Genome-Assisted Prediction of Quantitative Traits Usin

Citation Report

#	ARTICLE	IF	CITATIONS
1	Genomic models with genotypeâ€‰Ã—â€‰environment interaction for predicting hybrid performance: an application in maize hybrids. Theoretical and Applied Genetics, 2017, 130, 1431-1440.	1.8	46
2	SOFIA: An R Package for Enhancing Genetic Visualization With Circos. Journal of Heredity, 2017, 108, 443-448.	1.0	13
3	Construction of a High-Density American Cranberry (*Vaccinium macrocarpon* Ait.) Composite Map Using Genotyping-by-Sequencing for Multi-pedigree Linkage Mapping. G3: Genes, Genomes, Genetics, 2017, 7, 1177-1189.	0.8	37
4	Social and spatial effects on genetic variation between foraging flocks in a wild bird population. Molecular Ecology, 2017, 26, 5807-5819.	2.0	8
5	Strategies for Selecting Crosses Using Genomic Prediction in Two Wheat Breeding Programs. Plant Genome, 2017, 10, plantgenome2016.12.0128.	1.6	37
6	Prediction of genomic breeding values using new computing strategies for the implementation of MixP. Scientific Reports, 2017, 7, 17200.	1.6	6
7	Assessing the expected response to genomic selection of individuals and families in Eucalyptus breeding with an additive-dominant model. Heredity, 2017, 119, 245-255.	1.2	76
8	Polygenicity and Epistasis Underlie Fitness-Proximal Traits in the *Caenorhabditis elegans* Multiparental Experimental Evolution (CeMEE) Panel. Genetics, 2017, 207, 1663-1685.	1.2	81
9	Cell Membrane Stability and Association Mapping for Drought and Heat Tolerance in a Worldwide Wheat Collection. Sustainability, 2017, 9, 1606.	1.6	85
10	Beyond Genomic Prediction: Combining Different Types of *omics* Data Can Improve Prediction of Hybrid Performance in Maize. Genetics, 2018, 208, 1373-1385.	1.2	130
11	Genome-wide regression models considering general and specific combining ability predict hybrid performance in oilseed rape with similar accuracy regardless of trait architecture. Theoretical and Applied Genetics, 2018, 131, 299-317.	1.8	41
12	Improving the baking quality of bread wheat by genomic selection in early generations. Theoretical and Applied Genetics, 2018, 131, 477-493.	1.8	62
13	A fully automated pipeline for quantitative genotype calling from next generation sequencing data in autopolyploids. BMC Bioinformatics, 2018, 19, 398.	1.2	62
14	Multivariate GBLUP Improves Accuracy of Genomic Selection for Yield and Fruit Weight in Biparental Populations of Vaccinium macrocarpon Ait. Frontiers in Plant Science, 2018, 9, 1310.	1.7	41
15	Narrow-sense heritability and PST estimates of DNA methylation in three Populus nigra L. populations under contrasting water availability. Tree Genetics and Genomes, 2018, 14, 1.	0.6	15
16	Impact of residual covariance structures on genomic prediction ability in multi-environment trials. PLoS ONE, 2018, 13, e0201181.	1.1	8
17	Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar. G3: Genes, Genomes, Genetics, 2018, 8, 3961-3972.	0.8	114
18	Factors affecting genomic selection revealed by empirical evidence in maize. Crop Journal, 2018, 6, 341-352.	2.3	76

#	ARTICLE	IF	CITATIONS
19	Root architectural traits and yield: exploring the relationship in barley breeding trials. Euphytica, 2018, 214, 1.	0.6	46
20	Genome-Wide Association Analyses Identify QTL Hotspots for Yield and Component Traits in Durum Wheat Grown under Yield Potential, Drought, and Heat Stress Environments. Frontiers in Plant Science, 2018, 9, 81.	1.7	222
21	Prospects and Potential Uses of Genomic Prediction of Key Performance Traits in Tetraploid Potato. Frontiers in Plant Science, 2018, 9, 159.	1.7	51
22	Massive phenotyping of multiple cranberry populations reveals novel QTLs for fruit anthocyanin content and other important chemical traits. Molecular Genetics and Genomics, 2018, 293, 1379-1392.	1.0	35
23	Association mapping identifies loci for canopy temperature under drought in diverse soybean genotypes. Euphytica, 2018, 214, 1.	0.6	19
24	Heritability of drought resistance in Solanum aethiopicum Shum group and combining ability of genotypes for drought tolerance and recovery. Scientia Horticulturae, 2018, 240, 213-220.	1.7	14
25	Megaâ€Environmental Design: Using Genotype Ã— Environment Interaction to Optimize Resources for Cultivar Testing. Crop Science, 2019, 59, 1899-1915.	0.8	37
26	From mass selection to genomic selection: one century of breeding for quantitative yield components of oil palm (Elaeis guineensis Jacq.). Tree Genetics and Genomes, 2019, 15, 1.	0.6	17
27	Genomic selection for productive traits in biparental cassava breeding populations. PLoS ONE, 2019, 14, e0220245.	1.1	11
28	Efficiency of Genomic Prediction of Nonassessed Testcrosses. Crop Science, 2019, 59, 2020-2027.	0.8	8
29	Combining grain yield, protein content and protein quality by multi-trait genomic selection in bread wheat. Theoretical and Applied Genetics, 2019, 132, 2767-2780.	1.8	31
30	bWGR: Bayesian whole-genome regression. Bioinformatics, 2020, 36, 1957-1959.	1.8	13
31	Individual differences in behavior and heart rate variability across the preweaning period in the domestic horse in response to an ecologically relevant stressor. Physiology and Behavior, 2019, 210, 112652.	1.0	6
32	QTL mapping and genome-wide prediction of heat tolerance in multiple connected populations of temperate maize. Scientific Reports, 2019, 9, 14418.	1.6	26
33	Transcriptomic and presence/absence variation in the barley genome assessed from multi-tissue mRNA sequencing and their power to predict phenotypic traits. BMC Genomics, 2019, 20, 787.	1.2	16
34	Cassava yield traits predicted by genomic selection methods. PLoS ONE, 2019, 14, e0224920.	1.1	33
35	Epistasis Detection and Modeling for Genomic Selection in Cowpea (Vigna unguiculata L. Walp.). Frontiers in Genetics, 2019, 10, 677.	1.1	19
36	Analysis of Fusarium ear rot and fumonisin contamination in testcrosses of a maize biparental population. Crop Breeding and Applied Biotechnology, 2019, 19, 40-46.	0.1	6

