

# Variance component model to account for sample structure in genome-wide association studies

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Signaling Initiated by Overexpression of the Fibroblast Growth Factor Receptor-1 Investigated by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 29-36.	2.5	73
3	New approaches to population stratification in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 459-463.	7.7	1,047
4	Statistical analysis strategies for association studies involving rare variants. <i>Nature Reviews Genetics</i> , 2010, 11, 773-785.	7.7	426
5	Towards identifying genes underlying ecologically relevant traits in <i>Arabidopsis thaliana</i> . <i>Nature Reviews Genetics</i> , 2010, 11, 867-879.	7.7	297
6	Robust relationship inference in genome-wide association studies. <i>Bioinformatics</i> , 2010, 26, 2867-2873.	1.8	2,328
7	Conditions Under Which Genome-Wide Association Studies Will be Positively Misleading. <i>Genetics</i> , 2010, 186, 1045-1052.	1.2	178
8	Association mapping of local climate-sensitive quantitative trait loci in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21199-21204.	3.3	278
9	Genome-wide association studies in plants: the missing heritability is in the field. <i>Genome Biology</i> , 2011, 12, 232.	13.9	502
10	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	13.7	2,400
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16	The Genetics of Winterhardiness in Barley: Perspectives from Genome-Wide Association Mapping. <i>Plant Genome</i> , 2011, 4, .	1.6	62
17	Accounting for Population Stratification in Practice: A Comparison of the Main Strategies Dedicated to Genome-Wide Association Studies. <i>PLoS ONE</i> , 2011, 6, e28845.	1.1	53
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21	Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. <i>Molecular Ecology</i> , 2011, 20, 2555-2566.	2.0	217
22	Genome-wide association analysis of clinical vs. nonclinical origin provides insights into <i>Saccharomyces cerevisiae</i> pathogenesis. <i>Molecular Ecology</i> , 2011, 20, 4085-4097.	2.0	46
23	A Comparison of Association Methods Correcting for Population Stratification in Case-Control Studies. <i>Annals of Human Genetics</i> , 2011, 75, 418-427.	0.3	83
24	A Novel Method to Detect Gene-Gene Interactions in Structured Populations: MDR-SP. <i>Annals of Human Genetics</i> , 2011, 75, 742-754.	0.3	15
25	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011, 43, 519-525.	9.4	834
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29	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. <i>American Journal of Human Genetics</i> , 2011, 88, 706-717.	2.6	77
30	Complement Receptor 1 Gene Variants Are Associated with Erythrocyte Sedimentation Rate. <i>American Journal of Human Genetics</i> , 2011, 89, 131-138.	2.6	55
31	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , 2011, 89, 193-195.	2.6	27
32	Population Structure Can Inflate SNP-Based Heritability Estimates. <i>American Journal of Human Genetics</i> , 2011, 89, 191-193.	2.6	83
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39	A comparison of strategies for analyzing dichotomous outcomes in genome-wide association studies with general pedigrees. <i>Genetic Epidemiology</i> , 2011, 35, 650-657.	0.6	15
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52	Genome-Wide Association Study Identifies Chromosome 10q24.32 Variants Associated with Arsenic Metabolism and Toxicity Phenotypes in Bangladesh. <i>PLoS Genetics</i> , 2012, 8, e1002522.	1.5	156
53	Inheritance Beyond Plain Heritability: Variance-Controlling Genes in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2012, 8, e1002839.	1.5	130
54	Variation in Genes Related to Cochlear Biology Is Strongly Associated with Adult-Onset Deafness in Border Collies. <i>PLoS Genetics</i> , 2012, 8, e1002898.	1.5	20
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73	Robustness of Bayesian Multilocus Association Models to Cryptic Relatedness. <i>Annals of Human Genetics</i> , 2012, 76, 510-523.	0.3	31

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93	Inferences from Genomic Models in Stratified Populations. <i>Genetics</i> , 2012, 192, 693-704.	1.2	77
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133	MASTOR: Mixed-Model Association Mapping of Quantitative Traits in Samples with Related Individuals. <i>American Journal of Human Genetics</i> , 2013, 92, 652-666.	2.6	36
134	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
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152	Matrix Metalloproteinases and Educational Attainment in Refractive Error. <i>Ophthalmology</i> , 2013, 120, 298-305.	2.5	38
153	Improving the Accuracy and Efficiency of Partitioning Heritability into the Contributions of Genomic Regions. <i>American Journal of Human Genetics</i> , 2013, 92, 558-564.	2.6	24
