
43	A Large-Scale Genome-Wide Association Analyses of Ethiopian Sorghum Landrace Collection Reveal Loci Associated With Important Traits. <i>Frontiers in Plant Science</i> , 2019, 10, 691.	1.7	55
44	Genome-wide association mapping in a diverse spring barley collection reveals the presence of QTL hotspots and candidate genes for root and shoot architecture traits at seedling stage. <i>BMC Plant Biology</i> , 2019, 19, 216.	1.6	40
45	Genome-wide association study (GWAS) of leaf cuticular wax components in <i>Camelina sativa</i> identifies genetic loci related to intracellular wax transport. <i>BMC Plant Biology</i> , 2019, 19, 187.	1.6	22
46	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	9.4	219
47	Association mapping in common bean revealed regions associated with Anthracnose and Angular Leaf Spot resistance. <i>Scientia Agricola</i> , 2019, 76, 321-327.	0.6	18
48	Disease Resistance Genetics and Genomics in Octoploid Strawberry. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3315-3332.	0.8	26
49	Genome-Wide Association Mapping for Agronomic and Seed Quality Traits of Field Pea ( <i>Pisum sativum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	83
50	Genome-wide association mapping of total antioxidant capacity, phenols, tannins, and flavonoids in a panel of <i>Sorghum bicolor</i> and <i>S. bicolor</i> A— <i>S. halepense</i> populations using multi-locus models. <i>PLoS ONE</i> , 2019, 14, e0225979.	1.1	22
51	BLINK: a package for the next level of genome-wide association studies with both individuals and markers in the millions. <i>GigaScience</i> , 2019, 8, .	3.3	314
52	Discovering new alleles for yellow spot resistance in the Vavilov wheat collection. <i>Theoretical and Applied Genetics</i> , 2019, 132, 149-162.	1.8	21
53	Strong temporal dynamics of QTL action on plant growth progression revealed through high-throughput phenotyping in canola. <i>Plant Biotechnology Journal</i> , 2020, 18, 68-82.	4.1	45
54	Population Structure of the World Vegetable Center Mungbean Mini Core Collection and Genome-Wide Association Mapping of Loci Associated with Variation of Seed Coat Luster. <i>Tropical Plant Biology</i> , 2020, 13, 1-12.	1.0	31

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55	Genome-wide association mapping for adult resistance to powdery mildew in common wheat. <i>Molecular Biology Reports</i> , 2020, 47, 1241-1256.	1.0	22
56	Genetic variation associated with PPO-inhibiting herbicide tolerance in sorghum. <i>PLoS ONE</i> , 2020, 15, e0233254.	1.1	4
57	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	1.1	29
58	Genome-wide analysis and prediction of Fusarium head blight resistance in soft red winter wheat. <i>Crop Science</i> , 2020, 60, 2882-2900.	0.8	24
59	A SNP-Based Genome-Wide Association Study to Mine Genetic Loci Associated to Salinity Tolerance in Mungbean ( <i>Vigna radiata</i> L.). <i>Genes</i> , 2020, 11, 759.	1.0	18
60	Genome-Wide Association Study for Biomass Related Traits in a Panel of Sorghum bicolor and S. bicolor × S. halepense Populations. <i>Frontiers in Plant Science</i> , 2020, 11, 551305.	1.7	20
61	The apple REFPOP—a reference population for genomics-assisted breeding in apple. <i>Horticulture Research</i> , 2020, 7, 189.	2.9	37
62	Genetic mapping for agronomic traits in a MAGIC population of common bean ( <i>Phaseolus vulgaris</i> L.) under drought conditions. <i>BMC Genomics</i> , 2020, 21, 799.	1.2	41
63	Major-effect candidate genes identified in cultivated strawberry ( <i>Fragaria × ananassa</i> Duch.) for ellagic acid deoxyhexoside and pelargonidin-3-O-malonylglucoside biosynthesis, key polyphenolic compounds. <i>Horticulture Research</i> , 2020, 7, 125.	2.9	17
64	Analysis of Genetic Factors Defining Head Blight Resistance in an Old Hungarian Wheat Variety-Based Mapping Population. <i>Agronomy</i> , 2020, 10, 1128.	1.3	0
65	Identification of a candidate gene associated with isoflavone content in soybean seeds using genome-wide association and linkage mapping. <i>Plant Journal</i> , 2020, 104, 950-963.	2.8	39
66	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3741-3749.	0.8	16
67	mrMLM v4.0.2: An R Platform for Multi-locus Genome-wide Association Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 481-487.	3.0	91
