

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.	4.1	186
2	Variation of BMP3 Contributes to Dog Breed Skull Diversity. <i>PLoS Genetics</i> , 2012, 8, e1002849.	1.5	159
3	Imputation of Rare Variants in Next-Generation Association Studies. <i>Human Heredity</i> , 2012, 74, 196-204.	0.4	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.	2.6	36
5	Mapping Quantitative Trait Loci by Controlling Polygenic Background Effects. <i>Genetics</i> , 2013, 195, 1209-1222.	1.2	111
6	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	1.2	518
7	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2013, , .	1.0	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.	9.4	86
9	A Lasso multi-marker mixed model for association mapping with population structure correction. <i>Bioinformatics</i> , 2013, 29, 206-214.	1.8	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.	0.9	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.	9.4	667
14	Association mapping for seed size and shape traits in soybean cultivars. <i>Molecular Breeding</i> , 2013, 31, 785-794.	1.0	93
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16	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis. <i>Plant Cell</i> , 2013, 24, 4793-4805.	3.1	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.	3.5	627
18	Polygenic Modeling with Bayesian Sparse Linear Mixed Models. <i>PLoS Genetics</i> , 2013, 9, e1003264.	1.5	686

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19	The causal meaning of Fisher's average effect. <i>Genetical Research</i> , 2013, 95, 89-109.	0.3	29
20	The Genetics of Canine Skull Shape Variation. <i>Genetics</i> , 2013, 193, 317-325.	1.2	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.	0.8	58
22	A sequence of methodological changes due to sequencing. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2013, 13, 470-477.	1.1	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.	0.9	89
24	Efficiently Identifying Significant Associations in Genome-wide Association Studies. <i>Journal of Computational Biology</i> , 2013, 20, 817-830.	0.8	4
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26	Dissecting High-Dimensional Phenotypes with Bayesian Sparse Factor Analysis of Genetic Covariance Matrices. <i>Genetics</i> , 2013, 194, 753-767.	1.2	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.	1.1	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.	1.1	36
31	Association testing to detect gene-gene interactions on sex chromosomes in trio data. <i>Frontiers in Genetics</i> , 2013, 4, 239.	1.1	3
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33	Marker-Based Estimation of Genetic Parameters in Genomics. <i>PLoS ONE</i> , 2014, 9, e102715.	1.1	6
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35	A SUPER Powerful Method for Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e107684.	1.1	289
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37	Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky-Muller interactions. <i>ELife</i> , 2014, 3, .	2.8	107

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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.	1.5	189
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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.	1.2	24

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93	Genetic diversity and association mapping of seed vigor in rice (<i>Oryza sativa</i> L.). <i>Planta</i> , 2014, 239, 1309-1319.	1.6	93
94	A Unified Sparse Representation for Sequence Variant Identification for Complex Traits. <i>Genetic Epidemiology</i> , 2014, 38, 671-679.	0.6	9
95	A guide to genome-wide association analysis and post-analytic interrogation. <i>Statistics in Medicine</i> , 2015, 34, 3769-3792.	0.8	82
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107	Estimating genetic effect sizes under joint disease-endophenotype models in presence of gene-environment interactions. <i>Frontiers in Genetics</i> , 2015, 6, 248.	1.1	4
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109	Interacted QTL Mapping in Partial NCII Design Provides Evidences for Breeding by Design. <i>PLoS ONE</i> , 2015, 10, e0121034.	1.1	12

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111	Mapping of Craniofacial Traits in Outbred Mice Identifies Major Developmental Genes Involved in Shape Determination. <i>PLoS Genetics</i> , 2015, 11, e1005607.	1.5	67
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131	Detection of genomic loci associated with environmental variables using generalized linear mixed models. <i>Genomics</i> , 2015, 105, 69-75.	1.3	28
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167	Genome-Wide Association Study of Copy Number Variations (CNVs) with Opioid Dependence. <i>Neuropsychopharmacology</i> , 2015, 40, 1016-1026.	2.8	39
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#	ARTICLE	IF	CITATIONS
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995	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
998	Genome-Wide Association Study-Based Identification of SNPs and Haplotypes Associated With Goose Reproductive Performance and Egg Quality. <i>Frontiers in Genetics</i> , 2021, 12, 602583.	1.1	12
999	A platform for experimental precision medicine: The extended BXD mouse family. <i>Cell Systems</i> , 2021, 12, 235-247.e9.	2.9	115
1000	Identification of Major Loci and Candidate Genes for Meat Production-Related Traits in Broilers. <i>Frontiers in Genetics</i> , 2021, 12, 645107.	1.1	7
1001	A genome wide association study for lung function in the Korean population using an exome array. <i>Korean Journal of Internal Medicine</i> , 2021, 36, S142-S150.	0.7	1
1002	A populationâ€genomic approach for estimating selection on polygenic traits in heterogeneous environments. <i>Molecular Ecology Resources</i> , 2021, 21, 1529-1546.	2.2	2
1003	Variants at the MHC Region Associate With Susceptibility to <i>Clostridioides difficile</i> Infection: A Genome-Wide Association Study Using Comprehensive Electronic Health Records. <i>Frontiers in Immunology</i> , 2021, 12, 638913.	2.2	4
1005	A Missense Mutation in the KLF7 Gene Is a Potential Candidate Variant for Congenital Deafness in Australian Stumpy Tail Cattle Dogs. <i>Genes</i> , 2021, 12, 467.	1.0	5
1006	Genetic basis for variation in the number of cephalic pores in a hybrid zone between closely related species of goby, <i>Gymnogobius breunigii</i> and <i>Gymnogobius castaneus</i> . <i>Biological Journal of the Linnean Society</i> , 2021, 133, 143-154.	0.7	0
1007	Genomeâ€wide association study of fleece traits in Inner Mongolia Cashmere goats. <i>Animal Genetics</i> , 2021, 52, 375-379.	0.6	14
1008	Genomic association with pathogen carriage in bighorn sheep (<i>Ovis canadensis</i>). <i>Ecology and Evolution</i> , 2021, 11, 2488-2502.	0.8	4
1009	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
1011	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	3.0	396
1012	Discovery and fine-mapping of kidney function loci in first genome-wide association study in Africans. <i>Human Molecular Genetics</i> , 2021, 30, 1559-1568.	1.4	13
1013	Multivariate Analysis Identifies Eight Novel Loci Associated with Meat Productivity Traits in Sheep. <i>Genes</i> , 2021, 12, 367.	1.0	6
1014	Action detection using a neural network elucidates the genetics of mouse grooming behavior. <i>ELife</i> , 2021, 10, .	2.8	41
1015	Dissecting the genetic basis of grain morphology traits in Chinese wheat by genome wide association study. <i>Euphytica</i> , 2021, 217, 1.	0.6	6