154	Mixed models can correct for population structure for genomic regions under selection. <i>Nature Reviews Genetics</i> , 2013, 14, 300-300.	7.7	29
155	Pedigree Analysis and Exclusion of Alpha-Tocopherol Transfer Protein ( <i>TTPA</i> ) as a Candidate Gene for Neuroaxonal Dystrophy in the American Quarter Horse. <i>Journal of Veterinary Internal Medicine</i> , 2013, 27, 177-185.	0.6	32
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968	Reverse GWAS: Using genetics to identify and model phenotypic subtypes. <i>PLoS Genetics</i> , 2019, 15, e1008009.	1.5	34
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1027	Joint analysis of individual-level and summary-level GWAS data by leveraging pleiotropy. <i>Bioinformatics</i> , 2019, 35, 1729-1736.	1.8	3
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1042	Genome-wide association studies using binned genotypes. <i>Heredity</i> , 2020, 124, 288-298.	1.2	5
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1044	Trichome regulator SIMIXTA-like directly manipulates primary metabolism in tomato fruit. <i>Plant Biotechnology Journal</i> , 2020, 18, 354-363.	4.1	50
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1052	Natural variation in HsfA2 pre-mRNA splicing is associated with changes in thermotolerance during tomato domestication. <i>New Phytologist</i> , 2020, 225, 1297-1310.	3.5	55
1053	Joint multiple quantitative trait loci mapping for allometries of body compositions and metabolic traits to body weights in broiler. <i>Animal</i> , 2020, 14, 1120-1127.	1.3	0
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1065	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
1066	The impact of disregarding family structure on genome-wide association analysis of complex diseases in cohorts with simple pedigrees. <i>Journal of Applied Genetics</i> , 2020, 61, 75-86.	1.0	3
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1071	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
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1087	Genome-wide association studies for methane emission and ruminal volatile fatty acids using Holstein cattle sequence data. <i>BMC Genetics</i> , 2020, 21, 129.	2.7	7
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1100	Contrasting signatures of genomic divergence during sympatric speciation. <i>Nature</i> , 2020, 588, 106-111.	13.7	115
1101	Genome-wide association study of café-au-lait macule number in neurofibromatosis type 1. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1400.	0.6	4
1102	Meta-analysis of GWAS in canola blackleg ( <i>Leptosphaeria maculans</i> ) disease traits demonstrates increased power from imputed whole-genome sequence. <i>Scientific Reports</i> , 2020, 10, 14300.	1.6	19
1103	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 3854-3864.	1.8	9
1104	Extensive haplotypes are associated with population differentiation and environmental adaptability in Upland cotton ( <i>Gossypium hirsutum</i> ). <i>Theoretical and Applied Genetics</i> , 2020, 133, 3273-3285.	1.8	15
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1107	An evolutionary population structure model reveals pleiotropic effects of <i>GmPDAT</i> for traits related to seed size and oil content in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 6988-7002.	2.4	35
1108	Causal inference in genetic trio studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24117-24126.	3.3	25
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1114	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
1115	Genome-wide association studies in tropical maize germplasm reveal novel and known genomic regions for resistance to Northern corn leaf blight. <i>Scientific Reports</i> , 2020, 10, 21949.	1.6	22
1116	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	5.8	39
1117	Secondary Genome-Wide Association Study Using Novel Analytical Strategies Disentangle Genetic Components of Cleft Lip and/or Cleft Palate in 1q32.2. <i>Genes</i> , 2020, 11, 1280.	1.0	4
1118	Cohesion of Cortical Language Networks During Word Processing Is Predicted by a Common Polymorphism in the <i>SETBP1</i> Gene. <i>New Directions for Child and Adolescent Development</i> , 2020, 2020, 131-155.	1.3	1
1119	Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008766.	1.5	5
1120	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. <i>Nature Genetics</i> , 2020, 52, 634-639.	9.4	124
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1291	Genome-wide scan reveals important additive and non-additive genetic effects associated with resistance to <i>Haemonchus contortus</i> in Florida Native sheep. <i>International Journal for Parasitology</i> , 2021, 51, 535-543.	1.3	7
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1771	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