#	Article	IF	Citations
37	Improving and Maintaining Winter Hardiness and Frost Tolerance in Bread Wheat by Genomic Selection. Frontiers in Plant Science, 2019, 10, 1195.	1.7	20
38	Inclusion of herdmate data improves genomic prediction for milk-production and feed-efficiency traits within North American dairy herds. Journal of Dairy Science, 2019, 102, 11081-11091.	1.4	7
39	HaploBlocker: Creation of Subgroup-Specific Haplotype Blocks and Libraries. Genetics, 2019, 212, 1045-1061.	1.2	33
40	Genetic variation of biomass recalcitrance in a natural Salix viminalis (L.) population. Biotechnology for Biofuels, 2019, 12, 135.	6.2	17
41	A Novel Gene Underlies Bleomycin-Response Variation in<i>Caenorhabditis elegans</i>. Genetics, 2019, 212, 1453-1468.	1.2	43
42	Megaâ€environment identification for soybean (Glycine max) breeding and production in Brazilian Midwest region. Plant Breeding, 2019, 138, 336-347.	1.0	7
43	Genetic relatedness and the ratio of subpopulationâ€common alleles are related in genomic prediction across structured subpopulations in maize. Plant Breeding, 2019, 138, 802-809.	1.0	3
44	Estimation of metabolic syndrome heritability in three large populations including full pedigree and genomic information. Human Genetics, 2019, 138, 739-748.	1.8	4
45	QTL Ã— environment interactions underlie adaptive divergence in switchgrass across a large latitudinal gradient. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12933-12941.	3.3	75
46	Comparison of spaceâ€plant versus sward plot selection in thickspike wheatgrass (Elymus lanceolatus) Tj ETQq1 1 0.784314 rgBT /O	1.0	1
47	Genetic Correlations Between Photosynthetic and Yield Performance in Maize Are Different Under Two Heat Scenarios During Flowering. Frontiers in Plant Science, 2019, 10, 566.	1.7	18
48	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice (<i>Oryza sativa</i>L.) Grown in Subtropical Areas. G3: Genes, Genomes, Genetics, 2019, 9, 1519-1531.	0.8	59
49	An R Package for Bayesian Analysis of Multi-environment and Multi-trait Multi-environment Data for Genome-Based Prediction. G3: Genes, Genomes, Genetics, 2019, 9, 1355-1369.	0.8	39
50	Simultaneous selection for grain yield and protein content in genomics-assisted wheat breeding. Theoretical and Applied Genetics, 2019, 132, 1745-1760.	1.8	69
51	A framework for genomics-informed ecophysiological modeling in plants. Journal of Experimental Botany, 2019, 70, 2561-2574.	2.4	18
52	Fast and flexible linear mixed models for genome-wide genetics. PLoS Genetics, 2019, 15, e1007978.	1.5	54
53	Genomic Prediction using Existing Historical Data Contributing to Selection in Biparental Populations: A Study of Kernel Oil in Maize. Plant Genome, 2019, 12, 180025.	1.6	16
54	High-Throughput Phenotyping Enabled Genetic Dissection of Crop Lodging in Wheat. Frontiers in Plant Science, 2019, 10, 394.	1.7	104

#	ARTICLE	IF	CITATIONS
55	Mouse Skull Mean Shape and Shape Robustness Rely on Different Genetic Architectures and Different Loci. Frontiers in Genetics, 2019, 10, 64.	1.1	12
56	Multi-trait Improvement by Predicting Genetic Correlations in Breeding Crosses. G3: Genes, Genomes, Genetics, 2019, 9, 3153-3165.	0.8	34
57	Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. Genetics, 2019, 213, 1237-1253.	1.2	27
58	Effectiveness of Genomic Selection by Response to Selection for Winter Wheat Variety Improvement. Plant Genome, 2019, 12, 1-15.	1.6	18
59	Enhancing genomic selection by fitting large-effect SNPs as fixed effects and a genotype-by-environment effect using a maize BC1F3:4 population. PLoS ONE, 2019, 14, e0223898.	1.1	13
60	Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. Frontiers in Plant Science, 2019, 10, 1570.	1.7	24
61	Unraveling candidate genes underlying biomass digestibility in elephant grass (Cenchrus purpureus). BMC Plant Biology, 2019, 19, 548.	1.6	6
62	Evaluation of genomic selection and marker-assisted selection in Miscanthus and energycane. Molecular Breeding, 2019, 39, 1.	1.0	20
63	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. Plant Genome, 2019, 12, 180051.	1.6	58
64	Dissecting the genetics underlying the relationship between protein content and grain yield in a large hybrid wheat population. Theoretical and Applied Genetics, 2019, 132, 489-500.	1.8	44
65	Characterization of Early Blight Resistance in Potato Cultivars. Plant Disease, 2019, 103, 629-637.	0.7	24
66	A high density linkage map and quantitative trait loci for tree growth for New Zealand mānuka (Leptospermum scoparium). New Zealand Journal of Crop and Horticultural Science, 2019, 47, 261-272.	0.7	7
67	A miR-18a binding-site polymorphism in CDC42 3â€²UTR affects CDC42 mRNA expression in placentas and is associated with litter size in pigs. Mammalian Genome, 2019, 30, 34-41.	1.0	12
68	Exploring and exploiting the genetic variation of Fusarium head blight resistance for genomic-assisted breeding in the elite durum wheat gene pool. Theoretical and Applied Genetics, 2019, 132, 969-988.	1.8	57
69	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β-carotene and starch content in hexaploid sweetpotato [Ipomoea batatas (L.) Lam.]. Theoretical and Applied Genetics, 2020, 133, 23-36.	1.8	59
70	The remarkable morphological diversity of leaf shape in sweet potato (<i>Ipomoea batatas</i>): the influence of genetics, environment, and Gâ—E. New Phytologist, 2020, 225, 2183-2195.	3.5	32
71	The hybrid protein interactome contributes to rice heterosis as epistatic effects. Plant Journal, 2020, 102, 116-128.	2.8	10
72	Genetic structure of a germplasm for hybrid breeding in rye (Secale cereale L.). PLoS ONE, 2020, 15, e0239541.	1.1	16