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1016	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	3.5	46
1019	The genomics of rapid climatic adaptation and parallel evolution in North American house mice. <i>PLoS Genetics</i> , 2021, 17, e1009495.	1.5	26
1020	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. <i>International Journal of Obesity</i> , 2021, 45, 1532-1541.	1.6	8
1021	Genome-wide association mapping for resistance to bacterial blight and bacterial leaf streak in rice. <i>Planta</i> , 2021, 253, 94.	1.6	8
1022	Regional heritability mapping identifies several novel loci (STAT4, ULK4, and KCNH5) for primary biliary cholangitis in the Japanese population. <i>European Journal of Human Genetics</i> , 2021, 29, 1282-1291.	1.4	6
1024	On the use of GBLUP and its extension for GWAS with additive and epistatic effects. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
1025	Association of Genetic Variants for Plasma LRG1 With Rapid Decline in Kidney Function in Patients With Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 2384-2394.	1.8	9
1026	Functional phenomics and genetics of the root economics space in winter wheat using high-throughput phenotyping of respiration and architecture. <i>New Phytologist</i> , 2021, 232, 98-112.	3.5	26
1027	A Nonsense Variant in Hephaestin Like 1 (HEPHL1) Is Responsible for Congenital Hypotrichosis in Belted Galloway Cattle. <i>Genes</i> , 2021, 12, 643.	1.0	5
1028	Molecular Parallelism Underlies Convergent Highland Adaptation of Maize Landraces. <i>Molecular Biology and Evolution</i> , 2021, 38, 3567-3580.	3.5	35
1029	Hierarchical mixed-model expedites genome-wide longitudinal association analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
1030	Accounting for Population Structure and Phenotypes From Relatives in Association Mapping for Farm Animals: A Simulation Study. <i>Frontiers in Genetics</i> , 2021, 12, 642065.	1.1	11
1032	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2620-2629.	0.3	12
1033	Enriched-GWAS and Transcriptome Analysis to Refine and Characterize a Major QTL for Anaerobic Germination Tolerance in Rice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4445.	1.8	7
1035	Detecting local genetic correlations with scan statistics. <i>Nature Communications</i> , 2021, 12, 2033.	5.8	23
1038	Development of an Australian Bread Wheat Nested Association Mapping Population, a New Genetic Diversity Resource for Breeding under Dry and Hot Climates. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4348.	1.8	9
1039	Genomic Regions Related to White/Black Tail Feather Color in Dwarf Chickens Identified Using a Genome-Wide Association Study. <i>Frontiers in Genetics</i> , 2021, 12, 566047.	1.1	7
1040	Detection of loci exhibiting pleiotropic effects on body weight and egg number in female broilers. <i>Scientific Reports</i> , 2021, 11, 7441.	1.6	6

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1041	Performance of genome prediction for morphological and growth-related traits in Yellow River carp. <i>Aquaculture</i> , 2021, 536, 736463.	1.7	7
1042	Sex specific effect of gut microbiota on the risk of psychiatric disorders: A Mendelian randomisation study and PRS analysis using UK Biobank cohort. <i>World Journal of Biological Psychiatry</i> , 2021, 22, 495-504.	1.3	2
1044	Genome-wide detection of CNV regions and their potential association with growth and fatness traits in Duroc pigs. <i>BMC Genomics</i> , 2021, 22, 332.	1.2	25
1046	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. <i>American Journal of Human Genetics</i> , 2021, 108, 825-839.	2.6	25
1047	The morphometry of left cuneus mediating the genetic regulation on working memory. <i>Human Brain Mapping</i> , 2021, 42, 3470-3480.	1.9	14
1050	Statistical Learning Methods Applicable to Genome-Wide Association Studies on Unbalanced Case-Control Disease Data. <i>Genes</i> , 2021, 12, 736.	1.0	5
1051	Genome-wide association study of vitamin D concentrations and bone mineral density in the African American-Diabetes Heart Study. <i>PLoS ONE</i> , 2021, 16, e0251423.	1.1	6
1052	Five genetic variants explain over 70% of hair coat pheomelanin intensity variation in purebred and mixed breed domestic dogs. <i>PLoS ONE</i> , 2021, 16, e0250579.	1.1	6
1053	Clinical and Genetic Findings in 28 American Cocker Spaniels with Aural Ceruminous Gland Hyperplasia and Ectasia. <i>Journal of Comparative Pathology</i> , 2021, 185, 30-44.	0.1	2
1054	Computationally efficient whole-genome regression for quantitative and binary traits. <i>Nature Genetics</i> , 2021, 53, 1097-1103.	9.4	457
1056	Genome-Wide Association Studies Reveal Susceptibility Loci for Noninfectious Claw Lesions in Holstein Dairy Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 657375.	1.1	6
1057	The genetic architecture and population genomic signatures of glyphosate resistance in <i>Amaranthus tuberculatus</i> . <i>Molecular Ecology</i> , 2021, 30, 5373-5389.	2.0	22
1058	Characterization of effects of genetic variants via genome-scale metabolic modelling. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 5123-5138.	2.4	10
1059	Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. <i>Genetics Selection Evolution</i> , 2021, 53, 43.	1.2	4
1060	Design and evaluation of a custom 50K Infinium SNP array for egg-type chickens. <i>Poultry Science</i> , 2021, 100, 101044.	1.5	9
1061	A further look at quantitative trait loci for growth and fatness traits in a White Duroc × Erhualian F3 intercross population. <i>Animal Biotechnology</i> , 2021, , 1-12.	0.7	1
1062	Computational principles and challenges in single-cell data integration. <i>Nature Biotechnology</i> , 2021, 39, 1202-1215.	9.4	223
1063	Multi-omics approach identifies germline regulatory variants associated with hematopoietic malignancies in retriever dog breeds. <i>PLoS Genetics</i> , 2021, 17, e1009543.	1.5	9

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1066	The genetic mechanism of heterosis utilization in maize improvement. Genome Biology, 2021, 22, 148.	3.8	69
1067	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. Plant Physiology, 2021, 186, 2078-2092.	2.3	18
1068	Integration of evidence across human and model organism studies: A meeting report. Genes, Brain and Behavior, 2021, 20, e12738.	1.1	12
1070	Polygenic Risk Score for Alzheimer's Disease in Caribbean Hispanics. Annals of Neurology, 2021, 90, 366-376.	2.8	15
1071	A statistical pipeline for identifying physical features that differentiate classes of 3D shapes. Annals of Applied Statistics, 2021, 15, .	0.5	8
1072	lme4GS: An R-Package for Genomic Selection. Frontiers in Genetics, 2021, 12, 680569.	1.1	10
1073	Identifying the complex genetic architecture of growth and fatness traits in a Duroc pig population. Journal of Integrative Agriculture, 2021, 20, 1607-1614.	1.7	11
1074	Genome-wide association analysis of drought resistance based on seed germination vigor and germination rate at the bud stage in common bean. Agronomy Journal, 2021, 113, 2980-2990.	0.9	6
1075	Deleterious Mutations in the TPO Gene Associated with Familial Thyroid Follicular Cell Carcinoma in Dutch German Longhaired Pointers. Genes, 2021, 12, 997.	1.0	5
1076	Genome-wide association analysis of adaptation to oxygen stress in Nile tilapia (<i>Oreochromis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	1.2	15
1077	Identification of genomic regions affecting production traits in pigs divergently selected for feed efficiency. Genetics Selection Evolution, 2021, 53, 49.	1.2	19
1078	Development of polymorphic markers in the immune gene complex loci of cattle. Journal of Dairy Science, 2021, 104, 6897-6908.	1.4	2
1079	A genome-wide association study identifies <i>Arabidopsis thaliana</i> genes that contribute to differences in the outcome of infection with two <i>Turnip mosaic potyvirus</i> strains that differ in their evolutionary history and degree of host specialization. Virus Evolution, 2021, 7, veab063.	2.2	15
1080	Type 2 Diabetes Is Causally Associated With Reduced Serum Osteocalcin: A Genomewide Association and Mendelian Randomization Study. Journal of Bone and Mineral Research, 2020, 36, 1694-1707.	3.1	23
1081	An overview of current population genomics methods for the analysis of whole-genome resequencing data in eukaryotes. Molecular Ecology, 2021, 30, 6036-6071.	2.0	38
1083	Genetic evaluation of small ruminant lentivirus susceptibility in Valais blacknose sheep. Animal Genetics, 2021, 52, 781-782.	0.6	1
1084	Joint contributions of the gut microbiota and host genetics to feed efficiency in chickens. Microbiome, 2021, 9, 126.	4.9	58