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1873	Genotype by Environment Interactions for Chronic Wasting Disease in Farmed U.S. White-tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	2
1874	Canonical transformation for multivariate mixed model association analyses. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	1.8	0
1875	A high-density genome-wide association with absolute blood monocyte count in domestic sheep identifies novel loci. <i>PLoS ONE</i> , 2022, 17, e0266748.	1.1	0
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1881	Dissecting Meta-Analysis in GWAS Era: Bayesian Framework for Gene/Subnetwork-Specific Meta-Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	6
1882	Genome-Wide Association Study Identifies a Rice Panicle Blast Resistance Gene, Pb2, Encoding NLR Protein. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5668.	1.8	6
1883	Genome-wide association study of eigenvectors provides genetic insights into selective breeding for tomato metabolites. <i>BMC Biology</i> , 2022, 20, .	1.7	7
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1889	Natural allelic variation of <i>GmSTO5</i> controlling seed size and quality in soybean. <i>Plant Biotechnology Journal</i> , 2022, 20, 1807-1818.	4.1	44
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1894	Combining GWAS, Genome-Wide Domestication and a Transcriptomic Analysis Reveals the Loci and Natural Alleles of Salt Tolerance in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	13
1896	Phenotypic Variation and the Impact of Admixture in the <i>Oryza rufipogon</i> Species Complex (ORSC). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1897	Plant pan-genomics: recent advances, new challenges, and roads ahead. <i>Journal of Genetics and Genomics</i> , 2022, 49, 833-846.	1.7	27
1899	Genetics of Base Coat Colour Variations and Coat Colour-Patterns of the South African Nguni Cattle Investigated Using High-Density SNP Genotypes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
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1901	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. <i>Communications Biology</i> , 2022, 5, .	2.0	11
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1903	High-Altitude Genetic Selection and Genome-Wide Association Analysis of Yield-Related Traits in <i>Elymus sibiricus</i> L. Using SLAF Sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1904	Genome-Wide Association Study of Sheath Blight Resistance within a Core Collection of Rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.8	5
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1906	Genetic analysis and identification of VrFRO8, a salt tolerance-related gene in mungbean. <i>Gene</i> , 2022, 836, 146658.	1.0	5
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#	ARTICLE	IF	CITATIONS
1908	Control for population stratification in genetic association studies based on GWAS summary statistics. <i>Genetic Epidemiology</i> , 0, , .	0.6	0
1909	A genome-wide association study of lateral root number for Asian cotton ( <i>Gossypium arboreum</i> L.). <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	2
1910	An enhancer of <i>Agouti</i> contributes to parallel evolution of cryptically colored beach mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1911	Mendelian randomization for causal inference accounting for pleiotropy and sample structure using genome-wide summary statistics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	32
1913	Genomic insights into historical improvement of heterotic groups during modern hybrid maize breeding. <i>Nature Plants</i> , 2022, 8, 750-763.	4.7	36
1915	Genome-Wide Analysis Identifies Candidate Genes Encoding Feather Color in Ducks. <i>Genes</i> , 2022, 13, 1249.	1.0	9
1916	Genetic mapping of sorghum resistance to an Illinois isolate of <i>Colletotrichum sublineola</i> . <i>Plant Genome</i> , 0, , .	1.6	1
1917	Genome-wide association study in quinoa reveals selection pattern typical for crops with a short breeding history. <i>ELife</i> , 0, 11, .	2.8	14
1918	Integration of eQTL Analysis and GWAS Highlights Regulation Networks in Cotton under Stress Condition. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7564.	1.8	8
1919	Including diverse and admixed populations in genetic epidemiology research. <i>Genetic Epidemiology</i> , 2022, 46, 347-371.	0.6	11
1920	Genome-Wide Analysis Identifies Candidate Genes Encoding Beak Color of Duck. <i>Genes</i> , 2022, 13, 1271.	1.0	7
1921	Allopatric origin of sympatric whitefish morphs with insights on the genetic basis of their reproductive isolation. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1905-1913.	1.1	0
1922	High Levels of Complement Activating Enzyme MASP-2 Are Associated With the Risk of Future Incident Venous Thromboembolism. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 1186-1197.	1.1	4
