

Genome-wide efficient mixed-model analysis for associ

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A genome-wide association study on common SNPs and rare CNVs in anorexia nervosa. <i>Molecular Psychiatry</i> , 2011, 16, 949-959.	7.9	186
2	Variation of BMP3 Contributes to Dog Breed Skull Diversity. <i>PLoS Genetics</i> , 2012, 8, e1002849.	3.5	159
3	Imputation of Rare Variants in Next-Generation Association Studies. <i>Human Heredity</i> , 2012, 74, 196-204.	0.8	22
4	MASTOR: Mixed-Model Association Mapping of Quantitative Traits in Samples with Related Individuals. <i>American Journal of Human Genetics</i> , 2013, 92, 652-666.	6.2	36
5	Mapping Quantitative Trait Loci by Controlling Polygenic Background Effects. <i>Genetics</i> , 2013, 195, 1209-1222.	2.9	111
6	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	2.9	518
7	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2013, , .	1.3	17
8	Common variants in the HLA-DRB1 and HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	21.4	86
9	A Lasso multi-marker mixed model for association mapping with population structure correction. <i>Bioinformatics</i> , 2013, 29, 206-214.	4.1	99
10	Deciphering the complex: Methodological overview of statistical models to derive OMICS-based biomarkers. <i>Environmental and Molecular Mutagenesis</i> , 2013, 54, 542-557.	2.2	113
11	A missense mutation in growth differentiation factor 9 (GDF9) is strongly associated with litter size in sheep. <i>BMC Genetics</i> , 2013, 14, 1.	2.7	172
12	The convergent evolution of blue iris pigmentation in primates took distinct molecular paths. <i>American Journal of Physical Anthropology</i> , 2013, 151, 398-407.	2.1	14
13	Genome-wide association study identifies multiple susceptibility loci for pulmonary fibrosis. <i>Nature Genetics</i> , 2013, 45, 613-620.	21.4	667
14	Association mapping for seed size and shape traits in soybean cultivars. <i>Molecular Breeding</i> , 2013, 31, 785-794.	2.1	93
15	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. <i>Nature Communications</i> , 2013, 4, 2872.	12.8	77
16	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis. <i>Plant Cell</i> , 2013, 24, 4793-4805.	6.6	162
17	Testing for Associations between Loci and Environmental Gradients Using Latent Factor Mixed Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 1687-1699.	8.9	627
18	Polygenic Modeling with Bayesian Sparse Linear Mixed Models. <i>PLoS Genetics</i> , 2013, 9, e1003264.	3.5	686

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19	The causal meaning of Fisher's average effect. <i>Genetical Research</i> , 2013, 95, 89-109.	0.9	29
20	The Genetics of Canine Skull Shape Variation. <i>Genetics</i> , 2013, 193, 317-325.	2.9	82
21	Practical Considerations Regarding the Use of Genotype and Pedigree Data to Model Relatedness in the Context of Genome-Wide Association Studies. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1861-1867.	1.8	58
22	A sequence of methodological changes due to sequencing. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2013, 13, 470-477.	2.3	8
23	Arsenic metabolism efficiency has a causal role in arsenic toxicity: Mendelian randomization and gene-environment interaction. <i>International Journal of Epidemiology</i> , 2013, 42, 1862-1872.	1.9	89
24	Efficiently Identifying Significant Associations in Genome-wide Association Studies. <i>Journal of Computational Biology</i> , 2013, 20, 817-830.	1.6	4
25	Response to Sul and Eskin. <i>Nature Reviews Genetics</i> , 2013, 14, 300-300.	16.3	14
26	Dissecting High-Dimensional Phenotypes with Bayesian Sparse Factor Analysis of Genetic Covariance Matrices. <i>Genetics</i> , 2013, 194, 753-767.	2.9	61
28	Genome-wide Association Study of Chicken Plumage Pigmentation. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013, 26, 1523-1528.	2.4	11
29	QTL Analysis of Dietary Obesity in C57BL/6byj X 129P3/J F2 Mice: Diet- and Sex-Dependent Effects. <i>PLoS ONE</i> , 2013, 8, e68776.	2.5	21
30	The power of regional heritability analysis for rare and common variant detection: simulations and application to eye biometrical traits. <i>Frontiers in Genetics</i> , 2013, 4, 232.	2.3	36
31	Association testing to detect gene-gene interactions on sex chromosomes in trio data. <i>Frontiers in Genetics</i> , 2013, 4, 239.	2.3	3
32	Genome-Wide Association Analysis of Radiation Resistance in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2014, 9, e104858.	2.5	31
33	Marker-Based Estimation of Genetic Parameters in Genomics. <i>PLoS ONE</i> , 2014, 9, e102715.	2.5	6