68	Characterization of the Genetic Architecture for Fusarium Head Blight Resistance in Durum Wheat: The Complex Association of Resistance, Flowering Time, and Height Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 592064.	1.7	18
69	Genome-Wide Association Mapping and Genomic Prediction of Anther Extrusion in CIMMYT Hybrid Wheat Breeding Program via Modeling Pedigree, Genomic Relationship, and Interaction With the Environment. <i>Frontiers in Genetics</i> , 2020, 11, 586687.	1.1	10
70	Association mapping of resistance to emerging stem rust pathogen races in spring wheat using genotyping-by-sequencing. <i>Plant Genome</i> , 2020, 13, e20050.	1.6	8
71	Genome-wide association studies for waxy starch in cassava. <i>Euphytica</i> , 2020, 216, 1.	0.6	13
72	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. <i>Scientific Reports</i> , 2020, 10, 8165.	1.6	12

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73	Genome-wide association mapping of <i>Sclerotinia sclerotiorum</i> resistance in soybean using whole-genome resequencing data. <i>BMC Plant Biology</i> , 2020, 20, 195.	1.6	25
74	Genomic Prediction of Agronomic Traits in Common Bean ( <i>Phaseolus vulgaris</i> L.) Under Environmental Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 1001.	1.7	53
75	Differentiation, evolution and utilization of natural alleles for cold adaptability at the reproductive stage in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 2491-2503.	4.1	27
76	Environmental and genetic determinants of amphicarpy in <i>Pisum fulvum</i> , a wild relative of domesticated pea. <i>Plant Science</i> , 2020, 298, 110566.	1.7	3
77	Epigenetic Variation at a Genomic Locus Affecting Biomass Accumulation under Low Nitrogen in <i>Arabidopsis thaliana</i> . <i>Agronomy</i> , 2020, 10, 636.	1.3	8
78	Incorporating Genome-Wide Association Mapping Results Into Genomic Prediction Models for Grain Yield and Yield Stability in CIMMYT Spring Bread Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 197.	1.7	78
79	Identification of Stripe Rust Resistance Loci in U.S. Spring Wheat Cultivars and Breeding Lines Using Genome-Wide Association Mapping and <i>Yr</i> Gene Markers. <i>Plant Disease</i> , 2020, 104, 2181-2192.	0.7	34
80	Genetic Basis of Maize Resistance to Multiple Insect Pests: Integrated Genome-Wide Comparative Mapping and Candidate Gene Prioritization. <i>Genes</i> , 2020, 11, 689.	1.0	21
81	DArTseq Molecular Markers Associated with the Spiny-Tip Leaf Margin in Pineapple ( <i>Ananas comosus</i> )	1.8	3
82	The Genetics of Differential Gene Expression Related to Fruit Traits in Strawberry ( <i>Fragaria</i> )	1.1	20
83	Conserved defense responses between maize and sorghum to <i>Exserohilum turcicum</i> . <i>BMC Plant Biology</i> , 2020, 20, 67.	1.6	12
84	Genomic prediction for resistance to <i>Fusarium</i> ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2020, 60, 1863-1875.	0.8	20
85	Quantitative phenotyping of shell suture strength in walnut ( <i>Juglans regia</i> L.) enhances precision for detection of QTL and genome-wide association mapping. <i>PLoS ONE</i> , 2020, 15, e0231144.	1.1	25
86	Exploring transcriptional switches from pairwise, temporal and population RNA-Seq data using deepTS. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
87	MMAP: a cloud computing platform for mining the maximum accuracy of predicting phenotypes from genotypes. <i>Bioinformatics</i> , 2021, 37, 1324-1326.	1.8	3
88	Temporal dynamics of QTL effects on vegetative growth in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 476-490.	2.4	7
89	Temperature response of wheat affects final height and the timing of stem elongation under field conditions. <i>Journal of Experimental Botany</i> , 2021, 72, 700-717.	2.4	28
90	Natural variation in plant telomere length is associated with flowering time. <i>Plant Cell</i> , 2021, 33, 1118-1134.	3.1	29

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91	Tapping Diversity From the Wild: From Sampling to Implementation. <i>Frontiers in Plant Science</i> , 2021, 12, 626565.	1.7	23
92	Assessing Rice Salinity Tolerance: From Phenomics to Association Mapping. <i>Methods in Molecular Biology</i> , 2021, 2238, 339-375.	0.4	4
93	Nuclear and chloroplast genome diversity revealed by low-coverage whole-genome shotgun sequence in 44 <i>Brassica oleracea</i> breeding lines. <i>Horticultural Plant Journal</i> , 2021, 7, 539-551.	2.3	11
