

# Methodological implementation of mixed linear models association studies

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Citation Report

#	ARTICLE	IF	CITATIONS
1	pLARmEB: integration of least angle regression with empirical Bayes for multilocus genome-wide association studies. <i>Heredity</i> , 2017, 118, 517-524.	1.2	231
2	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478.	1.6	69
3	pKWmEB: integration of Kruskal-Wallis test with empirical Bayes under polygenic background control for multi-locus genome-wide association study. <i>Heredity</i> , 2018, 120, 208-218.	1.2	175
4	Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in <i>Coffea arabica</i> L. <i>Scientific Reports</i> , 2018, 8, 465.	1.6	53
5	Multi-Locus Genome-Wide Association Studies for 14 Main Agronomic Traits in Barley. <i>Frontiers in Plant Science</i> , 2018, 9, 1683.	1.7	40
6	Identification of QTNs Controlling Seed Protein Content in Soybean Using Multi-Locus Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 1690.	1.7	40
7	GWAS Analysis and QTL Identification of Fiber Quality Traits and Yield Components in Upland Cotton Using Enriched High-Density SNP Markers. <i>Frontiers in Plant Science</i> , 2018, 9, 1067.	1.7	99
8	The Application of Multi-Locus GWAS for the Detection of Salt-Tolerance Loci in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1464.	1.7	94
9	Genome-Wide Association Mapping of Starch Pasting Properties in Maize Using Single-Locus and Multi-Locus Models. <i>Frontiers in Plant Science</i> , 2018, 9, 1311.	1.7	71
10	Deciphering the Genetic Architecture of Cooked Rice Texture. <i>Frontiers in Plant Science</i> , 2018, 9, 1405.	1.7	34
11	Genome-wide generation and genotyping of informative SNPs to scan molecular signatures for seed yield in chickpea. <i>Scientific Reports</i> , 2018, 8, 13240.	1.6	27
12	Single-Locus and Multi-Locus Genome-Wide Association Studies in the Genetic Dissection of Fiber Quality Traits in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1083.	1.7	74
13	Multi-Locus Genome-Wide Association Studies of Fiber-Quality Related Traits in Chinese Early-Maturity Upland Cotton. <i>Frontiers in Plant Science</i> , 2018, 9, 1169.	1.7	54
14	Genome-Wide Association Studies of Free Amino Acid Levels by Six Multi-Locus Models in Bread Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1196.	1.7	59
15	Genome-Wide Association Studies of Photosynthetic Traits Related to Phosphorus Efficiency in Soybean. <i>Frontiers in Plant Science</i> , 2018, 9, 1226.	1.7	56
16	Genetic Dissection of Maize Embryonic Callus Regenerative Capacity Using Multi-Locus Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 561.	1.7	99
17	Multi-Locus Genome-Wide Association Study Reveals the Genetic Architecture of Stalk Lodging Resistance-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 611.	1.7	103
18	Genome-wide association study and genomic prediction using parental and breeding populations of Japanese pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Scientific Reports</i> , 2018, 8, 11994.	1.6	51

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19	Genome-Wide Association Studies for Five Forage Quality-Related Traits in Sorghum ( <i>Sorghum bicolor</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 T	1.7	34
20	Genetic Detection of Lint Percentage Applying Single-Locus and Multi-Locus Genome-Wide Association Studies in Chinese Early-Maturity Upland Cotton. <i>Frontiers in Plant Science</i> , 2019, 10, 964.	1.7	11
21	Single-Locus and Multi-Locus Genome-Wide Association Studies for Intramuscular Fat in Duroc Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 619.	1.1	47
22	Whole-genome re-sequencing association study for direct genetic effects and social genetic effects of six growth traits in Large White pigs. <i>Scientific Reports</i> , 2019, 9, 9667.	1.6	9
23	Combination of multi-locus genome-wide association study and QTL mapping reveals genetic basis of tassel architecture in maize. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1421-1440.	1.0	12
24	On the Population Dynamics of Junk: A Review on the Population Genomics of Transposable Elements. <i>Genes</i> , 2019, 10, 419.	1.0	94