34	Genome-Wide Association Studies and Heritability Estimates of Body Mass Index Related Phenotypes in Bangladeshi Adults. <i>PLoS ONE</i> , 2014, 9, e105062.	2.5	19
35	A SUPER Powerful Method for Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e107684.	2.5	289
36	Genome-Wide Association Study Reveals Novel Quantitative Trait Loci Associated with Resistance to Multiple Leaf Spot Diseases of Spring Wheat. <i>PLoS ONE</i> , 2014, 9, e108179.	2.5	189
37	Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky-Muller interactions. <i>ELife</i> , 2014, 3, .	6.0	107

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39	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.	1.8	195
40	Bridging Genomics and Phenomics. , 2014, , 299-333.		16
41	Combining genetic and nongenetic biomarkers to realize the promise of pharmacogenomics for inflammatory diseases. <i>Pharmacogenomics</i> , 2014, 15, 1931-1940.	1.3	7
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44	GPA: A Statistical Approach to Prioritizing GWAS Results by Integrating Pleiotropy and Annotation. <i>PLoS Genetics</i> , 2014, 10, e1004787.	3.5	189
45	Detecting Local Haplotype Sharing and Haplotype Association. <i>Genetics</i> , 2014, 197, 823-838.	2.9	51
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47	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. <i>Nature Communications</i> , 2014, 5, 5345.	12.8	60
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51	Poly-Omic Prediction of Complex Traits: OmicKriging. <i>Genetic Epidemiology</i> , 2014, 38, 402-415.	1.3	41
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54	Risk of false positive genetic associations in complex traits with underlying population structure: A case study. <i>Veterinary Journal</i> , 2014, 202, 543-549.	1.7	27
55	A genome-wide association analysis for porcine serum lipid traits reveals the existence of age-specific genetic determinants. <i>BMC Genomics</i> , 2014, 15, 758.	2.8	24

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60	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	21.4	136
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70	Using population isolates in genetic association studies. Briefings in Functional Genomics, 2014, 13, 371-377.	2.7	82
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94	A Unified Sparse Representation for Sequence Variant Identification for Complex Traits. Genetic Epidemiology, 2014, 38, 671-679.	1.3	9
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97	Genomic basis of the differences between cider and dessert apple varieties. Evolutionary Applications, 2015, 8, 650-661.	3.1	33
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99	Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. Scientific Reports, 2015, 5, 10298.	3.3	47
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111	Mapping of Craniofacial Traits in Outbred Mice Identifies Major Developmental Genes Involved in Shape Determination. PLoS Genetics, 2015, 11, e1005607.	3.5	67
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160	2½ plasmid in <i>Saccharomyces</i> species and in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov090.	2.3	19
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168	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	4.0	368
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174	Genome-wide imputation study identifies novel HLA locus for pulmonary fibrosis and potential role for auto-immunity in fibrotic idiopathic interstitial pneumonia. <i>BMC Genetics</i> , 2016, 17, 74.	2.7	84
175	Exploiting Single-Cell Quantitative Data to Map Genetic Variants Having Probabilistic Effects. <i>PLoS Genetics</i> , 2016, 12, e1006213.	3.5	11
176	CERAMIC: Case-Control Association Testing in Samples with Related Individuals, Based on Retrospective Mixed Model Analysis with Adjustment for Covariates. <i>PLoS Genetics</i> , 2016, 12, e1006329.	3.5	17
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181	Genome-Wide Association Study for Muscle Fat Content and Abdominal Fat Traits in Common Carp (<i>Cyprinus carpio</i>). <i>PLoS ONE</i> , 2016, 11, e0169127.	2.5	29
182	Genetic Diversity and Elite Allele Mining for Grain Traits in Rice (<i>Oryza sativa</i> L.) by Association Mapping. <i>Frontiers in Plant Science</i> , 2016, 7, 787.	3.6	26
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1173	Stratification of risk of progression to colectomy in ulcerative colitis via measured and predicted gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 1765-1779.	6.2	6