1923	Genome-Wide Association Mapping in Sunflower ( <i>Helianthus annuus</i> ) Reveals Common Loci and Putative Candidate Genes for Resistance to <i>Diaporthe gulyae</i> and <i>D. helianthi</i> Causing Phomopsis Stem Canker. <i>Plant Disease</i> , 2023, 107, 667-674.	0.7	1
1924	A Principal Component Informed Approach to Address Polygenic Risk Score Transferability Across European Cohorts. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1925	Genome-wide association analysis and transcriptome reveal novel loci and a candidate regulatory gene of fatty acid biosynthesis in sesame ( <i>Sesamum indicum</i> L.). <i>Plant Physiology and Biochemistry</i> , 2022, 186, 220-231.	2.8	8
1926	Locally adaptive temperature response of vegetative growth in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 0, 11, .	2.8	10
1927	Variation in Melatonin Contents and Genetic Dissection of Melatonin Biosynthesis in Sesame. <i>Plants</i> , 2022, 11, 2005.	1.6	7

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1928	A<scp>ir</scp>M<scp>easurer</scp>: openâ€source software to quantify static and dynamic traits derived from multiseason aerial phenotyping to empower genetic mapping studies in rice. <i>New Phytologist</i> , 2022, 236, 1584-1604.	3.5	8
1930	Bridging the splicing gap in human genetics with long-read RNA sequencing: finding the protein isoform drivers of disease. <i>Human Molecular Genetics</i> , 2022, 31, R123-R136.	1.4	10
1931	Genome-wide characterization of the Rho family in cotton provides insights into fiber development. <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	1
1932	Insights into the Genomic Regions and Candidate Genes of Senescence-Related Traits in Upland Cotton via GWAS. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8584.	1.8	4
1934	Phenomic selection in wheat breeding: prediction of the genotype-by-environment interaction in multi-environment breeding trials. <i>Theoretical and Applied Genetics</i> , 0, , .	1.8	1
1935	Mining alleles for tar spot complex resistance from CIMMYT's maize Germplasm Bank. <i>Frontiers in Sustainable Food Systems</i> , 0, 6, .	1.8	1
1936	Genetic association-based functional analysis detects HOGA1 as a potential gene involved in fat accumulation. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
1937	Genomic architecture of adaptive radiation and hybridization in Alpine whitefish. <i>Nature Communications</i> , 2022, 13, .	5.8	25
1938	Genomic analyses of wild argali, domestic sheep, and their hybrids provide insights into chromosome evolution, phenotypic variation, and germplasm innovation. <i>Genome Research</i> , 2022, 32, 1669-1684.	2.4	10
1940	Cellular Genome-wide Association Study Identifies Common Genetic Variation Influencing Lithium-Induced Neural Progenitor Proliferation. <i>Biological Psychiatry</i> , 2023, 93, 8-17.	0.7	6
1941	Breeding Dairy Cattle for Female Fertility and Production in the Age of Genomics. <i>Veterinary Sciences</i> , 2022, 9, 434.	0.6	4
1942	<scp>eQTLs</scp> play critical roles in regulating gene expression and identifying key regulators in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 2357-2371.	4.1	9
1943	Identification of candidate genes in cotton associated with specific seed traits and their initial functional characterization in <i>Arabidopsis</i>. <i>Plant Journal</i> , 0, , .	2.8	2
1944	Two variants of AUTS2 gene are associated with high lean meat percentage in Pekin ducks. <i>Gene</i> , 2023, 848, 146864.	1.0	0
1945	Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. <i>GigaScience</i> , 2022, 11, .	3.3	0
1946	GWAS of genetic factors affecting white blood cell morphological parameters in Sardinians uncovers influence of chromosome 11 innate immunity gene cluster on eosinophil morphology. <i>Human Molecular Genetics</i> , 0, , .	1.4	1
1948	Evaluation and characterization of expression quantitative trait analysis methods in the Hybrid Rat Diversity Panel. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
1949	Efficient permutation-based genome-wide association studies for normal and skewed phenotypic distributions. <i>Bioinformatics</i> , 2022, 38, ii5-ii12.	1.8	9

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1950	Genetic mapping and genome-wide association study identify BhYAB4 as the candidate gene regulating seed shape in wax gourd ( <i>Benincasa hispida</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1951	Efficient and accurate frailty model approach for genome-wide survival association analysis in large-scale biobanks. <i>Nature Communications</i> , 2022, 13, .	5.8	13
1952	Genetic variation underlying differential ammonium and nitrate responses in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2022, 34, 4696-4713.	3.1	10