25	Genome-wide association study of pre-harvest sprouting tolerance using a 90K SNP array in common wheat ( <i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2947-2963.	1.8	48
26	A Fast and Powerful Empirical Bayes Method for Genome-Wide Association Studies. <i>Animals</i> , 2019, 9, 305.	1.0	3
27	Multi-environments and multi-models association mapping identified candidate genes of lint percentage and seed index in <i>Gossypium hirsutum</i> L.. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	7
28	Genome-wide association studies in the genetic dissection of ovule number, seed number, and seed weight in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2019, 142, 111877.	2.5	32
29	Estimation of a significance threshold for genome-wide association studies. <i>BMC Genomics</i> , 2019, 20, 618.	1.2	100
30	Core set construction and association analysis of <i>Pinus massoniana</i> from Guangdong province in southern China using SLAF-seq. <i>Scientific Reports</i> , 2019, 9, 13157.	1.6	12
31	Population Structure and Implications on the Genetic Architecture of HIV-1 Phenotypes Within Southern Africa. <i>Frontiers in Genetics</i> , 2019, 10, 905.	1.1	15
32	Comparing Single-€SNP, Multi-€SNP, and Haplotype-€Based Approaches in Association Studies for Major Traits in Barley. <i>Plant Genome</i> , 2019, 12, 1-14.	1.6	48
33	Evaluation of Genomic Prediction for PasmO Resistance in Flax. <i>International Journal of Molecular Sciences</i> , 2019, 20, 359.	1.8	45
34	Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 5115-5130.	2.4	30
35	Genetic dissection of drought and heat-€responsive agronomic traits in wheat. <i>Plant, Cell and Environment</i> , 2019, 42, 2540-2553.	2.8	100
36	Candidate quantitative trait loci and genes for fiber quality in <i>Gossypium hirsutum</i> L. detected using single- and multi-locus association mapping. <i>Industrial Crops and Products</i> , 2019, 134, 356-369.	2.5	12

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37	High density linkage map construction and QTL mapping for runner production in allo-octoploid strawberry <i>Fragaria</i> × <i>Ananassa</i> based on ddRAD-seq derived SNPs. <i>Scientific Reports</i> , 2019, 9, 3275.	1.6	19
38	Genome-Wide Association Studies for PasmO Resistance in Flax ( <i>Linum usitatissimum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1982.	1.7	56
39	Editorial: The Applications of New Multi-Locus GWAS Methodologies in the Genetic Dissection of Complex Traits. <i>Frontiers in Plant Science</i> , 2019, 10, 100.	1.7	121
40	TSLRF: Two-Stage Algorithm Based on Least Angle Regression and Random Forest in genome-wide association studies. <i>Scientific Reports</i> , 2019, 9, 18034.	1.6	6
41	The Complex Genetic Architecture of Early Root and Shoot Traits in Flax Revealed by Genome-Wide Association Analyses. <i>Frontiers in Plant Science</i> , 2019, 10, 1483.	1.7	24
42	An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. <i>Briefings in Bioinformatics</i> , 2019, 20, 1913-1924.	3.2	74
43	Genome-wide association studies using binned genotypes. <i>Heredity</i> , 2020, 124, 288-298.	1.2	5
45	Genetic dissection of zinc, iron, copper, manganese and phosphorus in wheat ( <i>Triticum aestivum</i> L.) grain and rachis at two developmental stages. <i>Plant Science</i> , 2020, 291, 110338.	1.7	55
46	Genome-wide dissection of hybridization for fiber quality and yield-related traits in upland cotton. <i>Plant Journal</i> , 2020, 104, 1285-1300.	2.8	9
47	The improved FASTmrEMMA and GCIM algorithms for genome-wide association and linkage studies in large mapping populations. <i>Crop Journal</i> , 2020, 8, 723-732.	2.3	10
48	Identification of QTNs Controlling 100-Seed Weight in Soybean Using Multilocus Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2020, 11, 689.	1.1	26
49	Detection of QTL and QTN and candidate genes for oil content in soybean using a combination of four-way-RIL and germplasm populations. <i>Crop Journal</i> , 2020, 8, 802-811.	2.3	7
50	Genome-wide association studies and whole-genome prediction reveal the genetic architecture of KRN in maize. <i>BMC Plant Biology</i> , 2020, 20, 490.	1.6	14