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1195	Population Stratification of Rare Variants. , 2015, , 227-237.		2
1196	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. <i>Lecture Notes in Computer Science</i> , 2015, , 136-153.	1.3	1
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1199	Genetic influences on delayed reward discounting: A genome-wide prioritized subset approach.. <i>Experimental and Clinical Psychopharmacology</i> , 2019, 27, 29-37.	1.8	10
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1654	The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross. <i>Nature Communications</i> , 2022, 13, 1463.	12.8	19
1655	Genetic loci implicated in meta-analysis of body shape in Africans. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2022, , .	2.6	3
1657	Genetic modifiers of Huntington disease differentially influence motor and cognitive domains. <i>American Journal of Human Genetics</i> , 2022, 109, 885-899.	6.2	29
1658	METRO: Multi-ancestry transcriptome-wide association studies for powerful gene-trait association detection. <i>American Journal of Human Genetics</i> , 2022, 109, 783-801.	6.2	12

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1660	Estimating genetic variance contributed by a quantitative trait locus: A random model approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009923.	3.2	1
1661	Genomic landscape of Epstein-Barr virus in familial nasopharyngeal carcinoma. <i>Journal of General Virology</i> , 2022, 103, .	2.9	1
1662	Genomic heterozygosity is associated with parasite abundance, but the effects are not mediated by host condition. <i>Evolutionary Ecology</i> , 0, , 1.	1.2	2
1664	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.	8.3	53
1665	Admixture Mapping of Alzheimer's disease in Caribbean Hispanics identifies a new locus on 22q13.1. <i>Molecular Psychiatry</i> , 2022, 27, 2813-2820.	7.9	12
1666	Early onset adult deafness in the Rhodesian Ridgeback dog is associated with an in-frame deletion in the EPS8L2 gene. <i>PLoS ONE</i> , 2022, 17, e0264365.	2.5	3
1667	ExomeChip-based rare variant association study in restless legs syndrome. <i>Sleep Medicine</i> , 2022, 94, 26-30.	1.6	0
1668	Genome-Wide Association Study and FST Analysis Reveal Four Quantitative Trait Loci and Six Candidate Genes for Meat Color in Pigs. <i>Frontiers in Genetics</i> , 2022, 13, 768710.	2.3	4
1669	Genomic and Transcriptomic Characterization of Atypical Recurrent Flank Alopecia in the Cesky Fousek. <i>Genes</i> , 2022, 13, 650.	2.4	2
1670	A genome-wide epistatic network underlies the molecular architecture of continuous color variation of body extremities. <i>Genomics</i> , 2022, 114, 110361.	2.9	0
1671	GWAS and genomic prediction revealed potential for genetic improvement of large yellow croaker adapting to high plant protein diet. <i>Aquaculture</i> , 2022, 553, 738090.	3.5	18
1672	Potential genetic biomarkers are found to be associated with both cognitive function and blood pressure: A bivariate genome-wide association analysis. <i>Mechanisms of Ageing and Development</i> , 2022, 204, 111671.	4.6	0
1673	Maize Epistasis Detection by Multi-class Quantitative Multifactor Dimensionality Reduction. , 2021, , .		1
1675	Suitability of GWAS as a Tool to Discover SNPs Associated with Tick Resistance in Cattle: A Review. <i>Pathogens</i> , 2021, 10, 1604.	2.8	5
1676	GWAS in Mice Maps Susceptibility to HIV-Associated Nephropathy to the Ssbp2 Locus. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 108-120.	6.1	3
1677	Restricted maximum-likelihood method for learning latent variance components in gene expression data with known and unknown confounders. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	3
1678	Environmental and genome-wide association study on children anxiety and depression. , 2021, , .		1

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1680	Testing the accuracy of 3D automatic landmarking via genome-wide association studies. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	2
1681	Assessment of cold stress tolerance in maize through quantitative trait locus, genome-wide association study and transcriptome analysis. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12525.	1.1	3
1682	3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. <i>PeerJ</i> , 2021, 9, e12628.	2.0	4
1683	Pleiotropic Loci Associated With Foot Disorders and Common Periparturient Diseases in Holstein Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 742934.	2.3	2