1953	Deciphering signatures of natural selection via deep learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
1954	Genetic analyses of the electrocardiographic QT interval and its components identify additional loci and pathways. <i>Nature Communications</i> , 2022, 13, .	5.8	15
1955	Archetypes of inflorescence: genome-wide association networks of panicle morphometric, growth, and disease variables in a multiparent oat population. <i>Genetics</i> , 2023, 223, .	1.2	3
1956	Coordinate Descent for Variance-Component Models. <i>Algorithms</i> , 2022, 15, 354.	1.2	0
1957	Regain flood adaptation in rice through a 14-3-3 protein OsGF14h. <i>Nature Communications</i> , 2022, 13, .	5.8	20
1959	Genome-Wide Association Study in Bread Wheat Identifies Genomic Regions Associated with Grain Yield and Quality under Contrasting Water Availability. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10575.	1.8	6
1961	Robust association tests for quantitative traits on the X chromosome. <i>Heredity</i> , 2022, 129, 244-256.	1.2	1
1962	Rewiring of the seed metabolome during Tartary buckwheat domestication. <i>Plant Biotechnology Journal</i> , 2023, 21, 150-164.	4.1	15
1963	<i>Large Vascular Bundle Phloem Area 4</i> enhances grain yield and quality in rice via source-sink flow. <i>Plant Physiology</i> , 2023, 191, 317-334.	2.3	8
1964	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. <i>Genome Biology</i> , 2022, 23, .	3.8	6
1965	A Genome-Wide Association study in <i>Arabidopsis thaliana</i> to decipher the adaptive genetics of quantitative disease resistance in a native heterogeneous environment. <i>PLoS ONE</i> , 2022, 17, e0274561.	1.1	4
1966	Genetic insights into the crude protein and fiber content of ramie leaves. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1967	Recent advances and challenges of rare variant association analysis in the biobank sequencing era. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1968	Genomic insight into genetic changes and shaping of major inbred rice cultivars in China. <i>New Phytologist</i> , 0, , .	3.5	1
1969	Disentangling leaf-microbiome interactions in <i>Arabidopsis thaliana</i> by network mapping. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1

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1970	A combined polygenic score of 21,293 rare and 22 common variants improves diabetes diagnosis based on hemoglobin A1C levels. <i>Nature Genetics</i> , 2022, 54, 1609-1614.	9.4	20
1971	Natural variation of Dt2 determines branching in soybean. <i>Nature Communications</i> , 2022, 13, .	5.8	19
1972	Identification and validation of a key genomic region on chromosome 6 for resistance to Fusarium stalk rot in tropical maize. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4549-4563.	1.8	7
1973	Genome-wide identification and comparative analysis of CLE family in rapeseed and its diploid progenitors. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
1974	Genome-wide association studies provide genetic insights into natural variation of seed-size-related traits in mungbean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
1975	Genomic selection of orange-spotted grouper ( <i>Epinephelus coioides</i> ) based on multiplex PCR enrichment capture sequencing. <i>Aquaculture and Fisheries</i> , 2022, , .	1.2	0
1976	CottonMD: a multi-omics database for cotton biological study. <i>Nucleic Acids Research</i> , 2023, 51, D1446-D1456.	6.5	14
1977	Genomic and transcriptomic-based analysis of agronomic traits in sugar beet ( <i>Beta vulgaris</i> L.) pure line IMA1. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1979	Ozone and nitrogen dioxide regulate similar gene expression responses in <i>Arabidopsis</i> but natural variation in the extent of cell death is likely controlled by different genetic loci. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1980	Identification of elite fiber quality loci in upland cotton based on the genotyping-by-target-sequencing technology. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
1981	Underlying genetic architecture of resistance to mastitis in dairy cattle: A systematic review and gene prioritization analysis of genome-wide association studies. <i>Journal of Dairy Science</i> , 2023, 106, 323-351.	1.4	5
1982	Temperature-mediated flower size plasticity in <i>Arabidopsis</i> . <i>IScience</i> , 2022, 25, 105411.	1.9	6
1983	Leaf physiology variations are modulated by natural variations that underlie stomatal morphology in <i>Populus</i> . <i>Plant, Cell and Environment</i> , 2023, 46, 150-170.	2.8	6
1985	Genome-Wide Association with Uncertainty in the Genetic Similarity Matrix. <i>Journal of Computational Biology</i> , 0, , .	0.8	0
1986	Integrating Genome-Wide Association Study with RNA-Sequencing Reveals HDAC9 as a Candidate Gene Influencing Loin Muscle Area in Beijing Black Pigs. <i>Biology</i> , 2022, 11, 1635.	1.3	1