51	Identification of New Leaf Rust Resistance Loci in Wheat and Wild Relatives by Array-Based SNP Genotyping and Association Genetics. <i>Frontiers in Plant Science</i> , 2020, 11, 583738.	1.7	29
52	QTL mapping and GWAS for field kernel water content and kernel dehydration rate before physiological maturity in maize. <i>Scientific Reports</i> , 2020, 10, 13114.	1.6	6
53	Multi-locus genome-wide association studies reveal novel genomic regions associated with vegetative stage salt tolerance in bread wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2020, 112, 4608-4621.	1.3	32
54	Multi-trait multi-locus SEM model discriminates SNPs of different effects. <i>BMC Genomics</i> , 2020, 21, 490.	1.2	5
55	Multi-Locus GWAS of Quality Traits in Bread Wheat: Mining More Candidate Genes and Possible Regulatory Network. <i>Frontiers in Plant Science</i> , 2020, 11, 1091.	1.7	42

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56	ddRAD-seq derived genome-wide SNPs, high density linkage map and QTLs for fruit quality traits in strawberry ( <i>Fragaria x ananassa</i> ). <i>3 Biotech</i> , 2020, 10, 353.	1.1	4
57	Decryption of favourable haplotypes and potential candidate genes for five fibre quality properties using a relatively novel genome-wide association study procedure in upland cotton. <i>Industrial Crops and Products</i> , 2020, 158, 113004.	2.5	7
58	Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. <i>BMC Plant Biology</i> , 2020, 20, 404.	1.6	28
59	Genome-wide association studies of ionomic and agronomic traits in USDA mini core collection of rice and comparative analyses of different mapping methods. <i>BMC Plant Biology</i> , 2020, 20, 441.	1.6	25
60	Combining Random Forests and a Signal Detection Method Leads to the Robust Detection of Genotype-Phenotype Associations. <i>Genes</i> , 2020, 11, 892.	1.0	12
61	Appraising the Genetic Architecture of Kernel Traits in Hexaploid Wheat Using GWAS. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5649.	1.8	19
62	Genome-Wide Association Study (GWAS) for Resistance to <i>Sclerotinia sclerotiorum</i> in Common Bean. <i>Genes</i> , 2020, 11, 1496.	1.0	10
63	Genome-wide association identifies several QTLs controlling cysteine and methionine content in soybean seed including some promising candidate genes. <i>Scientific Reports</i> , 2020, 10, 21812.	1.6	12
64	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
65	JS-MA: A Jensen-Shannon Divergence Based Method for Mapping Genome-Wide Associations on Multiple Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 507038.	1.1	6
66	Genome-wide association study of partial resistance to sclerotinia stem rot of cultivated soybean based on the detached leaf method. <i>PLoS ONE</i> , 2020, 15, e0233366.	1.1	9
67	Genome-wide association analyses identify known and novel loci for teat number in Duroc pigs using single-locus and multi-locus models. <i>BMC Genomics</i> , 2020, 21, 344.	1.2	43
68	<i>HiG</i> was: how to compute longitudinal GWAS data in population designs. <i>Bioinformatics</i> , 2020, 36, 4222-4224.	1.8	1
69	Genome-Wide Association Mapping of Dark Green Color Index using a Diverse Panel of Soybean Accessions. <i>Scientific Reports</i> , 2020, 10, 5166.	1.6	13
70	Comparing Different Statistical Models and Multiple Testing Corrections for Association Mapping in Soybean and Maize. <i>Frontiers in Plant Science</i> , 2019, 10, 1794.	1.7	118
71	Linkage Analysis and Multi-Locus Genome-Wide Association Studies Identify QTNs Controlling Soybean Plant Height. <i>Frontiers in Plant Science</i> , 2020, 11, 9.	1.7	20
72	Genomic Prediction Accuracy of Seven Breeding Selection Traits Improved by QTL Identification in Flax. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1577.	1.8	21
73	Identification of QTNs and Their Candidate Genes for 100-Seed Weight in Soybean ( <i>Glycine max</i> L.) Using Multi-Locus Genome-Wide Association Studies. <i>Genes</i> , 2020, 11, 714.	1.0	22

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74	Identification of QTL and genes for pod number in soybean by linkage analysis and genome-wide association studies. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	14