#	Article	IF	Citations
73	Adoption and Optimization of Genomic Selection To Sustain Breeding for Apricot Fruit Quality. G3: Genes, Genomes, Genetics, 2020, 10, 4513-4529.	0.8	11
74	Genomic Studies Reveal Substantial Dominant Effects and Improved Genomic Predictions in an Open-Pollinated Breeding Population of <i>Eucalyptus pellita</i>. G3: Genes, Genomes, Genetics, 2020, 10, 3751-3763.	0.8	24
75	Metabolic and behavioral adaptations of greater white-toothed shrews to urban conditions. Behavioral Ecology, 2020, 31, 1334-1343.	1.0	8
76	Genome‐wide analysis and prediction of Fusarium head blight resistance in soft red winter wheat. Crop Science, 2020, 60, 2882-2900.	0.8	24
77	Genome‐wide association of volatiles reveals candidate loci for blueberry flavor. New Phytologist, 2020, 226, 1725-1737.	3.5	84
78	Shifts in the developmental rate of spadefoot toad larvae cause decreased complexity of post-metamorphic pigmentation patterns. Scientific Reports, 2020, 10, 19624.	1.6	1
79	Genomic selection for heterobothriosis resistance concurrent with body size in the tiger pufferfish, Takifugu rubripes. Scientific Reports, 2020, 10, 19976.	1.6	10
80	Genome-Wide Prediction of Complex Traits in Two Outcrossing Plant Species Through Deep Learning and Bayesian Regularized Neural Network. Frontiers in Plant Science, 2020, 11, 593897.	1.7	22
81	Making the most of all data: Combining non‐genotyped and genotyped potato individuals with HBLUP. Plant Genome, 2020, 13, e20056.	1.6	17
82	Synthetic hexaploid wheat as a source of novel genetic loci for aluminium tolerance. Euphytica, 2020, 216, 1.	0.6	3
83	Identifying inbred lines with resistance to endemic diseases in exotic maize germplasm. Crop Science, 2020, 60, 3141-3150.	0.8	5
84	Integration of genotypic, hyperspectral, and phenotypic data to improve biomass yield prediction in hybrid rye. Theoretical and Applied Genetics, 2020, 133, 3001-3015.	1.8	34
85	High-resolution characterization of male ornamentation and re-evaluation of sex linkage in guppies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201677.	1.2	10
86	Genomic Prediction and Selection for Fruit Traits in Winter Squash. G3: Genes, Genomes, Genetics, 2020, 10, 3601-3610.	0.8	15
87	Natural variation in a glucuronosyltransferase modulates propionate sensitivity in a C. elegans propionic acidemia model. PLoS Genetics, 2020, 16, e1008984.	1.5	18
88	Genome‐wide association study of resistance to Mal de Río Cuarto disease in maize. Agronomy Journal, 2020, 112, 4624-4633.	0.9	3
89	Mitigating the impact of selective phenotyping in training populations on the prediction ability by multi‐trait pedigree and genomic selection models. Plant Breeding, 2020, 139, 1067-1075.	1.0	6
90	Genomic Prediction of Rust Resistance in Tetraploid Wheat under Field and Controlled Environment Conditions. Agronomy, 2020, 10, 1843.	1.3	7

#	Article	IF	Citations
91	You Had Me at "MAGIC": Four Barley MAGIC Populations Reveal Novel Resistance QTL for Powdery Mildew. Genes, 2020, 11, 1512.	1.0	14
92	Prediction based on estimated breeding values using genealogy for tuber yield and late blight resistance in auto-tetraploid potato (Solanum tuberosum L.). Heliyon, 2020, 6, e05624.	1.4	8
93	Multi-Year Dynamics of Single-Step Genomic Prediction in an Applied Wheat Breeding Program. Agronomy, 2020, 10, 1591.	1.3	4
94	Multiple QTL Mapping in Autopolyploids: A Random-Effect Model Approach with Application in a Hexaploid Sweetpotato Full-Sib Population. Genetics, 2020, 215, 579-595.	1.2	42
95	Dominance and G×E interaction effects improve genomic prediction and genetic gain in intermediate wheatgrass (<i>Thinopyrum intermedium</i>). Plant Genome, 2020, 13, e20012.	1.6	19
96	Genomic prediction of maternal haploid induction rate in maize. Plant Genome, 2020, 13, e20014.	1.6	14
97	MoBPS - Modular Breeding Program Simulator. G3: Genes, Genomes, Genetics, 2020, 10, 1915-1918.	0.8	49
98	The maize shoot ionome: Its interaction partners, predictive power, and genetic determinants. Plant, Cell and Environment, 2020, 43, 2095-2111.	2.8	10
99	The value of early-stage phenotyping for wheat breeding in the age of genomic selection. Theoretical and Applied Genetics, 2020, 133, 2499-2520.	1.8	10
100	Can metabolic prediction be an alternative to genomic prediction in barley?. PLoS ONE, 2020, 15, e0234052.	1.1	17
101	QTL Mapping for Resistance to Early Blight in a Tetraploid Potato Population. Agronomy, 2020, 10, 728.	1.3	20
102	Multi-Trait Genome-Wide Association Studies Reveal Loci Associated with Maize Inflorescence and Leaf Architecture. Plant and Cell Physiology, 2020, 61, 1427-1437.	1.5	38
103	Genomic Prediction Accuracy of Seven Breeding Selection Traits Improved by QTL Identification in Flax. International Journal of Molecular Sciences, 2020, 21, 1577.	1.8	21
104	Estimating variances in time series kriging using convex optimization and empirical BLUPs. Statistical Papers, 2020, 62, 1899.	0.7	5
105	Evidence for Individual Differences in Behaviour and for Behavioural Syndromes in Adult Shelter Cats. Animals, 2020, 10, 962.	1.0	14
106	High-density genetic linkage map construction and cane cold hardiness QTL mapping for Vitis based on restriction site-associated DNA sequencing. BMC Genomics, 2020, 21, 419.	1.2	9
107	Identification of new QTL for yield-related traits in Chinese landrace and elite wheat varieties through a genome-wide linkage mapping. Euphytica, 2020, 216, 1.	0.6	7
108	On the usefulness of parental lines GWAS for predicting low heritability traits in tropical maize hybrids. PLoS ONE, 2020, 15, e0228724.	1.1	22