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1087	Genome wide study of tardive dyskinesia in schizophrenia. <i>Translational Psychiatry</i> , 2021, 11, 351.	2.4	13
1088	Standing variation rather than recent adaptive introgression probably underlies differentiation of the <i>Helianthus annuus</i> subspecies of <i>Helianthus annuus</i> . <i>Molecular Ecology</i> , 2021, 30, 6229-6245.	2.0	13
1089	Scalable and Robust Regression Methods for Phenome-Wide Association Analysis on Large-Scale Biobank Data. <i>Frontiers in Genetics</i> , 2021, 12, 682638.	1.1	2
1090	Single-marker and haplotype-based genome-wide association studies for the number of teats in two heavy pig breeds. <i>Animal Genetics</i> , 2021, 52, 440-450.	0.6	10
1091	Exploiting within-breed variability in the autochthonous Reggiana breed identified several candidate genes affecting pigmentation-related traits, stature and udder defects in cattle. <i>Animal Genetics</i> , 2021, 52, 579-597.	0.6	5
1092	Genome-wide association mapping of lentil (<i>Lens culinaris</i> Medikus) prebiotic carbohydrates toward improved human health and crop stress tolerance. <i>Scientific Reports</i> , 2021, 11, 13926.	1.6	19
1093	Genotype Groups of the Wheat Leaf Rust Fungus <i>Puccinia triticina</i> in the United States as Determined by Genotyping by Sequencing. <i>Phytopathology</i> , 2022, 112, 653-662.	1.1	4
1094	A sequence variant in the diacylglycerol O-acyltransferase 2 gene influences palmitoleic acid content in pig muscle. <i>Scientific Reports</i> , 2021, 11, 14797.	1.6	5
1095	Genome-Wide Association Studies Reveal Neurological Genes for Dog Herding, Predation, Temperament, and Trainability Traits. <i>Frontiers in Veterinary Science</i> , 2021, 8, 693290.	0.9	13
1096	The genetic basis of adaptation in phenology in an introduced population of Black Cottonwood (<i>Populus trichocarpa</i> , Torr. & Gray). <i>BMC Plant Biology</i> , 2021, 21, 317.	1.6	6
1097	Genetic Modulation of Initial Sensitivity to δ^9 -Tetrahydrocannabinol (THC) Among the BXD Family of Mice. <i>Frontiers in Genetics</i> , 2021, 12, 659012.	1.1	1
1099	Structural and Genomic Insights Into Pyrazinamide Resistance in <i>Mycobacterium tuberculosis</i> Underlie Differences Between Ancient and Modern Lineages. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 619403.	1.6	2
1100	Resequencing 250 Soybean Accessions: New Insights into Genes Associated with Agronomic Traits and Genetic Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 29-41.	3.0	21
1101	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , 2021, 187, 1481-1500.	2.3	44
1102	Genome-wide epistatic interactions of litter size at birth in Chinese indigenous pigs. <i>Animal Genetics</i> , 2021, 52, 739-743.	0.6	4
1103	MegaLMM: Mega-scale linear mixed models for genomic predictions with thousands of traits. <i>Genome Biology</i> , 2021, 22, 213.	3.8	25
1104	Genetic prediction of complex traits with polygenic scores: a statistical review. <i>Trends in Genetics</i> , 2021, 37, 995-1011.	2.9	55

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1106	Optimizing sampling design and sequencing strategy for the genomic analysis of quantitative traits in natural populations. <i>Molecular Ecology Resources</i> , 2022, 22, 137-152.	2.2	1
1108	Forest and Trees: Exploring Bacterial Virulence with Genome-wide Association Studies and Machine Learning. <i>Trends in Microbiology</i> , 2021, 29, 621-633.	3.5	34
1109	Detecting the footprint of selection on the genomes of Murciano-Granadina goats. <i>Animal Genetics</i> , 2021, 52, 683-693.	0.6	6
1110	Accurate prediction and genome-wide association analysis of digital intramuscular fat content in longissimus muscle of pigs. <i>Animal Genetics</i> , 2021, 52, 633-644.	0.6	12
1111	A Genome-Wide Association Study of Age-Related Hearing Impairment in Middle- and Old-Aged Chinese Twins. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	1
1113	Whole-genome resequencing of 240 <i>Gossypium barbadense</i> accessions reveals genetic variation and genes associated with fiber strength and lint percentage. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3249-3261.	1.8	19
1114	Telomere-to-telomere assembly of a fish Y chromosome reveals the origin of a young sex chromosome pair. <i>Genome Biology</i> , 2021, 22, 203.	3.8	34
1116	Genome-Wide Association Studies Provide Insights into the Genetic Determination of Flower and Leaf Traits of <i>Actinidia eriantha</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 730890.	1.7	4
1118	GWAS and Post-GWAS High-Resolution Mapping Analyses Identify Strong Novel Candidate Genes Influencing the Fatty Acid Composition of the Longissimus dorsi Muscle in Pigs. <i>Genes</i> , 2021, 12, 1323.	1.0	4
1120	Hearing Function: Identification of New Candidate Genes Further Explaining the Complexity of This Sensory Ability. <i>Genes</i> , 2021, 12, 1228.	1.0	1
1121	A large-scale genomic association analysis identifies a fragment in Dt11 chromosome conferring cotton <i>Verticillium</i> wilt resistance. <i>Plant Biotechnology Journal</i> , 2021, 19, 2126-2138.	4.1	21
1122	Identification of growth-related SNPs and genes in the genome of the Pacific abalone (<i>Haliotis discus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	1.7	14
1123	Gudgeon fish with and without genetically determined countershading coexist in heterogeneous littoral environments of an ancient lake. <i>Ecology and Evolution</i> , 2021, 11, 13283-13294.	0.8	3
1124	Multi-locus genome-wide association mapping for spike-related traits in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	1.2	12
1125	RNA-Seq reveals adaptive genetic potential of the rare Torrey pine (<i>Pinus torreyana</i>) in the face of Ips bark beetle outbreaks. <i>Conservation Genetics</i> , 2021, 22, 1035-1050.	0.8	2
1126	Killing two enemies with one stone? Genomics of resistance to two sympatric pathogens in Norway spruce. <i>Molecular Ecology</i> , 2021, 30, 4433-4447.	2.0	9
1128	High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. <i>Nature Genetics</i> , 2021, 53, 1385-1391.	9.4	76