75	Three-dimensional genetic networks among seed oil-related traits, metabolites and genes reveal the genetic foundations of oil synthesis in soybean. <i>Plant Journal</i> , 2020, 103, 1103-1124.	2.8	26
76	Loci harboring genes with important role in drought and related abiotic stress responses in flax revealed by multiple GWAS models. <i>Theoretical and Applied Genetics</i> , 2021, 134, 191-212.	1.8	23
77	Exploiting genetic diversity in two European maize landraces for improving <i>Gibberella</i> ear rot resistance using genomic tools. <i>Theoretical and Applied Genetics</i> , 2021, 134, 793-805.	1.8	18
78	Detection of QTNs for kernel moisture concentration and kernel dehydration rate before physiological maturity in maize using multi-locus GWAS. <i>Scientific Reports</i> , 2021, 11, 1764.	1.6	12
79	A Multi-Locus Association Model Framework for Nested Association Mapping With Discriminating QTL Effects in Various Subpopulations. <i>Frontiers in Genetics</i> , 2020, 11, 590012.	1.1	3
80	Fine mapping QTL and mining genes for protein content in soybean by the combination of linkage and association analysis. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1095-1122.	1.8	8
81	Mapping QTL/QTN and mining candidate genes for plant height and its response to planting densities in soybean [ <i>Glycine max</i> (L.) Merr.] through a FW-RIL population. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	2
82	Multi-Locus Genome-Wide Association Studies Reveal Fruit Quality Hotspots in Peach Genome. <i>Frontiers in Plant Science</i> , 2021, 12, 644799.	1.7	18
83	Genome-wide association study identified candidate genes for seed size and seed composition improvement in <i>M. truncatula</i> . <i>Scientific Reports</i> , 2021, 11, 4224.	1.6	11
84	A Fast Multi-Locus Ridge Regression Algorithm for High-Dimensional Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 649196.	1.1	1
85	Genome-Wide Association Study of Brown Rot ( <i>Monilinia</i> spp.) Tolerance in Peach. <i>Frontiers in Plant Science</i> , 2021, 12, 635914.	1.7	17
86	Uncovering genomic regions controlling plant architectural traits in hexaploid wheat using different GWAS models. <i>Scientific Reports</i> , 2021, 11, 6767.	1.6	33
87	Understanding the metabolome and metagenome as extended phenotypes: The next frontier in macroalgae domestication and improvement. <i>Journal of the World Aquaculture Society</i> , 2021, 52, 1009-1030.	1.2	6
88	Genetic dissection of flowering time in flax ( <i>Linum usitatissimum</i> L.) through single- and multi-locus genome-wide association studies. <i>Molecular Genetics and Genomics</i> , 2021, 296, 877-891.	1.0	16
89	Superior haplotypes towards development of low glycemic index rice with preferred grain and cooking quality. <i>Scientific Reports</i> , 2021, 11, 10082.	1.6	15
90	Genome-wide association mapping of the "super-soft"™ kernel texture in white winter wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2547-2559.	1.8	12
92	Genome-wide association study and its applications in the non-model crop <i>Sesamum indicum</i> . <i>BMC Plant Biology</i> , 2021, 21, 283.	1.6	20

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93	Genome-Wide Association Mapping of bc-1 and bc-u Reveals Candidate Genes and New Adjustments to the Host-Pathogen Interaction for Resistance to Bean Common Mosaic Necrosis Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 699569.	1.7	10
94	Identification of QTNs and their candidate genes for flowering time and plant height in soybean using multi-locus genome-wide association studies. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	7
95	Multi-Allelic Haplotype-Based Association Analysis Identifies Genomic Regions Controlling Domestication Traits in Intermediate Wheatgrass. <i>Agriculture (Switzerland)</i> , 2021, 11, 667.	1.4	9
96	Multi-Locus Genome-Wide Association Study and Genomic Selection of Kernel Moisture Content at the Harvest Stage in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 697688.	1.7	5
97	Exploiting natural variation in crown root traits via genome-wide association studies in maize. <i>BMC Plant Biology</i> , 2021, 21, 346.	1.6	10
98	Using chlorate as an analogue to nitrate to identify candidate genes for nitrogen use efficiency in barley. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	4