#	ARTICLE	IF	CITATIONS
109	Integrating host plant phylogeny, plant traits, intraspecific competition and repeated measures using a phylogenetic mixed model of field behaviour by polyphagous herbivores, the leaf-cutting ants. Journal of Tropical Ecology, 2020, 36, 80-86.	0.5	1
110	Seed Weight as a Covariate in Association and Prediction Studies for Biomass Traits in Maize Seedlings. Plants, 2020, 9, 275.	1.6	2
111	RAINBOW: Haplotype-based genome-wide association study using a novel SNP-set method. PLoS Computational Biology, 2020, 16, e1007663.	1.5	46
112	Influence of Genetic Ancestry on Human Serum Proteome. American Journal of Human Genetics, 2020, 106, 303-314.	2.6	19
113	Genomic predictions for Fusarium head blight resistance in a diverse durum wheat panel: an effective incorporation of plant height and heading date as covariates. Euphytica, 2020, 216, 1.	0.6	24
114	Linear models for diallel crosses: a review with R functions. Theoretical and Applied Genetics, 2021, 134, 585-601.	1.8	16
115	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. Theoretical and Applied Genetics, 2021, 134, 95-112.	1.8	103
116	Allelic variation in rice *Fertilization Independent Endosperm 1* contributes to grain width under high night temperature stress. New Phytologist, 2021, 229, 335-350.	3.5	28
117	Optimising accuracy of performance predictions using available morphophysiological information in wheat breeding germplasm. Annals of Applied Biology, 2021, 178, 367-376.	1.3	1
118	Nested association mapping reveals the genetic architecture of spike emergence and anthesis timing in intermediate wheatgrass. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	11
120	Evaluation of dominance in tropically adapted composite beef cattle. Animal Production Science, 2021, , .	0.6	1
121	Selection of Hancornia speciosa germplasm accessions based on the FAI-BLUP index. Pesquisa Agropecuaria Tropical, 0, 51, .	1.0	2
122	Merging Genomics and Transcriptomics for Predicting Fusarium Head Blight Resistance in Wheat. Genes, 2021, 12, 114.	1.0	10
123	Advances in Breeding for Mixed Cropping – Incomplete Factorials and the Producer/Associate Concept. Frontiers in Plant Science, 2020, 11, 620400.	1.7	26
124	Repeatable individual differences in behaviour and physiology in juvenile horses from an early age. Applied Animal Behaviour Science, 2021, 235, 105227.	0.8	6
125	Multi-Locus Genome-Wide Association Studies Reveal Fruit Quality Hotspots in Peach Genome. Frontiers in Plant Science, 2021, 12, 644799.	1.7	18
126	Multi-omics-based prediction of hybrid performance in canola. Theoretical and Applied Genetics, 2021, 134, 1147-1165.	1.8	23
128	Genotyping crossing parents and family bulks can facilitate cost-efficient genomic prediction strategies in small-scale line breeding programs. Theoretical and Applied Genetics, 2021, 134, 1575-1586.	1.8	1

#	ARTICLE	IF	CITATIONS
129	Early prediction of biomass in hybrid rye based on hyperspectral data surpasses genomic predictability in less-related breeding material. Theoretical and Applied Genetics, 2021, 134, 1409-1422.	1.8	15
131	Modeling first order additive Ã— additive epistasis improves accuracy of genomic prediction for sclerotinia stem rot resistance in canola. Plant Genome, 2021, 14, e20088.	1.6	8
132	Genome-wide association study on metabolite accumulation in a wild barley NAM population reveals natural variation in sugar metabolism. PLoS ONE, 2021, 16, e0246510.	1.1	5
133	Overcoming barriers to the registration of new plant varieties under the DUS system. Communications Biology, 2021, 4, 302.	2.0	12
134	Improving Genomic Prediction for Seed Quality Traits in Oat (Avena sativa L.) Using Trait-Specific Relationship Matrices. Frontiers in Genetics, 2021, 12, 643733.	1.1	14
135	First genomic prediction and genome€wide association for complex growth€related traits in Rock Bream (<i>Oplegnathus fasciatus</i>). Evolutionary Applications, 2022, 15, 523-536.	1.5	24
136	EigenGWAS: An online visualizing and interactive application for detecting genomic signatures of natural selection. Molecular Ecology Resources, 2021, 21, 1732-1744.	2.2	2
137	Drone phenotyping and machine learning enable discovery of loci regulating daily floral opening in lettuce. Journal of Experimental Botany, 2021, 72, 2979-2994.	2.4	8
138	QTL Ã— environment interactions underlie ionome divergence in switchgrass. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	6
139	Development of whole€genome prediction models to increase the rate of genetic gain in intermediate wheatgrass (<i>Thinopyrum intermedium</i>) breeding. Plant Genome, 2021, 14, e20089.	1.6	12
140	A genome-wide association study of heat tolerance in Pacific abalone based on genome resequencing. Aquaculture, 2021, 536, 736436.	1.7	34
141	High-Density Genetic Linkage Map Construction and White Rot Resistance Quantitative Trait Loci Mapping for Genus <i>Vitis</i> Based on Restriction Site-Associated DNA Sequencing. Phytopathology, 2021, 111, 659-670.	1.1	7
142	Genetic components of consumer liking based on visual appearance of leaf types in Brassica vegetables. Euphytica, 2021, 217, 1.	0.6	0
143	Assessment of Drought and Heat Tolerance of Durum Wheat Lines Derived from Interspecific Crosses Using Physiological Parameters and Stress Indices. Agronomy, 2021, 11, 695.	1.3	12
144	Diversifying maize genomic selection models. Molecular Breeding, 2021, 41, 1.	1.0	12
145	Genomic prediction and QTL mapping of root system architecture and above-ground agronomic traits in rice (<i>Oryza sativa</i> L.) with a multitrait index and Bayesian networks. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	10
147	Assessment of soybean test weight among genotypes, environments, agronomic and seed compositional traits. Agronomy Journal, 2021, 113, 2303-2313.	0.9	3
148	Improving Genomic Prediction Using High-Dimensional Secondary Phenotypes. Frontiers in Genetics, 2021, 12, 667358.	1.1	3