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1129	Novel Sources of Pre-Harvest Sprouting Resistance for Japonica Rice Improvement. <i>Plants</i> , 2021, 10, 1709.	1.6	11
1130	Evolutionary impacts of introgressive hybridization in a rapidly evolving group of jumping spiders (F. Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	2
1131	Large-scale transcriptome sequencing in broiler chickens to identify candidate genes for breast muscle weight and intramuscular fat content. <i>Genetics Selection Evolution</i> , 2021, 53, 66.	1.2	8
1132	Identification of genomic regions associated with resistance to blackleg (<i>Leptosphaeria maculans</i>) in canola using genome wide association study. <i>European Journal of Plant Pathology</i> , 2021, 161, 693.	0.8	1
1134	A combination of genome-wide association study and selection signature analysis dissects the genetic architecture underlying bone traits in chickens. <i>Animal</i> , 2021, 15, 100322.	1.3	18
1135	Global range expansion history of pepper (<i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
1136	Taking population stratification into account by local permutations in rare variant association studies on small samples. <i>Genetic Epidemiology</i> , 2021, 45, 821-829.	0.6	4
1137	Genome-wide association studies for production, respiratory disease, and immune-related traits in Landrace pigs. <i>Scientific Reports</i> , 2021, 11, 15823.	1.6	10
1138	Genomic prediction in a numerically small breed population using prioritized genetic markers from whole-genome sequence data. <i>Journal of Animal Breeding and Genetics</i> , 2021, , .	0.8	6
1139	Identification of candidate genomic regions for chicken egg number traits based on genome-wide association study. <i>BMC Genomics</i> , 2021, 22, 610.	1.2	13
1140	Genome-wide association studies. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	529
1141	Genomic selection in salmonids: new discoveries and future perspectives. <i>Aquaculture International</i> , 2021, 29, 2259-2289.	1.1	13
1142	Genomic Diversity and Antimicrobial Resistance of <i>Haemophilus</i> Colonizing the Airways of Young Children with Cystic Fibrosis. <i>MSystems</i> , 2021, 6, e0017821.	1.7	4
1143	Genome-wide association study of trypanosome prevalence and morphometric traits in purebred and crossbred Baoulé cattle of Burkina Faso. <i>PLoS ONE</i> , 2021, 16, e0255089.	1.1	6
1144	Genome-Wide Association Study for Body Length, Body Height, and Total Teat Number in Large White Pigs. <i>Frontiers in Genetics</i> , 2021, 12, 650370.	1.1	12
1145	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	2.3	23
1146	Genome-wide hierarchical mixed model association analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
1147	The Genetic Architecture of a Congenital Heart Defect Is Related to Its Fitness Cost. <i>Genes</i> , 2021, 12, 1368.	1.0	1

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1148	Genome-Wide Association Study Using Whole-Genome Sequencing Identifies a Genomic Region on Chromosome 6 Associated With Comb Traits in Nandan-Yao Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 682501.	1.1	4
1150	Multi-scale inference of genetic trait architecture using biologically annotated neural networks. <i>PLoS Genetics</i> , 2021, 17, e1009754.	1.5	13
1152	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	3.9	47
1155	Dynamics of sex chromosome evolution in a rapid radiation of cichlid fishes. <i>Science Advances</i> , 2021, 7, eabe8215.	4.7	33
1156	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. <i>Genetics</i> , 2021, 219, .	1.2	4
1157	Combined approaches identify known and novel genes associated with sheep litter size and non-seasonal breeding. <i>Animal Genetics</i> , 2021, 52, 857-867.	0.6	3
1158	Genetic control of arbuscular mycorrhizal colonization by <i>Rhizophagus intraradices</i> in <i>Helianthus annuus</i> (L.). <i>Mycorrhiza</i> , 2021, 31, 723-734.	1.3	9
1162	A genome-wide association analysis for body weight at 35 days measured on 137,343 broiler chickens. <i>Genetics Selection Evolution</i> , 2021, 53, 70.	1.2	12
1163	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	3.0	27
1164	Genome- and transcriptome-wide association studies reveal the genetic basis and the breeding history of seed glucosinolate content in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 211-225.	4.1	43
1165	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
1167	Quantitative trait locus mapping identifies a locus linked to striatal dopamine and points to collagen alpha6 chain as a novel regulator of striatal axonal branching in mice. <i>Genes, Brain and Behavior</i> , 2021, 20, e12769.	1.1	2
1168	Association of female reproductive tract microbiota with egg production in layer chickens. <i>GigaScience</i> , 2021, 10, .	3.3	7
1170	Genetic architecture and major genes for backfat thickness in pig lines of diverse genetic backgrounds. <i>Genetics Selection Evolution</i> , 2021, 53, 76.	1.2	35
1171	Controlling for human population stratification in rare variant association studies. <i>Scientific Reports</i> , 2021, 11, 19015.	1.6	8
1172	Identifying SNPs associated with birth weight and days to 100 kg traits in Yorkshire pigs based on genotyping-by-sequencing. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2483-2490.	1.7	2
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.	2.6	6
1174	Genome-wide association studies for canine hip dysplasia in single and multiple populations – implications and potential novel risk loci. <i>BMC Genomics</i> , 2021, 22, 636.	1.2	4

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1175	Genetic Dissection of Grain Yield Component Traits Under High Nighttime Temperature Stress in a Rice Diversity Panel. <i>Frontiers in Plant Science</i> , 2021, 12, 712167.	1.7	4
1176	Heritability and genome-wide association study of blood pressure in Chinese adult twins. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1828.	0.6	8
1177	Investigating anogenital distance and antral follicle count as novel markers of fertility within a herd of cows with positive or negative genetic merit for fertility traits. <i>Journal of Dairy Science</i> , 2021, 104, 12939-12952.	1.4	13
1179	GWAS for genetics of complex quantitative traits: Genome to pangenome and SNPs to SVs and <i>trans</i> -eQTLs. <i>BioEssays</i> , 2021, 43, e2100109.	1.2	15
1180	Controlling for background genetic effects using polygenic scores improves the power of genome-wide association studies. <i>Scientific Reports</i> , 2021, 11, 19571.	1.6	4
1181	Genetics, odor perception and food liking: The intriguing role of cinnamon. <i>Food Quality and Preference</i> , 2021, 93, 104277.	2.3	2
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1612	Comparison of mixed model based approaches for correcting for population substructure with application to extreme phenotype sampling. <i>BMC Genomics</i> , 2022, 23, 98.	1.2	1
1614	Sex-Specific Genomic Region Identification and Molecular Sex Marker Development of Rock Bream (<i>Oplegnathus fasciatus</i>). <i>Marine Biotechnology</i> , 2022, 24, 163-173.	1.1	11
1615	Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. <i>Gut Microbes</i> , 2022, 14, 2024415.	4.3	5
1616	Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts. <i>Gastroenterology</i> , 2022, 162, 1171-1182.e3.	0.6	9
1617	Sparse latent factor regression models for genome-wide and epigenome-wide association studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2022, 21, .	0.2	4
1619	Grid-based Gaussian process models for longitudinal genetic data. <i>Communications for Statistical Applications and Methods</i> , 2022, 29, 65-83.	0.1	1
1620	Genome-wide association, prediction and heritability in bacteria with application to <i>Streptococcus pneumoniae</i> . <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac011.	1.5	5
1623	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	1.1	13
1624	Genomic Landscapes of Epstein-Barr Virus in Pulmonary Lymphoepithelioma-Like Carcinoma. <i>Journal of Virology</i> , 2022, 96, JVI0169321.	1.5	5
1626	Genome-Wide Association Study of Body Conformation Traits by Whole Genome Sequencing in Dazhu Black Goats. <i>Animals</i> , 2022, 12, 548.	1.0	14
1627	Genomic insights into longan evolution from a chromosome-level genome assembly and population genomics of longan accessions. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
1629	AquaGWAS: A Genome-Wide Association Study Pipeline for Aquatic Animals and Its Application to Reference-Required and Reference-Free Genome-Wide Association Study for Abalone. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	0
1630	Genetic parameters estimation and genome-wide association studies for internal organ traits in an F ₂ chicken population. <i>Journal of Animal Breeding and Genetics</i> , 2022, , .	0.8	5
1631	Genome-Wide Association Analysis and Genomic Prediction of Thyroglobulin Plasma Levels. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2173.	1.8	1
1632	A Genome Wide Association Study Revealed Key Single Nucleotide Polymorphisms/Genes Associated With Seed Germination in <i>Gossypium hirsutum</i> L.. <i>Frontiers in Plant Science</i> , 2022, 13, 844946.	1.7	3
1634	IPRS: Leveraging Gene-Environment Interaction to Reconstruct Polygenic Risk Score. <i>Frontiers in Genetics</i> , 2022, 13, 801397.	1.1	4
1635	Do leaf nitrogen resorption dynamics align with the slow-fast continuum? A test at the intraspecific level. <i>Functional Ecology</i> , 2022, 36, 1315-1328.	1.7	6