99	Identification and validation of a novel locus, Qpm-3BL, for adult plant resistance to powdery mildew in wheat using multilocus GWAS. <i>BMC Plant Biology</i> , 2021, 21, 357.	1.6	14
100	Genetic Dissection of Seedling Root System Architectural Traits in a Diverse Panel of Hexaploid Wheat through Multi-Locus Genome-Wide Association Mapping for Improving Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7188.	1.8	20
101	Favorable pleiotropic loci for fiber yield and quality in upland cotton ( <i>Gossypium hirsutum</i> ). <i>Scientific Reports</i> , 2021, 11, 15935.	1.6	5
102	QTL for Main Stem Node Number and Its Response to Plant Densities in 144 Soybean FW-RILs. <i>Frontiers in Plant Science</i> , 2021, 12, 666796.	1.7	2
103	Multi-locus genome-wide association studies for five yield-related traits in rice. <i>BMC Plant Biology</i> , 2021, 21, 364.	1.6	22
104	Genome-Wide Association Analysis Reveals Loci and Candidate Genes Involved in Fiber Quality Traits Under Multiple Field Environments in Cotton ( <i>Gossypium hirsutum</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 695503.	1.7	12
105	Genetic architecture of maize yield traits dissected by QTL mapping and GWAS in maize. <i>Crop Journal</i> , 2022, 10, 436-446.	2.3	17
106	Validation of Genes Affecting Rice Grain Zinc Content Through Candidate Gene-Based Association Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 701658.	1.1	4
107	Genome-wide association mapping reveals key genomic regions for physiological and yield-related traits under salinity stress in wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2021, 113, 3198-3215.	1.3	22
108	Genome-Wide Association Study of QTLs Conferring Resistance to Bacterial Leaf Streak in Rice. <i>Plants</i> , 2021, 10, 2039.	1.6	6
109	The Effect of Population Structure on Murine Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 745361.	1.1	7
110	An Efficient Score Test Integrated with Empirical Bayes for Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 742752.	1.1	1

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111	Status and prospects of genome-wide association studies in plants. <i>Plant Genome</i> , 2021, 14, e20077.	1.6	200
114	Novel stripe rust all-stage resistance loci identified in a worldwide collection of durum wheat using genome-wide association mapping. <i>Plant Genome</i> , 2021, 14, e20136.	1.6	7
115	Advances and Challenges for QTL Analysis and GWAS in the Plant-Breeding of High-Yielding: A Focus on Rapeseed. <i>Biomolecules</i> , 2021, 11, 1516.	1.8	19
116	Genome-Wide Association Study Identifies Genomic Regions for Important Morpho-Agronomic Traits in Mesoamerican Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 748829.	1.7	6
117	Genome-Wide Composite Interval Mapping (GCIM) of Expressional Quantitative Trait Loci in Backcross Population. <i>Methods in Molecular Biology</i> , 2020, 2082, 63-71.	0.4	1
118	SNP- and Haplotype-Based GWAS of Flowering-Related Traits in <i>Brassica napus</i> . <i>Plants</i> , 2021, 10, 2475.	1.6	12
119	Complex adaptive architecture underlies adaptation to quantitative host resistance in a fungal plant pathogen. <i>Molecular Ecology</i> , 2021, , .	2.0	0
120	Genome-Wide Association Studies of Soybean Yield-Related Hyperspectral Reflectance Bands Using Machine Learning-Mediated Data Integration Methods. <i>Frontiers in Plant Science</i> , 2021, 12, 777028.	1.7	26
121	Identification of quantitative trait nucleotides and candidate genes for tuber yield and mosaic virus tolerance in an elite population of white guinea yam ( <i>Dioscorea rotundata</i> ) using genome-wide association scan. <i>BMC Plant Biology</i> , 2021, 21, 552.	1.6	15
122	Uncovering Novel Genomic Regions and Candidate Genes for Senescence-Related Traits by Genome-Wide Association Studies in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 809522.	1.7	3
123	Genome-wide association studies for growth traits in broilers. <i>BMC Genomic Data</i> , 2022, 23, 1.	0.7	16
126	Application of multi-locus GWAS for the detection of bruchid resistance loci in cowpea ( <i>Vigna unguiculata</i> ). <i>Plant Breeding</i> , 2022, 141, 439-450.	1.0	5