#	Article	IF	Citations
149	Genome wide association study reveals plant loci controlling heritability of the rhizosphere microbiome. ISME Journal, 2021, 15, 3181-3194.	4.4	97
150	The genetic mechanism of heterosis utilization in maize improvement. Genome Biology, 2021, 22, 148.	3.8	69
151	lme4GS: An R-Package for Genomic Selection. Frontiers in Genetics, 2021, 12, 680569.	1.1	10
152	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. Genetics, 2021, 218, .	1.2	24
153	Genomic signatures of selection for resistance to stripe rust in Austrian winter wheat. Theoretical and Applied Genetics, 2021, 134, 3111-3121.	1.8	2
154	Genetic dissection of natural variation in oilseed traits of camelina by wholeâ€genome resequencing and QTL mapping. Plant Genome, 2021, 14, e20110.	1.6	24
155	Genomic Prediction of Yield Traits in Single-Cross Hybrid Rice (Oryza sativa L.). Frontiers in Genetics, 2021, 12, 692870.	1.1	7
156	Genomic prediction with non-additive effects in beef cattle: stability of variance component and genetic effect estimates against population size. BMC Genomics, 2021, 22, 512.	1.2	7
159	Optimizing Genomic-Enabled Prediction in Small-Scale Maize Hybrid Breeding Programs: A Roadmap Review. Frontiers in Plant Science, 2021, 12, 658267.	1.7	14
160	Pre-emptive Breeding Against Karnal Bunt Infection in Common Wheat: Combining Genomic and Agronomic Information to Identify Suitable Parents. Frontiers in Plant Science, 2021, 12, 675859.	1.7	4
161	Heterotic quantitative trait loci analysis and genomic prediction of seedling biomass-related traits in maize triple testcross populations. Plant Methods, 2021, 17, 85.	1.9	1
162	Resistance to Phytophthora infestans Clonal Lineage US-23 in Potato Cultivars and Its Relationship with Early Blight Resistance and Tuber Yield. Plant Disease, 2021, , PDIS03210594RE.	0.7	0
163	Quantitative Trait Loci and Candidate Genes Associated with Photoperiod Sensitivity in Lettuce (Lactuca spp.). Theoretical and Applied Genetics, 2021, 134, 3473-3487.	1.8	2
164	A multivariate heterogeneous variance components model for multi-environment studies with locational genetic effects. Soft Computing, 2021, 25, 13195-13200.	2.1	0
165	Genomeâ€wide Association Study Identified Chromosome 8 Locus Associated with Medicationâ€Related Osteonecrosis of the Jaw. Clinical Pharmacology and Therapeutics, 2021, 110, 1558-1569.	2.3	8
166	Genetics components of rice root architecture and carbon isotopic fractionation parameters: a tracer for breeding in a water-saving irrigation management. Journal of Crop Science and Biotechnology, 2022, 25, 19-32.	0.7	0
167	Combining abilities and elite germplasm enhancement across US public sorghum breeding programs. Crop Science, 0, , .	0.8	2
168	Genetic Dissection of Phosphorus Use Efficiency in a Maize Association Population under Two P Levels in the Field. International Journal of Molecular Sciences, 2021, 22, 9311.	1.8	12

#	ARTICLE	IF	CITATIONS
169	Natural variation in Caenorhabditis elegans responses to the anthelmintic emodepside. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 16, 1-8.	1.4	14
170	Genome-Wide Scanning Enabled SNP Discovery, Linkage Disequilibrium Patterns and Population Structure in a Panel of Fonio (Digitaria exilis [Kippist] Stapf) Germplasm. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	5
172	Genetic and phenotypic characterization of rice grain quality traits to define research strategies for improving rice milling, appearance, and cooking qualities in Latin America and the Caribbean. Plant Genome, 2021, 14, e20134.	1.6	13
173	Genetic dissection of complex traits using hierarchical biological knowledge. PLoS Computational Biology, 2021, 17, e1009373.	1.5	1
174	Development of a Genomic Prediction Pipeline for Maintaining Comparable Sample Sizes in Training and Testing Sets across Prediction Schemes Accounting for the Genotype-by-Environment Interaction. Agriculture (Switzerland), 2021, 11, 932.	1.4	5
176	Runs of homozygosity analysis reveals consensus homozygous regions affecting production traits in Chinese Simmental beef cattle. BMC Genomics, 2021, 22, 678.	1.2	8
177	LightGBM: accelerated genomically designed crop breeding through ensemble learning. Genome Biology, 2021, 22, 271.	3.8	76
178	Mapping causal genes and genetic interactions for agronomic traits using a large F2 population in rice. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
179	Contribution of Wild Relatives to Durum Wheat (Triticum turgidum subsp. durum) Yield Stability across Contrasted Environments. Agronomy, 2021, 11, 1992.	1.3	11
180	Genetic improvement of survival in Pacific oysters to the Tomales Bay strain of OsHV-1 over two cycles of selection. Aquaculture, 2021, 543, 737020.	1.7	14
181	Evaluation of Bayesian methods of genomic association via chromosomic regions using simulated data. Scientia Agricola, 2022, 79, .	0.6	2
182	Dissecting the phenotypic response of maize to low phosphorus soils by field screening of a large diversity panel. Euphytica, 2021, 217, 1.	0.6	8
184	Distinct genetic architectures for phenotype means and plasticities in Zea mays. Nature Plants, 2017, 3, 715-723.	4.7	98
185	Genome-wide approaches to understanding and improving complex traits in aquaculture species.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , 1-10.	0.6	8
186	AlphaSimR: an R package for breeding program simulations. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	109
187	Tolerance to oxidative stress is associated with both oxidative stress response and inherent growth in a fungal wheat pathogen. Genetics, 2021, 217, .	1.2	11
197	Genetic study and molecular breeding for high phosphorus use efficiency in maize. Frontiers of Agricultural Science and Engineering, 2019, 6, 366.	0.9	2
198	Accuracy of Single and Multi-Trait Genomic Prediction Models for Grain Yield in US Pacific Northwest Winter Wheat. Crop Breeding Genetics and Genomics, 0, , .	1.7	23

#	ARTICLE	IF	CITATIONS
199	Factors Influencing Genomic Prediction Accuracies of Tropical Maize Resistance to Fall Armyworm and Weevils. Plants, 2021, 10, 29.	1.6	6
200	Development of Optimized Phenomic Predictors for Efficient Plant Breeding Decisions Using Phenomic-Assisted Selection in Soybean. Plant Phenomics, 2019, 2019, 5809404.	2.5	50
201	Natural variation in C. elegans arsenic toxicity is explained by differences in branched chain amino acid metabolism. ELife, 2019, 8, .	2.8	66
202	Image-based phenotyping for identification of QTL determining fruit shape and size in American cranberry (<i>Vaccinium macrocarpon</i>L.). PeerJ, 2018, 6, e5461.	0.9	32
203	Increased Predictive Accuracy of Multi-Environment Genomic Prediction Model for Yield and Related Traits in Spring Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2021, 12, 720123.	1.7	10
205	Surveying Grassland Islands: the genetics and performance of Appalachian switchgrass (Panicum) Tj ETQq1 1 0.784314 rgBT /Overloo	0.8	0
206	Subsampling and DNA pooling can increase gains through genomic selection in switchgrass. Plant Genome, 2021, 14, e20149.	1.6	3
207	Genomic selection of parents and crosses beyond the native gene pool of a breeding program. Plant Genome, 2021, 14, e20153.	1.6	1
208	QTL for seed shattering and threshability in intermediate wheatgrass align closely with well†studied orthologs from wheat, barley, and rice. Plant Genome, 2021, 14, e20145.	1.6	8
217	Population genomic analysis of Aegilops tauschii identifies targets for bread wheat improvement. Nature Biotechnology, 2022, 40, 422-431.	9.4	102
218	Identification of superior parental lines for biparental crossing via genomic prediction. PLoS ONE, 2020, 15, e0243159.	1.1	5
220	Genotyping-by-Sequencing Identifies Historical Breeding Stages of the Recently Domesticated American Cranberry. Frontiers in Plant Science, 2020, 11, 607770.	1.7	11
221	Evaluation of a new additive-dominance genomic model and implications for quantitative genetics and genomic selection. Scientia Agricola, 2022, 79, .	0.6	0
228	Strategies to Increase Prediction Accuracy in Genomic Selection of Complex Traits in Alfalfa (Medicago sativa L.). Cells, 2021, 10, 3372.	1.8	8
229	Genomic studies with preselected markers reveal dominance effects influencing growth traits in <i>Eucalyptus nitens</i>. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	8
230	Variation for Nitrogen Use Efficiency Traits in Wheat Under Contrasting Nitrogen Treatments in South-Eastern Europe. Frontiers in Plant Science, 2021, 12, 682333.	1.7	14
231	Identification of an Elite Core Panel as a Key Breeding Resource to Accelerate the Rate of Genetic Improvement for Irrigated Rice. Rice, 2021, 14, 92.	1.7	19
232	Genomic prediction of the recombination rate variation in barley â€" A route to highly recombinogenic genotypes. Plant Biotechnology Journal, 2022, 20, 676-690.	4.1	16