1685	Genome evolution in an agricultural pest following adoption of transgenic crops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	23
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1691	Average semivariance directly yields accurate estimates of the genomic variance in complex trait analyses. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
1692	Genomic changes underlying repeated niche shifts in an adaptive radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1301-1319.	2.3	3
1693	Efficient estimation of SNP heritability using Gaussian predictive process in large scale cohort studies. <i>PLoS Genetics</i> , 2022, 18, e1010151.	3.5	4
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1697	A novel distribution of supergene genotypes is present in the socially polymorphic ant <i>Formica neoclara</i> . <i>Bmc Ecology and Evolution</i> , 2022, 22, 47.	1.6	1
1699	A natural genetic variation screen identifies insulin signaling, neuronal communication, and innate immunity as modifiers of hyperglycemia in the absence of <i>Sirt1</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	2
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1859	Identification of two new recessive <i>MC1R</i> alleles in red-coloured Evoliner cattle and other breeds. <i>Animal Genetics</i> , 2022, 53, 427-435.	1.7	1
1860	Aquaculture Molecular Breeding Platform (AMBP): a comprehensive web server for genotype imputation and genetic analysis in aquaculture. <i>Nucleic Acids Research</i> , 2022, 50, W66-W74.	14.5	7
1861	Association of Predicted Expression and Multimodel Association Analysis of Substance Abuse Traits. <i>Complex Psychiatry</i> , 2022, 8, 35-46.	0.9	0
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1863	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. <i>Nature</i> , 2022, 606, 358-367.	27.8	67
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1866	Genetic architectures and selection signatures of body height in Chinese indigenous donkeys revealed by next-generation sequencing. <i>Animal Genetics</i> , 2022, 53, 487-497.	1.7	5
1867	Identification of crucial factors involved in <i>Cynoglossus semilaevis</i> sexual size dimorphism by GWAS and demonstration of <i>zbed1</i> regulatory network by DAP-seq. <i>Genomics</i> , 2022, 114, 110376.	2.9	4
1870	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.	3.6	5
1871	Genome-wide association study of platelet factor 4/heparin antibodies in heparin-induced thrombocytopenia. <i>Blood Advances</i> , 2022, 6, 4137-4146.	5.2	7
1872	Genotype by Environment Interactions for Chronic Wasting Disease in Farmed U.S. White-tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	2
1873	Canonical transformation for multivariate mixed model association analyses. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	3.6	0
1874	Evaluation of genomic selection for high salinity tolerance traits in Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Aquaculture</i> , 2022, 557, 738320.	3.5	9
1876	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	21.4	55
1877	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1730-1742.	8.3	21
1878	InDels Identification and Association Analysis with Spike and Awn Length in Chinese Wheat Mini-Core Collection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5587.	4.1	3

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1883	Hybridization alters the shape of the genotypic fitness landscape, increasing access to novel fitness peaks during adaptive radiation. <i>ELife</i> , 0, 11, .	6.0	6
1884	Electrical responses from human retinal cone pathways associate with a common genetic polymorphism implicated in myopia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	8
1885	Host-genotype-dependent cecal microbes are linked to breast muscle metabolites in Chinese chickens. <i>IScience</i> , 2022, 25, 104469.	4.1	5
1886	Large scale across-breed genome-wide association study reveals a variant in HMGA2 associated with inguinal cryptorchidism risk in dogs. <i>PLoS ONE</i> , 2022, 17, e0267604.	2.5	2
1887	Robust High-Throughput Phenotyping with Deep Segmentation Enabled by a Web-Based Annotator. <i>Plant Phenomics</i> , 2022, 2022, .	5.9	2
1889	Genome Wide Association (GWAS) Analysis and genomic heritability for parasite resistance and growth in European seabass. <i>Aquaculture Reports</i> , 2022, 24, 101178.	1.7	2
1890	ZNF652 Gene and its SNP Variant Affect the Abdominal Fat Percentage of Chicken. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1891	Genome-Wide Association Study Statistical Models: A Review. <i>Methods in Molecular Biology</i> , 2022, , 43-62.	0.9	10