94	Genome-wide association study in hexaploid wheat identifies novel genomic regions associated with resistance to root lesion nematode ( <i>Pratylenchus thornei</i> ). <i>Scientific Reports</i> , 2021, 11, 3572.	1.6	20
95	<i>OsGRETCHENHAGEN3-2</i> modulates rice seed storability via accumulation of abscisic acid and protective substances. <i>Plant Physiology</i> , 2021, 186, 469-482.	2.3	24
96	Genetic Architecture and Genomic Prediction of Cooking Time in Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 622213.	1.7	27
97	Exploring genetic architecture for pod-related traits in soybean using image-based phenotyping. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	10
98	Identification of resistance loci against new pathotypes of <i>Plasmodiophora brassicae</i> in <i>Brassica napus</i> based on genome-wide association mapping. <i>Scientific Reports</i> , 2021, 11, 6599.	1.6	14
99	Reconstruction of the Origin of a Neo-Y Sex Chromosome and Its Evolution in the Spotted Knifejaw, <i>Oplegnathus punctatus</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2615-2626.	3.5	21
100	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	3.0	396
101	<i>Arabidopsis thaliana</i> Genes Associated with Cucumber mosaic virus Virulence and Their Link to Virus Seed Transmission. <i>Microorganisms</i> , 2021, 9, 692.	1.6	13
102	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. <i>Genome Biology</i> , 2021, 22, 113.	3.8	32
103	Strawberry sweetness and consumer preference are enhanced by specific volatile compounds. <i>Horticulture Research</i> , 2021, 8, 66.	2.9	55
104	Genome-Wide Association Study Reveals the QTLs for Seed Storability in World Rice Core Collections. <i>Plants</i> , 2021, 10, 812.	1.6	9
105	Genomic prediction for growth using a low-density SNP panel in dromedary camels. <i>Scientific Reports</i> , 2021, 11, 7675.	1.6	10
106	Pathway-based analysis of anthocyanin diversity in diploid potato. <i>PLoS ONE</i> , 2021, 16, e0250861.	1.1	9
107	Genome-wide association study for septoria tritici blotch resistance reveals the occurrence and distribution of <i>Stb6</i> in a historic Swiss landrace collection. <i>Euphytica</i> , 2021, 217, 1.	0.6	3
108	MultiGWAS: An integrative tool for Genome Wide Association Studies in tetraploid organisms. <i>Ecology and Evolution</i> , 2021, 11, 7411-7426.	0.8	5

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109	Genomic Characterization of the Fruity Aroma Gene, FaFAD1, Reveals a Gene Dosage Effect on Î³-Decalactone Production in Strawberry ( <i>Fragaria Å— ananassa</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 639345.	1.7	20
110	Genetic Analysis of Methyl Anthranilate, Mesifurane, Linalool, and Other Flavor Compounds in Cultivated Strawberry ( <i>Fragaria Å— ananassa</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 615749.	1.7	20
111	Whole-genome resequencing of <i>Osmanthus fragrans</i> provides insights into flower color evolution. <i>Horticulture Research</i> , 2021, 8, 98.	2.9	35
112	Genome-wide association study of myrtle rust ( <i>Austropuccinia psidii</i> ) resistance in <i>Eucalyptus obliqua</i> (subgenus <i>Eucalyptus</i> ). <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	8
115	Genome-wide association analysis permits characterization of <i>Stagonospora nodorum</i> blotch (SNB) resistance in hard winter wheat. <i>Scientific Reports</i> , 2021, 11, 12570.	1.6	13
116	Genome-Wide Association Study for Ultraviolet-B Resistance in Soybean ( <i>Glycine max</i> L.). <i>Plants</i> , 2021, 10, 1335.	1.6	7
117	Leveraging breeding programs and genomic data in Norway spruce ( <i>Picea abies</i> L. Karst) for GWAS analysis. <i>Genome Biology</i> , 2021, 22, 179.	3.8	29
118	Genetic and Morphological Approach for Western Corn Rootworm Resistance Management. <i>Agriculture (Switzerland)</i> , 2021, 11, 585.	1.4	4
119	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , 2021, 12, 3551.	5.8	21
120	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 642828.	1.7	16
121	Robustification of GWAS to explore effective SNPs addressing the challenges of hidden population stratification and polygenic effects. <i>Scientific Reports</i> , 2021, 11, 13060.	1.6	4