1987	Gene-Based Genome-Wide Association Study Identified Genes for Agronomic Traits in Maize. <i>Biology</i> , 2022, 11, 1649.	1.3	2
1989	Genome-wide association studies for soybean epicotyl length in two environments using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1990	BICOSS: Bayesian iterative conditional stochastic search for GWAS. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	5

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1991	<sc> <i>HvGST</i> </sc> plays a key role in anthocyanin accumulation in colored barley. Plant Journal, 0, , .	2.8	0
1992	A comparison of classical and machine learning-based phenotype prediction methods on simulated data and three plant species. Frontiers in Plant Science, 0, 13, .	1.7	10
1993	Privacy-aware estimation of relatedness in admixed populations. Briefings in Bioinformatics, 2022, 23, .	3.2	7
1994	Genome-Wide Association Study Identifies a Rice Panicle Blast Resistance Gene Pb3 Encoding NLR Protein. International Journal of Molecular Sciences, 2022, 23, 14032.	1.8	6
1996	Single-cell genome-wide association reveals that a nonsynonymous variant in ERAP1 confers increased susceptibility to influenza virus. Cell Genomics, 2022, 2, 100207.	3.0	2
1997	Genome-wide association study uncovers major genetic loci associated with flowering time in response to active accumulated temperature in wild soybean population. BMC Genomics, 2022, 23, .	1.2	6
1998	Comprehensive transcriptional variability analysis reveals gene networks regulating seed oil content of Brassica napus. Genome Biology, 2022, 23, .	3.8	6
1999	Mendelian randomization study reveals a causal relationship between adiponectin and LDL cholesterol in Africans. Scientific Reports, 2022, 12, .	1.6	2
2000	Local diversity of drought resistance and resilience in <i>Populus tomentosa</i> correlates with the variation of DNA methylation. Plant, Cell and Environment, 2023, 46, 479-497.	2.8	5
2001	Molecular mapping of Chilli veinal mottle virus (ChiVMV) resistance in hot pepper (Capsicum annuum) Tj ETQq1 1 0.784314 rgBT /Over 1.4	1.4	0
2003	Dissecting Complex Traits Using Omics Data: A Review on the Linear Mixed Models and Their Application in GWAS. Plants, 2022, 11, 3277.	1.6	1
2004	TeaGVD: A comprehensive database of genomic variations for uncovering the genetic architecture of metabolic traits in tea plants. Frontiers in Plant Science, 0, 13, .	1.7	9
2005	RNA-Seq and Genome-Wide Association Studies Reveal Potential Genes for Rice Seed Shattering. International Journal of Molecular Sciences, 2022, 23, 14633.	1.8	1
2006	Increasing plant group productivity through latent genetic variation for cooperation. PLoS Biology, 2022, 20, e3001842.	2.6	12
2007	Quality Control Procedures for Genome-Wide Association Studies. Current Protocols, 2022, 2, .	1.3	5
2008	The impact of SNP density on quantitative genetic analyses of body size traits in a wild population of Soay sheep. Ecology and Evolution, 2022, 12, .	0.8	2
2009	Genome-Wide Association Studies in Sunflower: Towards Sclerotinia sclerotiorum and Diaporthe/Phomopsis Resistance Breeding. Genes, 2022, 13, 2357.	1.0	2
2010	Identification of new resistance loci against wheat sharp eyespot through genome-wide association study. Frontiers in Plant Science, 0, 13, .	1.7	1

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2011	Genome-wide association study of salt tolerance at the germination stage in hemp. <i>Euphytica</i> , 2023, 219, .	0.6	2
2013	Two decades of association mapping: Insights on disease resistance in major crops. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
2014	Application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary statistics from a whole-genome association study. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	0
2015	Whole-genome identification of transposable elements reveals the equine repetitive element insertion polymorphism in Chinese horses. <i>Animal Genetics</i> , 0, , .	0.6	0
2017	Genome-Wide Association Study for Non-Photochemical Quenching Traits in <i>Oryza sativa</i> L.. <i>Agronomy</i> , 2022, 12, 3216.	1.3	3
2018	Genomes of the cosmopolitan fruit pest <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) reveal its global invasion history and thermal adaptation. <i>Journal of Advanced Research</i> , 2023, 53, 61-74.	4.4	15
2019	Genome-Wide Association Studies of Salt Tolerance at the Seed Germination Stage and Yield-Related Traits in <i>Brassica napus</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15892.	1.8	3
2020	Modern drug discovery for inflammatory bowel disease: The role of computational methods. <i>World Journal of Gastroenterology</i> , 0, 29, 310-331.	1.4	3
2021	East African cichlid fishes. <i>EvoDevo</i> , 2023, 14, .	1.3	14