1892	Genome-Wide Association Study of Six Forage Traits in Ramie (<i>Boehmeria nivea</i> L. Gaud). <i>Plants</i> , 2022, 11, 1443.	3.5	4
1893	Genome-Wide Association Study of Potential Meat Quality Trait Loci in Ducks. <i>Genes</i> , 2022, 13, 986.	2.4	7
1894	Genome-Wide Association Studies, Runs of Homozygosity Analysis, and Copy Number Variation Detection to Identify Reproduction-Related Genes in Bama Xiang Pigs. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	5
1895	Genome-Wide Associations with Resistance to <i>Bipolaris</i> Leaf Spot (<i>Bipolaris oryzae</i> (Breda de Haan)) Tj ETQq1 1 0.784314 rgBT /Overl	3.5	80
1897	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. <i>Genome Medicine</i> , 2022, 14, .	8.2	2
1898	Testing for fitness epistasis in a transplant experiment identifies a candidate adaptive locus in <i>Timema</i> stick insects. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	6
1899	Genome-wide association mapping within a local <i>Arabidopsis thaliana</i> population more fully reveals the genetic architecture for defensive metabolite diversity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	12
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1905	Genetic characterization of outbred Sprague Dawley rats and utility for genome-wide association studies. PLoS Genetics, 2022, 18, e1010234.	3.5	27
1906	Time-resolved multiomics analysis of the genetic regulation of maize kernel moisture. Crop Journal, 2023, 11, 247-257.	5.2	8
1908	Mass spectrometry-based draft of the mouse proteome. Nature Methods, 2022, 19, 803-811.	19.0	19
1909	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	12.8	30
1911	Quantitative trait loci controlling swimming performance and their effect on growth in Nile tilapia (<i>Oreochromis niloticus</i>). Aquaculture, 2022, 560, 738522.	3.5	1
1912	Complex Feline Disease Mapping Using a Dense Genotyping Array. Frontiers in Veterinary Science, 0, 9, .	2.2	2
1914	Identifying alcohol misuse biotypes from neural connectivity markers and concurrent genetic associations. Translational Psychiatry, 2022, 12, .	4.8	8
1917	High-Altitude Genetic Selection and Genome-Wide Association Analysis of Yield-Related Traits in <i>Elymus sibiricus</i> L. Using SLAF Sequencing. Frontiers in Plant Science, 0, 13, .	3.6	4
1918	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, .	3.6	6
1919	Genome-Wide Association Study for Lactation Performance in the Early and Peak Stages of Lactation in Holstein Dairy Cows. Animals, 2022, 12, 1541.	2.3	0
1920	Genetic analysis and identification of VrFRO8, a salt tolerance-related gene in mungbean. Gene, 2022, 836, 146658.	2.2	5
1921	Genome-wide association study and gene editing reveals the causal gene responsible for abnormal red skin color in Yellow River carp. Aquaculture, 2022, 560, 738530.	3.5	5
1922	High-quality genome assembly and pan-genome studies facilitate genetic discovery in mung bean and its improvement. Plant Communications, 2022, 3, 100352.	7.7	21
1923	Genome-wide association and multi-omics studies identify <i>MGMT</i> as a novel risk gene for Alzheimer's disease among women. Alzheimer's and Dementia, 2023, 19, 896-908.	0.8	19
1924	An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. Human Genetics and Genomics Advances, 2022, 3, 100118.	1.7	4
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1929	A genome-wide screen for resilient responses in growing pigs. Genetics Selection Evolution, 2022, 54, .	3.0	2
1930	Rapid adaptive radiation of Darwin's finches depends on ancestral genetic modules. Science Advances, 2022, 8, .	10.3	18
1931	Genome-wide association study for reproduction-related traits in Chinese domestic goose. British Poultry Science, 0, , .	1.7	2
1932	Genome-Wide Association and Genomic Prediction of Growth Traits in the European Flat Oyster (<i>Ostrea edulis</i>). Frontiers in Genetics, 0, 13, .	2.3	6
1934	Reconstructing queen genotypes by pool sequencing colonies in eusocial insects: statistical methods and their application to honeybee. Molecular Ecology Resources, 0, , .	4.8	7
1935	EEF1A1 transcription cofactor gene polymorphism is associated with muscle gene expression and residual feed intake in Nelore cattle. Mammalian Genome, 2022, 33, 619-628.	2.2	1
1936	A super pan-genomic landscape of rice. Cell Research, 2022, 32, 878-896.	12.0	99
1937	Integration of genome-wide association study and selection signatures reveals genetic determinants for skeletal muscle production traits in an F2 chicken population. Journal of Integrative Agriculture, 2022, 21, 2065-2075.	3.5	7