#	Article	IF	Citations
233	The genetic basis of the root economics spectrum in a perennial grass. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
234	Reproductive barriers in cassava: Factors and implications for genetic improvement. PLoS ONE, 2021, 16, e0260576.	1.1	8
235	Population-tailored mock genome enables genomic studies in species without a reference genome. Molecular Genetics and Genomics, 2022, 297, 33-46.	1.0	4
237	Phenomic selection is competitive with genomic selection for breeding of complex traits. The Plant Phenome Journal, 2021, 4, .	1.0	15
238	Phenomic selection in wheat breeding: identification and optimisation of factors influencing prediction accuracy and comparison to genomic selection. Theoretical and Applied Genetics, 2022, 135, 895-914.	1.8	20
239	Uncovering Novel Genomic Regions and Candidate Genes for Senescence-Related Traits by Genome-Wide Association Studies in Upland Cotton (Gossypium hirsutum L.). Frontiers in Plant Science, 2021, 12, 809522.	1.7	3
241	Strategies for Multi-trait Selection of Sweet Sorghum Progenies. Crop Breeding and Applied Biotechnology, 2021, 21, .	0.1	0
242	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. Theoretical and Applied Genetics, 2021, 134, 4043-4054.	1.8	20
244	Genomic prediction using composite training sets is an effective method for exploiting germplasm conserved in rice gene banks. Crop Journal, 2022, 10, 1073-1082.	2.3	4
245	Genome-wide association study of cassava starch paste properties. PLoS ONE, 2022, 17, e0262888.	1.1	3
246	Dissecting the Genetics of Early Vigour to Design Drought-Adapted Wheat. Frontiers in Plant Science, 2021, 12, 754439.	1.7	9
248	No disruption of rhizobial symbiosis during early stages of cowpea domestication. Evolution; International Journal of Organic Evolution, 2022, 76, 496-511.	1.1	4
249	Multiple haplotype-based analyses provide genetic and evolutionary insights into tomato fruit weight and composition. Horticulture Research, 2022, 9, .	2.9	14
250	Insights Into the Genetic Architecture of Complex Traits in Napier Grass (Cenchrus purpureus) and QTL Regions Governing Forage Biomass Yield, Water Use Efficiency and Feed Quality Traits. Frontiers in Plant Science, 2021, 12, 678862.	1.7	12
251	Genetic basis of a spontaneous mutationâ€™s expressivity. Genetics, 2022, 220, .	1.2	4
252	Genetic architecture of yield component traits in the new perennial grain crop, intermediate wheatgrass (Thinopyrum intermedium). Crop Science, 0, , .	0.8	1
253	Balancing selection gain and genetic diversity in the genomic planning of crosses. Plant Breeding, 0, , .	1.0	1
255	Analysis of genotype-by-environment interactions in a maize mapping population. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	10

#	Article	IF	Citations
257	Evaluation of Methods for Measuring Fusarium-Damaged Kernels of Wheat. Agronomy, 2022, 12, 532.	1.3	6
261	Genetic Dissection of Early Blight Resistance in Tetraploid Potato. Frontiers in Plant Science, 2022, 13, 851538.	1.7	5
262	Genome-wide association study and genomic prediction for yield and grain quality traits of hybrid rice. Molecular Breeding, 2022, 42, 1.	1.0	4
264	The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross. Nature Communications, 2022, 13, 1463.	5.8	19
265	Migration Drives the Replacement of Xanthomonas perforans Races in the Absence of Widely Deployed Resistance. Frontiers in Microbiology, 2022, 13, 826386.	1.5	4
266	Catch crop mixtures have higher potential for nutrient carry-over than pure stands under changing environments. European Journal of Agronomy, 2022, 136, 126504.	1.9	7
267	A Method for Identifying Environmental Stimuli and Genes Responsible for Genotype-by-Environment Interactions From a Large-Scale Multi-Environment Data Set. Frontiers in Genetics, 2021, 12, 803636.	1.1	7
268	Can Cross-Country Genomic Predictions Be a Reasonable Strategy to Support Germplasm Exchange? â€" A Case Study With Hydrogen Cyanide in Cassava. Frontiers in Plant Science, 2021, 12, 742638.	1.7	1
269	Harnessing Genetic Diversity in the USDA Pea Germplasm Collection Through Genomic Prediction. Frontiers in Genetics, 2021, 12, 707754.	1.1	18
270	Selection for seed size has uneven effects on specialized metabolite abundance in oat (<i>Avena) Tj ETQq1 1 0.784314 rgBT /Overloc	0.8	9
272	Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112516119.	3.3	10
273	Average semivariance directly yields accurate estimates of the genomic variance in complex trait analyses. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
274	There and back again; historical perspective and future directions for <i>Vaccinium</i> breeding and research studies. Horticulture Research, 2022, 9, .	2.9	27
317	Overview of Major Computer Packages for Genomic Prediction of Complex Traits. Methods in Molecular Biology, 2022, 2467, 157-187.	0.4	0
318	Genome and EnvironmentÂBased Prediction Models and Methods of Complex Traits Incorporating Genotype Ã— Environment Interaction. Methods in Molecular Biology, 2022, 2467, 245-283.	0.4	13
319	Enabling Breeding Selection for Biomass in Slash Pine Using UAV-Based Imaging. Plant Phenomics, 2022, 2022, 9783785.	2.5	6
320	Strong parallel evidence of selection during switchgrass sward establishment in hybrid and lowland ecotypes. , 2022, 1, 31-42.		3
321	Insights into the Genetic Architecture and Genomic Prediction of Powdery Mildew Resistance in Flax (Linum usitatissimum L.). International Journal of Molecular Sciences, 2022, 23, 4960.	1.8	12