2022	Genetic architecture of fresh-market tomato yield. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
2023	Identification of multiple novel genetic mechanisms that regulate chilling tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
2024	From SNP to pathway-based GWAS meta-analysis: do current meta-analysis approaches resolve power and replication in genetic association studies?. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	1
2025	Integrating GWAS and transcriptomics to identify candidate genes conferring heat tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
2026	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. <i>ELife</i> , 0, 12, .	2.8	2
2027	Rare variant analyses across multiethnic cohorts identify novel genes for refractive error. <i>Communications Biology</i> , 2023, 6, .	2.0	2
2029	Fast integration and accumulation of beneficial breeding alleles through an ABâ€“NAMIC strategy in wheat. <i>Plant Communications</i> , 2023, 4, 100549.	3.6	5
2031	Genome-wide association study reveals the genetic determinism of serum biochemical indicators in ducks. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
2032	Independent Evolution of Sex Chromosomes and Male Pregnancy-Related Genes in Two Seahorse Species. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4

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2033	Association of Early Childhood Caries with Bitter Taste Receptors: A Meta-Analysis of Genome-Wide Association Studies and Transcriptome-Wide Association Study. <i>Genes</i> , 2023, 14, 59.	1.0	8
2034	A comparison between similarity matrices for principal component analysis to assess population stratification in sequenced genetic data sets. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	3
2035	Genetic association of wool quality characteristics in United States Rambouillet sheep. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
2036	Genome-wide association studies demonstrate the genes associated with perimysial thickness in ducks. <i>Animal Genetics</i> , 2023, 54, 363-374.	0.6	3
2037	Efficient penalized generalized linear mixed models for variable selection and genetic risk prediction in high-dimensional data. <i>Bioinformatics</i> , 2023, 39, .	1.8	3
2038	Unraveling the genetics underlying micronutrient signatures of diversity panel present in brown rice through genome-wide linkage disequilibrium. <i>Plant Journal</i> , 2023, 113, 749-771.	2.8	5
2039	Heritable defects in telomere and mitotic function selectively predispose to sarcomas. <i>Science</i> , 2023, 379, 253-260.	6.0	13
2040	A 21-bp InDel in the promoter of <i>STP1</i> selected during tomato improvement accounts for soluble solid content in fruits. <i>Horticulture Research</i> , 2023, 10, .	2.9	3
2042	Genome-wide association and genomic prediction for a reproductive index summarizing fertility outcomes in U.S. Holsteins. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	0
2044	Genomic insights into the genetic basis of cotton breeding in China. <i>Molecular Plant</i> , 2023, 16, 662-677.	3.9	8
2045	Fine mapping of QTL conferring resistance to calcareous soil in mungbean reveals VrYSL3 as candidate gene for the resistance. <i>Plant Science</i> , 2023, 332, 111698.	1.7	0
2046	PSReliP: an integrated pipeline for analysis and visualization of population structure and relatedness based on genome-wide genetic variant data. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
2047	Structural variation (SV)-based pan-genome and GWAS reveal the impacts of SVs on the speciation and diversification of allotetraploid cottons. <i>Molecular Plant</i> , 2023, 16, 678-693.	3.9	14
2048	Metabolome-Based Genome-Wide Association Study of Duck Meat Leads to Novel Genetic and Biochemical Insights. <i>Advanced Science</i> , 2023, 10, .	5.6	1
2049	Genetic fine-mapping reveals single nucleotide polymorphism mutations in the <i>MC1R</i> regulatory region associated with duck melanism. <i>Molecular Ecology</i> , 2023, 32, 3076-3088.	2.0	2
2050	Loci for insulin processing and secretion provide insight into type 2 diabetes risk. <i>American Journal of Human Genetics</i> , 2023, 110, 284-299.	2.6	9
2051	Identification of QTNs, QTN-by-environment interactions, and their candidate genes for grain size traits in main crop and ratoon rice. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	7
2052	A fast linkage method for population GWAS cohorts with related individuals. <i>Genetic Epidemiology</i> , 2023, 47, 231-248.	0.6	1

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2053	Genome-wide association study identifies novel candidate malaria resistance genes in Cameroon. <i>Human Molecular Genetics</i> , 0, , .	1.4	1
2054	Interaction-integrated linear mixed model reveals 3D-genetic basis underlying Autism. <i>Genomics</i> , 2023, 115, 110575.	1.3	3