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1939	Genomic regions associate with major axes of variation driven by gas exchange and leaf construction traits in cultivated sunflower (<i>Helianthus annuus</i> L.). Plant Journal, 2022, 111, 1425-1438.	5.7	4
1940	A genome-wide association study of important reproduction traits in large white pigs. Gene, 2022, 838, 146702.	2.2	2
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1942	Combining GWAS and population genomic analyses to characterize coevolution in a legume-rhizobia symbiosis. Molecular Ecology, 2023, 32, 3798-3811.	3.9	8
1943	Plant genetic effects on microbial hubs impact host fitness in repeated field trials. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	43
1944	Genome-Wide Association Analysis and Genetic Parameters for Feed Efficiency and Related Traits in Yorkshire and Duroc Pigs. Animals, 2022, 12, 1902.	2.3	1
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1947	An imputation-based genome-wide association study for growth and fatness traits in Sujiang pigs. <i>Animal</i> , 2022, 16, 100591.	3.3	3
1948	Structured hierarchical models for probabilistic inference from perturbation screening data. <i>Annals of Applied Statistics</i> , 2022, 16, .	1.1	0
1949	Multivariate genome-wide association study of depression, cognition, and memory phenotypes and validation analysis identify 12 cross-ethnic variants. <i>Translational Psychiatry</i> , 2022, 12, .	4.8	3
1950	Locally adaptive temperature response of vegetative growth in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 0, 11, .	6.0	10
1951	Association analyses of host genetics, root-colonizing microbes, and plant phenotypes under different nitrogen conditions in maize. <i>ELife</i> , 0, 11, .	6.0	22
1952	Genome-Wide Association Study and Selective Sweep Analysis Reveal the Genetic Architecture of Body Weights in a Chicken F2 Resource Population. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	6
1953	Genome-wide association study of handgrip strength in the Northern Chinese adult twins. <i>Connective Tissue Research</i> , 0, , 1-9.	2.3	1
1954	Population genomics of Group B <i>Streptococcus</i> reveals the genetics of neonatal disease onset and meningial invasion. <i>Nature Communications</i> , 2022, 13, .	12.8	7
1956	Potential regulation of linoleic acid and volatile organic compound contents in meat of chickens by PLCD1. <i>Journal of Integrative Agriculture</i> , 2023, 22, 222-234.	3.5	6
1957	Genetic networks underlying salinity tolerance in wheat uncovered with genome-wide analyses and selective sweeps. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2925-2941.	3.6	7
1958	Genome-wide association study identifying genetic variants associated with carcass backfat thickness, lean percentage and fat percentage in a four-way crossbred pig population using SLAF-seq technology. <i>BMC Genomics</i> , 2022, 23, .	2.8	10
1959	Genome-wide association studies of global <i>Mycobacterium tuberculosis</i> resistance to 13 antimicrobials in 10,228 genomes identify new resistance mechanisms. <i>PLoS Biology</i> , 2022, 20, e3001755.	5.6	27
1960	A significant quantitative trait locus on chromosome Z and its impact on egg production traits in seven maternal lines of meat-type chicken. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	5.3	2
1961	Fine mapping of candidate quantitative trait loci for plant and ear height in a maize nested-association mapping population. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
1963	Fatty acid metabolism-related genes are associated with flavor-presenting aldehydes in Chinese local chicken. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	5
1965	Mining alleles for tar spot complex resistance from CIMMYT's maize Germplasm Bank. <i>Frontiers in Sustainable Food Systems</i> , 0, 6, .	3.9	1
1966	Genomic analysis of the rare British Lop pig and identification of distinctive genomic markers. <i>PLoS ONE</i> , 2022, 17, e0271053.	2.5	2

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1968	Clinical and genotypic analysis in determining dystonia non-motor phenotypic heterogeneity: a UK Biobank study. <i>Journal of Neurology</i> , 2022, 269, 6436-6451.	3.6	9
1969	A composite strategy of genome-wide association study and copy number variation analysis for carcass traits in a Duroc pig population. <i>BMC Genomics</i> , 2022, 23, .	2.8	11