122	Genetic dissection of natural variation in oilseed traits of camelina by whole-€genome resequencing and QTL mapping. <i>Plant Genome</i> , 2021, 14, e20110.	1.6	24
123	Resequencing of 672 Native Rice Accessions to Explore Genetic Diversity and Trait Associations in Vietnam. <i>Rice</i> , 2021, 14, 52.	1.7	12
124	Genome-Wide Association Mapping and Gene Expression Analysis Reveal the Negative Role of OsMYB21 in Regulating Bacterial Blight Resistance in Rice. <i>Rice</i> , 2021, 14, 58.	1.7	11
125	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021, 14, 874-887.	3.9	56
126	Integrating GWAS and transcriptomics to identify genes involved in seed dormancy in rice. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3553-3562.	1.8	6
127	Genetic basis and network underlying synergistic roots and shoots biomass accumulation revealed by genome-wide association studies in rice. <i>Scientific Reports</i> , 2021, 11, 13769.	1.6	4
128	Genome-Wide Association Study in Rice Revealed a Novel Gene in Determining Plant Height and Stem Development, by Encoding a WRKY Transcription Factor. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8192.	1.8	16



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129	High throughput can produce better decisions than high accuracy when phenotyping plant populations. <i>Crop Science</i> , 2021, 61, 3301-3313.	0.8	22
130	Genome-Wide Association Mapping for Stomata and Yield Indices in Bread Wheat under Water Limited Conditions. <i>Agronomy</i> , 2021, 11, 1646.	1.3	13
131	Breeding With Major and Minor Genes: Genomic Selection for Quantitative Disease Resistance. <i>Frontiers in Plant Science</i> , 2021, 12, 713667.	1.7	22
132	Genomic selection in salmonids: new discoveries and future perspectives. <i>Aquaculture International</i> , 2021, 29, 2259-2289.	1.1	13
133	Genome-Wide Association Mapping of Mixed Linkage (1,3;1,4)- $\beta$ -Glucan and Starch Contents in Rice Whole Grain. <i>Frontiers in Plant Science</i> , 2021, 12, 665745.	1.7	6
134	Multi-Trait Multi-Environment Genomic Prediction of Agronomic Traits in Advanced Breeding Lines of Winter Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 709545.	1.7	25
136	Genome-Wide Association Study Reveals Novel Genetic Loci for Quantitative Resistance to Septoria Tritici Blotch in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 671323.	1.7	8
137	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. <i>Nature Communications</i> , 2021, 12, 5466.	5.8	24
138	GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 629-640.	3.0	345
139	Mapping the adaptive landscape of a major agricultural pathogen reveals evolutionary constraints across heterogeneous environments. <i>ISME Journal</i> , 2021, 15, 1402-1419.	4.4	25
140	Status and prospects of genome-wide association studies in plants. <i>Plant Genome</i> , 2021, 14, e20077.	1.6	200
141	Identifying barley pan-genome sequence anchors using genetic mapping and machine learning. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2535-2544.	1.8	9
152	Allelic Variation of <i>MYB10</i> Is the Major Force Controlling Natural Variation in Skin and Flesh Color in Strawberry ( <i>Fragaria</i> spp.) Fruit. <i>Plant Cell</i> , 2020, 32, 3723-3749.	3.1	111
153	The Candidate Genes Underlying a Stably Expressed QTL for Low Temperature Germinability in Rice ( <i>Oryza sativa</i> L.). <i>Rice</i> , 2020, 13, 74.	1.7	14
154	Dissecting seed pigmentation-associated genomic loci and genes by employing dual approaches of reference-based and k-mer-based GWAS with 438 Glycine accessions. <i>PLoS ONE</i> , 2020, 15, e0243085.	1.1	8
155	Species-Specific Duplication Event Associated with Elevated Levels of Nonstructural Carbohydrates in <i>Sorghum bicolor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1511-1520.	0.8	13
156	Application of Genomics Tools in Wheat Breeding to Attain Durable Rust Resistance. <i>Frontiers in Plant Science</i> , 2020, 11, 567147.	1.7	27
157	Evaluating the Utility of Carbon Isotope Discrimination for Wheat Breeding in the Pacific Northwest. <i>Plant Phenomics</i> , 2019, 2019, 4528719.	2.5	6

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158	Molecular characterization of bacterial leaf streak resistance in hard winter wheat. PeerJ, 2019, 7, e7276.	0.9	19
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