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1637	Parallel reduction in flowering time from de novo mutations enable evolutionary rescue in colonizing lineages. <i>Nature Communications</i> , 2022, 13, 1461.	5.8	20
1638	Likelihood-based Mendelian randomization analysis with automated instrument selection and horizontal pleiotropic modeling. <i>Science Advances</i> , 2022, 8, eabl5744.	4.7	13
1641	A genome-wide association study of mare fertility in the Pura Raza Español horse. <i>Animal</i> , 2022, 16, 100476.	1.3	6
1642	Genomic consequences of domestication of the Siamese fighting fish. <i>Science Advances</i> , 2022, 8, eabm4950.	4.7	20
1643	Patterns of genomic divergence in sympatric and allopatric speciation of three <i>Mihoutao</i> (<i>Actinidia</i>) species. <i>Horticulture Research</i> , 2022, 9, uhac054.	2.9	5
1644	A multi-trait multi-locus stepwise approach for conducting GWAS on correlated traits. <i>Plant Genome</i> , 2022, 15, e20200.	1.6	4
1645	Multi-omics analysis dissects the genetic architecture of seed coat content in <i>Brassica napus</i> . <i>Genome Biology</i> , 2022, 23, 86.	3.8	23
1646	Trade-offs of Linear Mixed Models in Genome-Wide Association Studies. <i>Journal of Computational Biology</i> , 2022, 29, 233-242.	0.8	5
1647	GWAS for main effects and epistatic interactions for grain morphology traits in wheat. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 651-668.	1.4	6
1648	Comparison of genomic prediction methods for residual feed intake in broilers. <i>Animal Genetics</i> , 2022, 53, 466-469.	0.6	2
1649	Genome-Wide Association Studies and Haplotype-Sharing Analysis Targeting the Egg Production Traits in Shaoxing Duck. <i>Frontiers in Genetics</i> , 2022, 13, 828884.	1.1	1
1650	Genome-wide detection of non-additive quantitative trait loci for semen production traits in beef and dairy bulls. <i>Animal</i> , 2022, 16, 100472.	1.3	11
1651	Target-oriented prioritization: targeted selection strategy by integrating organismal and molecular traits through predictive analytics in breeding. <i>Genome Biology</i> , 2022, 23, 80.	3.8	13
1652	Habitat-linked genetic variation supports microgeographic adaptive divergence in an island endemic bird species. <i>Molecular Ecology</i> , 2022, 31, 2830-2846.	2.0	6
1654	The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross. <i>Nature Communications</i> , 2022, 13, 1463.	5.8	19
1655	Genetic loci implicated in meta-analysis of body shape in Africans. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2022, , .	1.1	3
1657	Genetic modifiers of Huntington disease differentially influence motor and cognitive domains. <i>American Journal of Human Genetics</i> , 2022, 109, 885-899.	2.6	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.	2.6	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.	1.5	1
1661	Genomic landscape of Epstein-Barr virus in familial nasopharyngeal carcinoma. <i>Journal of General Virology</i> , 2022, 103, .	1.3	1
1662	Genomic heterozygosity is associated with parasite abundance, but the effects are not mediated by host condition. <i>Evolutionary Ecology</i> , 0, , 1.	0.5	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.	3.9	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.	4.1	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.	1.1	3
1667	ExomeChip-based rare variant association study in restless legs syndrome. <i>Sleep Medicine</i> , 2022, 94, 26-30.	0.8	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.	1.1	4
1669	Genomic and Transcriptomic Characterization of Atypical Recurrent Flank Alopecia in the Cesky Fousek. <i>Genes</i> , 2022, 13, 650.	1.0	2
1670	A genome-wide epistatic network underlies the molecular architecture of continuous color variation of body extremities. <i>Genomics</i> , 2022, 114, 110361.	1.3	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.	1.7	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.	2.2	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.	1.2	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.	3.0	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, .	0.8	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, .	0.8	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.	0.5	3
1682	3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. <i>PeerJ</i> , 2021, 9, e12628.	0.9	4
1683	Pleiotropic Loci Associated With Foot Disorders and Common Periparturient Diseases in Holstein Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 742934.	1.1	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, .	3.3	23
1686	Genome-Wide Analyses for Osteosarcoma in Leonberger Dogs Reveal the CDKN2A/B Gene Locus as a Major Risk Locus. <i>Genes</i> , 2021, 12, 1964.	1.0	8
1688	Hyperspectral and genome-wide association analyses of leaf phosphorus status in local Thai indica rice. <i>PLoS ONE</i> , 2022, 17, e0267304.	1.1	5
1689	Limited evidence of a genetic basis for sex determination in the common creek chub, <i>Semotilus atromaculatus</i> . <i>Journal of Evolutionary Biology</i> , 2022, 35, 1635-1645.	0.8	3
1691	Average semivariance directly yields accurate estimates of the genomic variance in complex trait analyses. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
1692	Genomic changes underlying repeated niche shifts in an adaptive radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1301-1319.	1.1	3
1693	Efficient estimation of SNP heritability using Gaussian predictive process in large scale cohort studies. <i>PLoS Genetics</i> , 2022, 18, e1010151.	1.5	4
1694	Utilization Strategies of Two Environment Phenotypes in Genomic Prediction. <i>Genes</i> , 2022, 13, 722.	1.0	0
1695	A genealogical estimate of genetic relationships. <i>American Journal of Human Genetics</i> , 2022, 109, 812-824.	2.6	13
1696	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
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.	0.7	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, , .	0.8	2
1701	Genome-wide association studies and haplotype sharing analysis targeting the growth traits in Yandang partridge chickens. <i>Animal Biotechnology</i> , 2022, , 1-7.	0.7	0