127	A compressed variance component mixed model for detecting QTNs and QTN-by-environment and QTN-by-QTN interactions in genome-wide association studies. <i>Molecular Plant</i> , 2022, 15, 630-650.	3.9	53
128	Maize Epistasis Detection by Multi-class Quantitative Multifactor Dimensionality Reduction. , 2021, , .		1
129	Coding Mutations in Vacuolar Protein-Sorting 4 AAA+ ATPase Endosomal Sorting Complexes Required for Transport Protein Homologs Underlie bc-2 and New bc-4 Gene Conferring Resistance to Bean Common Mosaic Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 769247.	1.7	12
130	Association analysis for resistance to <i>Striga hermonthica</i> in diverse tropical maize inbred lines. <i>Scientific Reports</i> , 2021, 11, 24193.	1.6	15
131	Multi-locus genome-wide association studies (ML-GWAS) reveal novel genomic regions associated with seedling and adult plant stage leaf rust resistance in bread wheat ( <i>Triticum aestivum</i> L.). <i>Heredity</i> , 2022, 128, 434-449.	1.2	15
224	Genetic Bases of Complex Traits: From Quantitative Trait Loci to Prediction. <i>Methods in Molecular Biology</i> , 2022, 2467, 1-44.	0.4	0



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225	Insights into the Genetic Architecture and Genomic Prediction of Powdery Mildew Resistance in Flax ( <i>Linum usitatissimum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 4960.	1.8	12
226	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
227	Genetic diversity analysis and GWAS reveal the adaptive loci of milling and appearance quality of japonica rice ( <i>Oryza sativa</i> L.) in Northeast China. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1539-1550.	1.7	3
228	Machine-Learning-Based Genome-Wide Association Studies for Uncovering QTL Underlying Soybean Yield and Its Components. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5538.	1.8	20
230	Genome-Wide Association Study Statistical Models: A Review. <i>Methods in Molecular Biology</i> , 2022, , 43-62.	0.4	10
231	Domestication and improvement genes reveal the differences of seed size- and oil-related traits in soybean domestication and improvement. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2951-2964.	1.9	7
232	Identification of QTNs Associated With Flowering Time, Maturity, and Plant Height Traits in <i>Linum usitatissimum</i> L. Using Genome-Wide Association Study. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
233	Genetic architecture of end-use quality traits in soft white winter wheat. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
234	Association mapping of plant sex and cross-compatibility related traits in white Guinea yam ( <i>Dioscorea</i> ) Tj ETQq0 0,0rgBT /Oylock 10	1.6	4
235	Identification of major genomic regions for soybean seed weight by genome-wide association study. <i>Molecular Breeding</i> , 2022, 42, .	1.0	4
237	Genome-Wide Association Study of Grain Quality Traits in Rice Detected Genomic Regions of High-Quality Rice for Increasing Rice Consumption. <i>Biosciences, Biotechnology Research Asia</i> , 2022, 19, 333-346.	0.2	1
238	Genome-Wide Association Studies of Root-Related Traits in <i>Brassica napus</i> L. under Low-Potassium Conditions. <i>Plants</i> , 2022, 11, 1826.	1.6	3
239	Integrating multi-locus genome-wide association studies with transcriptomic data to identify genetic loci underlying adult root trait responses to drought stress in flax ( <i>Linum usitatissimum</i> L.). <i>Environmental and Experimental Botany</i> , 2022, 202, 105019.	2.0	4
240	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
241	Genome-wide association study identified genes associated with ammonia nitrogen tolerance in <i>Litopenaeus vannamei</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
242	Genetic architecture behind developmental and seasonal control of tree growth and wood properties in Norway spruce. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
243	A multi-locus genome-wide association study reveals the genetics underlying muscadine antioxidant in berry skin. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
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