1970	Variation in CFHR3 determines susceptibility to meningococcal disease by controlling factor H concentrations. <i>American Journal of Human Genetics</i> , 2022, 109, 1680-1691.	6.2	3
1971	Mycobacterium abscessus pathogenesis identified by phenogenomic analyses. <i>Nature Microbiology</i> , 2022, 7, 1431-1441.	13.3	14
1972	A multi-omics framework reveals strawberry flavor genes and their regulatory elements. <i>New Phytologist</i> , 2022, 236, 1089-1107.	7.3	18
1973	Candidate genes and signature of selection associated with different biological aspects and general characteristics of goat. , 2022, 5, 100013.		6
1974	Whole-genome sequence association study identifies CDK8 as a key gene for the number of mummified piglets. <i>Animal Bioscience</i> , 0, , .	2.0	0
1975	Epi-MEIF: detecting higher order epistatic interactions for complex traits using mixed effect conditional inference forests. <i>Nucleic Acids Research</i> , 2022, 50, e114-e114.	14.5	5
1976	Significant compositional and functional variation reveals the patterns of gut microbiota evolution among the widespread Asian honeybee populations. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
1977	A genome-wide association study to investigate genetic loci associated with primary glaucoma in American Cocker Spaniels. <i>American Journal of Veterinary Research</i> , 2022, 83, .	0.6	2
1978	Integrative analysis of GWAS and transcriptome reveals p53 signaling pathway mediates resistance to visceral white-nodules disease in large yellow croaker. <i>Fish and Shellfish Immunology</i> , 2022, 130, 350-358.	3.6	3
1979	Whole-genome sequence-based association analyses on an eight-breed crossed heterogeneous stock of pigs reveal the genetic basis of skeletal muscle fiber characteristics. <i>Meat Science</i> , 2022, 194, 108974.	5.5	4
1980	Genomic and Bioinformatic Resources for Next-Generation Breeding Approaches Towards Enhanced Stress Tolerance in Cereals. , 2022, , 453-493.		2
1981	Assessing the Relationship between the Predicted Deleteriousness of 97 Missense Mutations in 68 Lipid Genes and Phenotypic Variation of Complex Fatness Traits in Pigs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1982	Nested-Association Mapping (NAM) Based Genetic Dissection Reveals Candidate QTLs and Genes for Ear-Kernel Related Traits in Maize. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1983	Genome-Wide Association Mapping and Genomic Selection Approaches for Stress Resilience in Rice. , 2022, , 45-94.		1
1984	A mechanism for red coloration in vertebrates. <i>Current Biology</i> , 2022, 32, 4201-4214.e12.	3.9	20

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1987	Genome-wide association analysis of 101 accessions dissects the genetic basis of shell thickness for genetic improvement in Persian walnut (<i>Juglans regia</i> L.). BMC Plant Biology, 2022, 22, .	3.6	3
1988	<i>Waxy</i> is an important factor for grain fissure resistance and head rice yield as revealed by a genome-wide association study. Journal of Experimental Botany, 2022, 73, 6942-6954.	4.8	8
1989	Genetic adaptation of skin pigmentation in highland Tibetans. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
1990	An SNN retrocopy insertion upstream of <i>GPR22</i> is associated with dark red coat color in Poodles. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	3
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1992	Dissecting the genetic architecture of glucosinolate compounds for quality improvement in flowering stalk tissues of <i>Brassica napus</i> . Horticultural Plant Journal, 2023, 9, 553-562.	5.0	2
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2361	Differential gene expression analysis based on linear mixed model corrects false positive inflation for studying quantitative traits. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
2362	Identification of novel genetic risk factors of dilated cardiomyopathy: from canine to human. <i>Genome Medicine</i> , 2023, 15, .	8.2	1
2363	Genome-wide association studies using multi-models and multi-SNP datasets provide new insights into pasmo resistance in flax. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
2365	Accurate haplotype construction and detection of selection signatures enabled by high quality pig genome sequences. <i>Nature Communications</i> , 2023, 14, .	12.8	2
2366	Machine Learning of Functional Connectivity to Biotype Alcohol and Nicotine Use Disorders. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2024, 9, 326-336.	1.5	2
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