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1858	Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize. <i>Genetics</i> , 2022, 221, .	1.2	8
1859	Identification of two new recessive <i>MC1R</i> alleles in red-coloured EvolÄner cattle and other breeds. <i>Animal Genetics</i> , 2022, 53, 427-435.	0.6	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.	6.5	7
1861	Association of Predicted Expression and Multimodel Association Analysis of Substance Abuse Traits. <i>Complex Psychiatry</i> , 2022, 8, 35-46.	1.3	0
1862	A genome-wide association and prediction study in grapevine deciphers the genetic architecture of multiple traits and identifies genes under many new QTLs. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	18
1863	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. <i>Nature</i> , 2022, 606, 358-367.	13.7	67
1864	Genome-Wide Association Studies of Salt-Alkali Tolerance at Seedling and Mature Stages in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 857149.	1.7	5
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.	0.6	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.	1.3	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.	1.8	5
1871	Genome-wide association study of platelet factor 4/heparin antibodies in heparin-induced thrombocytopenia. <i>Blood Advances</i> , 2022, 6, 4137-4146.	2.5	7
1872	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
1873	Canonical transformation for multivariate mixed model association analyses. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	1.8	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.	1.7	9
1876	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	9.4	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.	4.1	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.	1.8	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, .	2.8	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, .	3.3	8
1885	Host-genotype-dependent cecal microbes are linked to breast muscle metabolites in Chinese chickens. <i>IScience</i> , 2022, 25, 104469.	1.9	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.	1.1	2
1887	Robust High-Throughput Phenotyping with Deep Segmentation Enabled by a Web-Based Annotator. <i>Plant Phenomics</i> , 2022, 2022, .	2.5	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.	0.7	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.	0.4	10
1892	Genome-Wide Association Study of Six Forage Traits in Ramie (<i>Boehmeria nivea</i> L. Gaud). <i>Plants</i> , 2022, 11, 1443.	1.6	4
1893	Genome-Wide Association Study of Potential Meat Quality Trait Loci in Ducks. <i>Genes</i> , 2022, 13, 986.	1.0	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, .	0.9	5
1895	Genome-Wide Associations with Resistance to Bipolaris Leaf Spot (<i>Bipolaris oryzae</i> (Breda de Haan)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 16 0		0
1897	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. <i>Genome Medicine</i> , 2022, 14, .	3.6	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, .	1.8	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, .	1.8	12
1900	Sorghum Association Panel whole-genome sequencing establishes cornerstone resource for dissecting genomic diversity. <i>Plant Journal</i> , 2022, 111, 888-904.	2.8	20
1901	Genome-wide analyses reveal a strong association between LEPR gene variants and body fat reserves in ewes. <i>BMC Genomics</i> , 2022, 23, .	1.2	2

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1902	GWAS reveals heritable individual variations in the inherent swimming performance of juvenile large yellow croaker. <i>Aquaculture</i> , 2022, 559, 738419.	1.7	8
1905	Genetic characterization of outbred Sprague Dawley rats and utility for genome-wide association studies. <i>PLoS Genetics</i> , 2022, 18, e1010234.	1.5	27
1906	Time-resolved multiomics analysis of the genetic regulation of maize kernel moisture. <i>Crop Journal</i> , 2023, 11, 247-257.	2.3	8
1908	Mass spectrometry-based draft of the mouse proteome. <i>Nature Methods</i> , 2022, 19, 803-811.	9.0	19
1909	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. <i>Nature Communications</i> , 2022, 13, .	5.8	30
1911	Quantitative trait loci controlling swimming performance and their effect on growth in Nile tilapia (<i>Oreochromis niloticus</i>). <i>Aquaculture</i> , 2022, 560, 738522.	1.7	1
1912	Complex Feline Disease Mapping Using a Dense Genotyping Array. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
1914	Identifying alcohol misuse biotypes from neural connectivity markers and concurrent genetic associations. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	8
1917	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
1918	Detection of Stable Elite Haplotypes and Potential Candidate Genes of Boll Weight Across Multiple Environments via GWAS in Upland Cotton. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
1919	Genome-Wide Association Study for Lactation Performance in the Early and Peak Stages of Lactation in Holstein Dairy Cows. <i>Animals</i> , 2022, 12, 1541.	1.0	0
1920	Genetic analysis and identification of VrFRO8, a salt tolerance-related gene in mungbean. <i>Gene</i> , 2022, 836, 146658.	1.0	5
1921	Genome-wide association study and gene editing reveals the causal gene responsible for abnormal red skin color in Yellow River carp. <i>Aquaculture</i> , 2022, 560, 738530.	1.7	5
1922	High-quality genome assembly and pan-genome studies facilitate genetic discovery in mung bean and its improvement. <i>Plant Communications</i> , 2022, 3, 100352.	3.6	21
1923	Genome-wide association and multi-omics studies identify <i>MGMT</i> as a novel risk gene for Alzheimer's disease among women. <i>Alzheimer's and Dementia</i> , 2023, 19, 896-908.	0.4	19
1924	An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100118.	1.0	4
1926	A socially polymorphic <i>Formica</i> ant species exhibits a novel distribution of social supergene genotypes. <i>Journal of Evolutionary Biology</i> , 2022, 35, 1031-1044.	0.8	3
1927	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. <i>BMC Genomics</i> , 2022, 23, .	1.2	11

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1929	A genome-wide screen for resilient responses in growing pigs. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	2
1930	Rapid adaptive radiation of Darwin's finches depends on ancestral genetic modules. <i>Science Advances</i> , 2022, 8, .	4.7	18
1931	Genome-wide association study for reproduction-related traits in Chinese domestic goose. <i>British Poultry Science</i> , 0, , .	0.8	2
1932	Genome-Wide Association and Genomic Prediction of Growth Traits in the European Flat Oyster (<i>Ostrea edulis</i>). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
1934	Reconstructing queen genotypes by pool sequencing colonies in eusocial insects: statistical methods and their application to honeybee. <i>Molecular Ecology Resources</i> , 0, , .	2.2	7
1935	EEF1A1 transcription cofactor gene polymorphism is associated with muscle gene expression and residual feed intake in Nelore cattle. <i>Mammalian Genome</i> , 2022, 33, 619-628.	1.0	1
1936	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	5.7	99
1937	Integration of genome-wide association study and selection signatures reveals genetic determinants for skeletal muscle production traits in an F2 chicken population. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2065-2075.	1.7	7
1938	Including diverse and admixed populations in genetic epidemiology research. <i>Genetic Epidemiology</i> , 2022, 46, 347-371.	0.6	11
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.). <i>Plant Journal</i> , 2022, 111, 1425-1438.	2.8	4
1940	A genome-wide association study of important reproduction traits in large white pigs. <i>Gene</i> , 2022, 838, 146702.	1.0	2
1941	Host genetic determinants drive compartment-specific assembly of tea plant microbiomes. <i>Plant Biotechnology Journal</i> , 2022, 20, 2174-2186.	4.1	10
1942	Combining GWAS and population genomic analyses to characterize coevolution in a legume-rhizobia symbiosis. <i>Molecular Ecology</i> , 2023, 32, 3798-3811.	2.0	8
1943	Plant genetic effects on microbial hubs impact host fitness in repeated field trials. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	43
1944	Genome-Wide Association Analysis and Genetic Parameters for Feed Efficiency and Related Traits in Yorkshire and Duroc Pigs. <i>Animals</i> , 2022, 12, 1902.	1.0	1
1945	Key features of the genetic architecture and evolution of host-microbe interactions revealed by high-resolution genetic mapping of the mucosa-associated gut microbiome in hybrid mice. <i>ELife</i> , 0, 11, .	2.8	9
1946	PHARP: a pig haplotype reference panel for genotype imputation. <i>Scientific Reports</i> , 2022, 12, .	1.6	12

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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.	1.3	3
1948	Structured hierarchical models for probabilistic inference from perturbation screening data. <i>Annals of Applied Statistics</i> , 2022, 16, .	0.5	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, .	2.4	3
1950	Locally adaptive temperature response of vegetative growth in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 0, 11, .	2.8	10
1951	Association analyses of host genetics, root-colonizing microbes, and plant phenotypes under different nitrogen conditions in maize. <i>ELife</i> , 0, 11, .	2.8	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, .	0.9	6
1953	Genome-wide association study of handgrip strength in the Northern Chinese adult twins. <i>Connective Tissue Research</i> , 0, , 1-9.	1.1	1
1954	Population genomics of Group B <i>Streptococcus</i> reveals the genetics of neonatal disease onset and meningal invasion. <i>Nature Communications</i> , 2022, 13, .	5.8	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.	1.7	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.	1.8	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, .	1.2	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.	2.6	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, .	2.1	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, .	1.7	5
1963	Fatty acid metabolism-related genes are associated with flavor-presenting aldehydes in Chinese local chicken. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1965	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
1966	Genomic analysis of the rare British Lop pig and identification of distinctive genomic markers. <i>PLoS ONE</i> , 2022, 17, e0271053.	1.1	2
1967	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