#	ARTICLE	IF	CITATIONS
322	Dissecting the Genetic Architecture of Carbon Partitioning in Sorghum Using Multiscale Phenotypes. Frontiers in Plant Science, 2022, 13, .	1.7	7
323	Host genomic influence on bacterial composition in the switchgrass rhizosphere. Molecular Ecology, 2022, 31, 3934-3950.	2.0	13
324	Sorghum Association Panelâwholeâ€genome sequencing establishes cornerstone resource for dissecting genomic diversity. Plant Journal, 2022, 111, 888-904.	2.8	20
325	Geographical Variation in the Growth and Nutritional Traits of Leaf Powder from Broussonetia papyrifera (L.) Lâ€™HÃ©r. ex Vent. from Different Provenances. Forests, 2022, 13, 868.	0.9	1
326	Phenotypic and Genetic Characterization of the Lentil Single Plant-Derived Core Collection for Resistance to Root Rot Caused by <i>Fusarium avenaceum</i>. Phytopathology, 2022, 112, 1979-1987.	1.1	3
328	Biomass yield improvement in switchgrass through genomic prediction of flowering time. GCB Bioenergy, 2022, 14, 1023-1034.	2.5	2
329	The impact of species-wide gene expression variation on Caenorhabditis elegans complex traits. Nature Communications, 2022, 13, .	5.8	23
330	Genetic correlations between switchgrass performance in sward conditions and surrogate measures. Crop Science, 2022, 62, 1511-1521.	0.8	3
331	Detection of Stable Elite Haplotypes and Potential Candidate Genes of Boll Weight Across Multiple Environments via GWAS in Upland Cotton. Frontiers in Plant Science, 0, 13, .	1.7	6
332	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. BMC Genomics, 2022, 23, .	1.2	11
333	Contrasting Water Withholding Responses of Young Maize Plants Reveal Link Between Lipid Peroxidation and Osmotic Regulation Corroborated by Genetic Analysis. Frontiers in Plant Science, 0, 13, .	1.7	1
334	The Unique Seed Protein Composition of Quality Protein Popcorn Promotes Growth of Beneficial Bacteria From the Human Gut Microbiome. Frontiers in Microbiology, 0, 13, .	1.5	1
335	The genetic basis for panicle trait variation in switchgrass (Panicum virgatum). Theoretical and Applied Genetics, 2022, 135, 2577-2592.	1.8	2
337	Accurate predictions of barley phenotypes using genomewide markers and environmental covariates. Crop Science, 0, , .	0.8	4
338	Training population optimization for genomic selection improves the predictive ability of a costly measure in bread wheat, the gliadin to glutenin ratio. Euphytica, 2022, 218, .	0.6	3
339	Selection of parental lines for plant breeding via genomic prediction. Frontiers in Plant Science, 0, 13, .	1.7	3
340	Genome-wide association mapping identifies common bunt (Tilletia caries) resistance loci in bread wheat (Triticum aestivum) accessions of the USDA National Small Grains Collection. Theoretical and Applied Genetics, 2022, 135, 3103-3115.	1.8	4
341	Association analyses of host genetics, root-colonizing microbes, and plant phenotypes under different nitrogen conditions in maize. ELife, 0, 11, .	2.8	22

#	ARTICLE	IF	CITATIONS
342	Analysis of historical selection in winter wheat. Theoretical and Applied Genetics, 2022, 135, 3005-3023.	1.8	6
344	Host genotype controls ecological change in the leaf fungal microbiome. PLoS Biology, 2022, 20, e3001681.	2.6	14
345	Phenomic selection in wheat breeding: prediction of the genotype-by-environment interaction in multi-environment breeding trials. Theoretical and Applied Genetics, 0, , .	1.8	1
346	Multitrait Bayesian shrinkage and variable selection models with the BGLR-R package. Genetics, 2022, 222, .	1.2	16
347	Genetic Parameters and Genomic Regions Underlying Growth and Linear Type Traits in Akkaraman Sheep. Genes, 2022, 13, 1414.	1.0	13
348	Integrated Approach in Genomic Selection to Accelerate Genetic Gain in Sugarcane. Plants, 2022, 11, 2139.	1.6	9
351	Genetic analysis of maize grain yield components and physiological determinants under contrasting nitrogen availability. Crop and Pasture Science, 2023, 74, 182-193.	0.7	1
352	Association mapping across a multitude of traits collected in diverse environments in maize. GigaScience, 2022, 11, .	3.3	14
353	Geographic variation in growth and wood traits of <i>Neolamarckia cadamba</i> in China. Forestry Research, 2022, 2, 0-0.	0.5	1
354	learnMET: an R package to apply machine learning methods for genomic prediction using multi-environment trial data. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	9
355	A Pleiotropic Flowering Time QTL Exhibits Gene-by-Environment Interaction for Fitness in a Perennial Grass. Molecular Biology and Evolution, 2022, 39, .	3.5	2
357	Live soil inocula, not host population or domestication status, is the predominant driver of growth benefits to cowpea. Plant and Soil, 0, , .	1.8	0
358	Accuracy of Genomic Prediction of Yield and Sugar Traits in Saccharum spp. Hybrids. Agriculture (Switzerland), 2022, 12, 1436.	1.4	2
359	Identification of a <scp>UDP</scp>â€glucosyltransferase conferring deoxynivalenol resistance in <i>Aegilops tauschii</i> and wheat. Plant Biotechnology Journal, 2023, 21, 109-121.	4.1	4
362	Genomic footprints of selection in early-and late-flowering pearl millet landraces. Frontiers in Plant Science, 0, 13, .	1.7	1
363	Genotyping marker density and prediction models effects in long-term breeding schemes of cross-pollinated crops. Theoretical and Applied Genetics, 2022, 135, 4523-4539.	1.8	3
364	Quantitative trait loci related to growth and wood quality traits in Eucalyptus grandis W. Hill identified through single- and multi-trait genome-wide association studies. Tree Genetics and Genomes, 2022, 18, .	0.6	0
365	Relationship between total and differential quarter somatic cell counts at dry-off and early lactation. PLoS ONE, 2022, 17, e0275755.	1.1	6