2055	The SIDOG1 Affect Biosynthesis of Steroidal Glycoalkaloids by Regulating GAME Expression in Tomato. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3360.	1.8	5
2056	<sc>TaTPP</sc> positively feedback regulates grain filling and wheat grain yield through <sc>T6</sc> signalling pathway and <sc>sugar</sc>“ABA” interaction. <i>Plant Biotechnology Journal</i> , 2023, 21, 1159-1175.	4.1	13
2057	512. The application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary. , 2022, , .		0
2058	373. Fine-mapping young-stock survival QTL on chromosome 6 in Nordic Red Dairy Cattle. , 2022, , .		0
2059	Genomic decoding of breeding history to guide breeding-by-design in rice. <i>National Science Review</i> , 2023, 10, .	4.6	6
2060	High-Throughput Association Mapping in Brassica napus L.: Methods and Applications. <i>Methods in Molecular Biology</i> , 2023, , 67-91.	0.4	1
2062	Convergently selected NPF2.12 coordinates root growth and nitrogen use efficiency in wheat and barley. <i>New Phytologist</i> , 2023, 238, 2175-2193.	3.5	2
2064	A heterophil/lymphocyte-selected population reveals the phosphatase PTPRJ is associated with immune defense in chickens. <i>Communications Biology</i> , 2023, 6, .	2.0	2
2065	Genome-wide association study identifies GhSAL1 affects cold tolerance at the seedling emergence stage in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	9
2066	Re-Evaluation of Genotyping Methodologies in Cattle: The Proficiency of Imputation. <i>Genes</i> , 2023, 14, 547.	1.0	0
2067	Genetic association models are robust to common population kinship estimation biases. <i>Genetics</i> , 0, , .	1.2	2
2068	Genetic and Genomic Analysis of Cow Mortality in the Israeli Holstein Population. <i>Genes</i> , 2023, 14, 588.	1.0	3
2069	QTL Mapping: Strategy, Progress, and Prospects in Flax. <i>Compendium of Plant Genomes</i> , 2023, , 69-99.	0.3	0
2070	Three amphioxus reference genomes reveal gene and chromosome evolution of chordates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	11
2071	Genome-wide association study to identify SNPs and candidate genes associated with body size traits in donkeys. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
2072	Genome-wide significant risk loci for mood disorders in the Old Order Amish founder population. <i>Molecular Psychiatry</i> , 0, , .	4.1	3



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2073	The giant diploid faba genome unlocks variation in a global protein crop. <i>Nature</i> , 2023, 615, 652-659.	13.7	40
2074	Genome-Wide Association Studies (GWAS) for Agronomic Traits in Maize. , 2023, , 83-98.		0
2075	A chromosome-scale genome sequence of sudangrass ( <i>Sorghum sudanense</i> ) highlights the genome evolution and regulation of dhurrin biosynthesis. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	1
2076	Identification of a key locus, qNL3.1, associated with seed germination under salt stress via a genome-wide association study in rice. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	1
2077	Genome-Wide Association Study of Growth and Sex Traits Provides Insight into Heritable Mechanisms Underlying Growth Development of <i>Macrobrachium nipponense</i> (Oriental River Prawn). <i>Biology</i> , 2023, 12, 429.	1.3	0
2079	Genetic architecture of spatial electrical biomarkers for cardiac arrhythmia and relationship with cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	5.8	1
2080	The trouble with triples: Examining the impact of measurement error in mediation analysis. <i>Genetics</i> , 0, , .	1.2	0
2082	Genome-wide characterization of ubiquitin-conjugating enzyme gene family explores its genetic effects on the oil content and yield of <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
2083	Multi-omics analysis identifies drivers of protein phosphorylation. <i>Genome Biology</i> , 2023, 24, .	3.8	5
2084	Genome-wide association mapping for LLS resistance in a MAGIC population of groundnut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	2
2085	Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. <i>GigaScience</i> , 2023, 12, .	3.3	1
2086	Large haploblocks underlie rapid adaptation in the invasive weed <i>Ambrosia artemisiifolia</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	13
2087	The genomics of linkage drag in inbred lines of sunflower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	14
2088	Population analysis reveals the roles of DNA methylation in tomato domestication and metabolic diversity. <i>Science China Life Sciences</i> , 2023, 66, 1888-1902.	2.3	2
2089	Height-Related Polygenic Variants Are Associated with Metabolic Syndrome Risk and Interact with Energy Intake and a Rice-Main Diet to Influence Height in KoGES. <i>Nutrients</i> , 2023, 15, 1764.	1.7	4
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