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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.	1.8	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, .	1.2	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.	2.6	3
1971	<i>Mycobacterium abscessus</i> pathogenesis identified by phenogenomic analyses. <i>Nature Microbiology</i> , 2022, 7, 1431-1441.	5.9	14
1972	A multi-omics framework reveals strawberry flavor genes and their regulatory elements. <i>New Phytologist</i> , 2022, 236, 1089-1107.	3.5	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, , .	0.8	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.	6.5	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, .	1.5	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, .	0.3	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.	1.6	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.	2.7	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.	1.8	20
1985	A comprehensive comparison of multilocus association methods with summary statistics in genome-wide association studies. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	4

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1988	<i>Waxy</i> is an important factor for grain fissure resistance and head rice yield as revealed by a genome-wide association study. <i>Journal of Experimental Botany</i> , 2022, 73, 6942-6954.	2.4	8
1989	Genetic adaptation of skin pigmentation in highland Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1990	An SNN retrocopy insertion upstream of <i>GPR22</i> is associated with dark red coat color in Poodles. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
1991	Unequal reproduction early in a social transition: insights from invasive wasps. <i>American Naturalist</i> , 0, , .	1.0	0
1992	Dissecting the genetic architecture of glucosinolate compounds for quality improvement in flowering stalk tissues of <i>Brassica napus</i> . <i>Horticultural Plant Journal</i> , 2023, 9, 553-562.	2.3	2
1993	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
1994	Insights into the architecture of human-induced polygenic selection in Duroc pigs. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	4
1996	The genetic architecture of phenotypic diversity in the Betta fish (<i>Betta splendens</i>). <i>Science Advances</i> , 2022, 8, .	4.7	10
1997	Genome-wide association study and transcriptome analysis reveal key genes controlling fruit branch angle in cotton. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1998	Prediction of evolutionary constraint by genomic annotations improves functional prioritization of genomic variants in maize. <i>Genome Biology</i> , 2022, 23, .	3.8	7
1999	Natural variation and artificial selection at the <i>BnaC2.MYB28</i> locus modulate <i>Brassica napus</i> seed glucosinolate. <i>Plant Physiology</i> , 2023, 191, 352-368.	2.3	5
2000	Identification and single-base gene-editing functional validation of a cis-EPO variant as a genetic predictor for EPO-increasing therapies. <i>American Journal of Human Genetics</i> , 2022, 109, 1638-1652.	2.6	5
2001	Identification of a missense variant in the porcine <i>AGPAT</i> gene family associated with intramuscular fat content through whole-genome sequencing. <i>Animal Genetics</i> , 2022, 53, 782-793.	0.6	3
2002	Uncovering natural variation in root system architecture and growth dynamics using a robotics-assisted phenomics platform. <i>ELife</i> , 0, 11, .	2.8	9
2003	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
2005	Genetic Dissection of Epistatic Interactions Contributing Yield-Related Agronomic Traits in Rice Using the Compressed Mixed Model. <i>Plants</i> , 2022, 11, 2504.	1.6	2
2007	Syringohydromyelia in Dogs: The Genomic Component Underlying a Complex Neurological Disease. <i>Animals</i> , 2022, 12, 2622.	1.0	0

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2009	Pepper variome reveals the history and key loci associated with fruit domestication and diversification. <i>Molecular Plant</i> , 2022, 15, 1744-1758.	3.9	16
2010	GWAS, MWAS and mGWAS provide insights into precision agriculture based on genotype-dependent microbial effects in foxtail millet. <i>Nature Communications</i> , 2022, 13, .	5.8	30
2011	ExPRSweb: An online repository with polygenic risk scores for common health-related exposures. <i>American Journal of Human Genetics</i> , 2022, 109, 1742-1760.	2.6	9
2012	Prophage-encoded immune evasion factors are critical for <i>Staphylococcus aureus</i> host infection, switching, and adaptation. <i>Cell Genomics</i> , 2022, , 100194.	3.0	11
2013	Genome-Wide Association and Expression Analysis Revealed the Candidate Variants and Molecular Underpinnings of Cold-Stress Response in Large Yellow Croaker. <i>Marine Biotechnology</i> , 2022, 24, 927-941.	1.1	2
2014	Identification of QTNs, QTN-by-environment interactions and genes for yield-related traits in rice using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
2015	Genome-Wide Association Studies Revealed Significant QTLs and Candidate Genes Associated with Backfat and Loin Muscle Area in Pigs Using Imputation-Based Whole Genome Sequencing Data. <i>Animals</i> , 2022, 12, 2911.	1.0	1
2016	Integrative QTL mapping and selection signatures in Groningen White Headed cattle inferred from whole-genome sequences. <i>PLoS ONE</i> , 2022, 17, e0276309.	1.1	3
2017	Variation Pattern and Genome-Wide Association Study of Leaf Phenotypic Traits among Ancient <i>CinkgoÂbiloba L.</i> Populations. <i>Forests</i> , 2022, 13, 1764.	0.9	0
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2020	Time series canopy phenotyping enables the identification of genetic variants controlling dynamic phenotypes in soybean. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 117-132.	4.1	12
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2022	Genome-wide association and transcriptome studies reveal the segregation mechanism of mantle markings in three-way cross hybrid abalone. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
2023	CottonMD: a multi-omics database for cotton biological study. <i>Nucleic Acids Research</i> , 2023, 51, D1446-D1456.	6.5	14
2024	The regulatory landscape of multiple brain regions in outbred heterogeneous stock rats. <i>Nucleic Acids Research</i> , 2022, 50, 10882-10895.	6.5	20
2025	New insights into the novel sequences of the chicken pangenome by liquid chip. <i>Journal of Animal Science</i> , 0, , .	0.2	1
2026	SLC16A7 Promotes Triglyceride Deposition by De Novo Lipogenesis in Chicken Muscle Tissue. <i>Biology</i> , 2022, 11, 1547.	1.3	4

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2028	Resequencing of 558 Chinese mungbean landraces identifies genetic loci associated with key agronomic traits. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2029	Genome-wide association study meta-analysis of suicide death and suicidal behavior. <i>Molecular Psychiatry</i> , 2023, 28, 891-900.	4.1	15
2031	Identification of candidate genes related to highland adaptation from multiple Chinese local chicken breeds by whole genome sequencing analysis. <i>Animal Genetics</i> , 2023, 54, 55-67.	0.6	2
2032	Genomic regions underlying the species-specific mating songs of green lacewings. <i>Insect Molecular Biology</i> , 0, , .	1.0	0
2033	Prioritized candidate causal haplotype blocks in plant genome-wide association studies. <i>PLoS Genetics</i> , 2022, 18, e1010437.	1.5	3
2036	The Genetic Architecture of Meat Quality Traits in a Crossbred Commercial Pig Population. <i>Foods</i> , 2022, 11, 3143.	1.9	3
2037	Genome-Wide Association to Study the Host-Specificity Determinants of <i>Xanthomonas perforans</i> . <i>Phytopathology</i> , 2023, 113, 400-412.	1.1	4
2039	Identification of key adipogenic transcription factors for the pork belly parameters via the association weight matrix. <i>Meat Science</i> , 2023, 195, 109015.	2.7	2
2040	Gene-Based Genome-Wide Association Study Identified Genes for Agronomic Traits in Maize. <i>Biology</i> , 2022, 11, 1649.	1.3	2
2041	Markhor-derived Introgression of a Genomic Region Encompassing <i>PAPSS2</i> Confers High-altitude Adaptability in Tibetan Goats. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
2042	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	7
2043	THP9 enhances seed protein content and nitrogen-use efficiency in maize. <i>Nature</i> , 2022, 612, 292-300.	13.7	48
2046	Genetic insights into smoking behaviours in 10,558 men of African ancestry from continental Africa and the UK. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
2047	Genome-wide association studies of five free amino acid levels in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
2048	Genome-wide association studies for soybean epicotyl length in two environments using 3VmrMLM. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2049	A novel splice-affecting HNF1A variant with large population impact on diabetes in Greenland. <i>Lancet Regional Health - Europe</i> , The, 2023, 24, 100529.	3.0	3
2050	Modified screening method of middle american dry bean genotypes reveals new genomic regions on Pv10 associated with anthracnose resistance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1