#	Article	IF	Citations
366	Estimates of genomic heritability and genome-wide association studies for blood parameters in Akkaraman sheep. Scientific Reports, 2022, 12, .	1.6	4
367	Revealing the interaction effect on the accuracy of genomic selection between marker density and genetic architecture. Aquaculture, 2023, 563, 739022.	1.7	0
368	Bite Force Performance from wild Derived mice has Undetectable Heritability Despite Having Heritable Morphological Components. Evolutionary Biology, 0, , .	0.5	0
369	Genotype A— <math xmlns="http://www.w3.org/1998/Math/MathML" altimg="urn:x-wiley:00029122:media:ajb216091:ajb216091-math-0001" wiley:location="equation/ajb216091-math-0001.png"><mrow><mrow><mo>unicode{x000D7}</mo><mrow environment interaction obscures genetic sources of variation in seed size in <i>Dithyrea californica</i> but provides the opportunity for selection on phenotypic plasticity. American Journal of Botany, 2022, 109, 1847-1860.	0.8	2
371	Stacked kinship CNN vs. GBLUP for genomic predictions of additive and complex continuous phenotypes. Scientific Reports, 2022, 12, .	1.6	7
372	Multi-Trait Genomic Prediction Improves Accuracy of Selection among Doubled Haploid Lines in Maize. International Journal of Molecular Sciences, 2022, 23, 14558.	1.8	1
373	Genomic Analysis of Gastrointestinal Parasite Resistance in Akkaraman Sheep. Genes, 2022, 13, 2177.	1.0	5
374	Effects of Different Methods and Genomic Relationship Matrices on Reliabilities of Genomic Selection in Dairy Cattle. RIMAK International Journal of Humanities and Social Sciences, 0, , .	0.0	0
375	Improving the efficiency of multi-location field trials with complete and incomplete relationship information. Euphytica, 2023, 219, .	0.6	0
376	The Development of Forest Genetic Breeding and the Application of Genome Selection and CRISPR/Cas9 in Forest Breeding. Forests, 2022, 13, 2116.	0.9	0
377	Genomic prediction of hybrid performance for agronomic traits in sorghum. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	2
378	Modelling internal tree attributes for breeding applications in Douglas-fir progeny trials using RPAS-ALS. Science of Remote Sensing, 2023, 7, 100072.	2.2	1
379	Increasing cassava root yield: Additive-dominant genetic models for selection of parents and clones. Frontiers in Plant Science, 0, 13, .	1.7	3
380	Genomic prediction of switchgrass winter survivorship across diverse lowland populations. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	1
381	Switchgrass sward establishment selection is consistent across multiple environments and fertilization levels. , 0, , .		0
382	Modeling the influence of phenotypic plasticity on maize hybrid performance. Plant Communications, 2023, 4, 100548.	3.6	3
383	Alternative scoring methods of fusarium head blight resistance for genomic assisted breeding. Frontiers in Plant Science, 0, 13, .	1.7	0
385	Genetic analyses of tropical maize lines under artificial infestation of fall armyworm and foliar diseases under optimum conditions. Frontiers in Plant Science, 0, 14, .	1.7	2

#	Article	IF	Citations
386	Genome-wide association and genomic prediction for resistance to southern corn rust in DH and testcross populations. Frontiers in Plant Science, 0, 14, .	1.7	1
387	Initiation of genomics-assisted breeding in Virginia-type peanuts through the generation of a de novo reference genome and informative markers. Frontiers in Plant Science, 0, 13, .	1.7	3
388	Combining datasets to routinely predict fusarium head blight resistance in a wheat breeding program. Crop Science, 2023, 63, 1197-1208.	0.8	0
389	Genomics Assisted Breeding Strategy in Flax. Compendium of Plant Genomes, 2023, , 253-272.	0.3	1
390	White Lupin Adaptation to Moderately Calcareous Soils: Phenotypic Variation and Genome-Enabled Prediction. Plants, 2023, 12, 1139.	1.6	0
391	Genome-Wide Scan of Wool Production Traits in Akkaraman Sheep. Genes, 2023, 14, 713.	1.0	7
393	Marker-assisted selection in a Pacific oyster population for an antiviral QTL conferring increased survival to OsHV-1 mortality events in Tomales Bay. Aquaculture, 2023, 567, 739291.	1.7	6
394	Genetic diversity and local adaption of alfalfa populations (Medicago sativa L.) under long-term grazing. Scientific Reports, 2023, 13, .	1.6	3
395	Genomeâ€wide association study for bacterial leaf streak resistance in maize. Agronomy Journal, 2023, 115, 1051-1058.	0.9	1
396	Genetic analysis and elite tree selection of the main resin components of slash pine. Frontiers in Plant Science, 0, 14, .	1.7	5
397	Which mouse multiparental population is right for your study? The Collaborative Cross inbred strains, their F1 hybrids, or the Diversity Outbred population. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	7
398	Inbred phenotypic data and nonâ€additive effects can enhance genomic prediction models for hybrid grain sorghum. Crop Science, 2023, 63, 1183-1196.	0.8	2
399	Syntenic Cell Wall QTLs as Versatile Breeding Tools: Intraspecific Allelic Variability and Predictability of Biomass Quality Loci in Target Plant Species. Plants, 2023, 12, 779.	1.6	0
400	284. Considering chromosomal trait correlations improves accuracy of genomic prediction. , 2022, , .		0
401	Construction of a high-density genetic map and dissection of genetic architecture of six agronomic traits in tobacco (Nicotiana tabacum L.). Frontiers in Plant Science, 0, 14, .	1.7	1
402	HIBLUP: an integration of statistical models on the BLUP framework for efficient genetic evaluation using big genomic data. Nucleic Acids Research, 2023, 51, 3501-3512.	6.5	13
403	Genomeâ€wide association mapping for preâ€harvest sprouting in European winter wheat detects novel resistance QTL, pleiotropic effects, and structural variation in multiple genomes. Plant Genome, 0, , .	1.6	2
404	Comparison of genotypic and phenotypic selection of breeding parents in a carrot (<i>Daucus) Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	0

#	Article	IF	Citations
405	Genetics of destemming in pepper: A step towards mechanical harvesting. Frontiers in Genetics, 0, 14, .	1.1	0
406	Fully efficient, two-stage analysis of multi-environment trials with directional dominance and multi-trait genomic selection. Theoretical and Applied Genetics, 2023, 136, .	1.8	5
407	Toward combining qualitative race-specific and quantitative race-nonspecific disease resistance by genomic selection. Theoretical and Applied Genetics, 2023, 136, .	1.8	2
408	Interplay Between Polymorphic Short Tandem Repeats and Gene Expression Variation in <i>Caenorhabditis elegans</i>. Molecular Biology and Evolution, 2023, 40, .	3.5	2
409	Genomic prediction of rice mesocotyl length indicative of directing seeding suitability using a half-sib hybrid population. PLoS ONE, 2023, 18, e0283989.	1.1	0
410	Single and multi-trait genomic prediction for agronomic traits in Euterpe edulis. PLoS ONE, 2023, 18, e0275407.	1.1	1
411	Genetic determinants of switchgrass-root-associated microbiota in field sites spanning its natural range. Current Biology, 2023, 33, 1926-1938.e6.	1.8	11