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2052	High-throughput phenotyping-based quantitative trait loci mapping reveals the genetic architecture of the salt stress tolerance of <i>Brassica napus</i> . <i>Plant, Cell and Environment</i> , 2023, 46, 549-566.	2.8	5
2053	Identifying causal serum protein-cardiometabolic trait relationships using whole genome sequencing. <i>Human Molecular Genetics</i> , 2023, 32, 1266-1275.	1.4	4
2055	Investigation of high gamma-glutamyltransferase syndrome in California Thoroughbred racehorses. <i>Journal of Veterinary Internal Medicine</i> , 2022, 36, 2203-2212.	0.6	2
2056	Genome-wide association study uncovers major genetic loci associated with flowering time in response to active accumulated temperature in wild soybean population. <i>BMC Genomics</i> , 2022, 23, .	1.2	6
2057	Genomic Assembly of Clinical <i>Candida glabrata</i> (Nakaseomyces glabrata) Isolates Reveals within-Species Structural Plasticity and Association with <i>In Vitro</i> Antifungal Susceptibility. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
2058	Genomic Variation across a Clinical <i>Cryptococcus</i> Population Linked to Disease Outcome. <i>MBio</i> , 2022, 13, .	1.8	11
2059	SLAF-Seq Technology-Based Genome-Wide Association and Population Structure Analyses of Ancient <i>Camellia sinensis</i> (L.) Kuntze in Sandu County, China. <i>Forests</i> , 2022, 13, 1885.	0.9	5
2060	Population genetic structure analysis and identification of backfat thickness loci of Chinese synthetic Yunan pigs. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
2062	H3AGWAS: a portable workflow for genome wide association studies. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	6
2063	Genome-Wide Association Studies for Flesh Color and Intramuscular Fat in (Duroc \times Landrace \times Large) Tj ETQq000 rgBT ₅ Overlock		
2064	Design and characterization of a high-resolution multiple-SNP capture array by target sequencing for sheep. <i>Journal of Animal Science</i> , 0, , .	0.2	4
2065	Identifying Genetic Loci Associated with Complex Trait Variability. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 257-270.	0.2	0
2067	Application of Machine Learning to Ranking Predictors of Anti-VEGF Response. <i>Life</i> , 2022, 12, 1926.	1.1	1
2068	Hypothesis-driven genome-wide association studies provide novel insights into genetics of reading disabilities. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	6
2069	Genetic variation and microbiota in bumble bees cross-infected by different strains of <i>C. bombi</i> . <i>PLoS ONE</i> , 2022, 17, e0277041.	1.1	3
2070	Joint Analysis of Phenotypic and Genomic Diversity Sheds Light on the Evolution of Xenobiotic Metabolism in Humans. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	1
2071	Pistachio genomes provide insights into nut tree domestication and ZW sex chromosome evolution. <i>Plant Communications</i> , 2023, 4, 100497.	3.6	13

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2073	Meta-analysis of genome-wide association studies uncovers shared candidate genes across breeds for pig fatness trait. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
2074	Genome-wide association study for wattles trait in the dairy goat breed. <i>Animal Biotechnology</i> , 0, , 1-7.	0.7	2
2075	Identification of New Genes and Genetic Variant Loci Associated with Breast Muscle Development in the Mini-Cobb F2 Chicken Population Using a Genome-Wide Association Study. <i>Genes</i> , 2022, 13, 2153.	1.0	4
2077	An Improved Bayesian Shrinkage Regression Algorithm for Genomic Selection. <i>Genes</i> , 2022, 13, 2193.	1.0	1
2078	Quality Control Procedures for Genome-Wide Association Studies. <i>Current Protocols</i> , 2022, 2, .	1.3	5
2079	Identification of candidate genomic regions for thermogelled egg yolk traits based on a genome-wide association study. <i>Poultry Science</i> , 2023, 102, 102402.	1.5	1
2082	A genome-wide association study identifies novel players in Na and Fe homeostasis in <i>Arabidopsis thaliana</i> under alkaline salinity stress. <i>Plant Journal</i> , 2023, 113, 225-245.	2.8	2
2084	Genome-wide association study of salt tolerance at the germination stage in hemp. <i>Euphytica</i> , 2023, 219, .	0.6	2
2085	Harnessing underutilized gene bank diversity and genomic prediction of cross usefulness to enhance resistance to <i>Phytophthora cactorum</i> in strawberry. <i>Plant Genome</i> , 2023, 16, .	1.6	8
2087	The environmental adaptation to production and price risks of cayenne pepper: Learning from the Lombok Island - Indonesia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2022, 1107, 012007.	0.2	0
2088	Two decades of association mapping: Insights on disease resistance in major crops. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
2091	A genetic correlation and bivariate genome-wide association study of grip strength and depression. <i>PLoS ONE</i> , 2022, 17, e0278392.	1.1	2
2092	Across-breed genetic investigation of canine hip dysplasia, elbow dysplasia, and anterior cruciate ligament rupture using whole-genome sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
2093	Genome-Wide Association Study Revealed the Effect of rs312715211 in ZNF652 Gene on Abdominal Fat Percentage of Chickens. <i>Biology</i> , 2022, 11, 1849.	1.3	1
2094	<i>Neurog2</i> regulates <i>Isl1</i> to modulate horizontal cell number. <i>Development (Cambridge)</i> , 0, , .	1.2	0
2096	Plant GWAS. , 2022, , 181-189.		0
2098	Genetic dissection of yield-related traits in response to drought stress in common bean. <i>Crop Journal</i> , 2022, , .	2.3	1

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2101	Genetic architecture and evolution of color variation in American black bears. <i>Current Biology</i> , 2023, 33, 86-97.e10.	1.8	9
2102	Genetic architecture of inducible and constitutive metabolic profile related to drought resistance in qingke (Tibetan hulless barley). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2103	First genome-wide association study and genomic prediction for growth traits in spotted sea bass (<i>Lateolabrax maculatus</i>) using whole-genome resequencing. <i>Aquaculture</i> , 2023, 566, 739194.	1.7	6
2104	Genome-wide association studies of viral infections—A short guide to a successful experimental and statistical analysis. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.5	1
2105	Incorporating genome-wide and transcriptome-wide association studies to identify genetic elements of longissimus dorsi muscle in Huaxi cattle. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
2106	Genome–phenotype–environment associations identify signatures of selection in a panmictic population of threespine stickleback. <i>Molecular Ecology</i> , 2023, 32, 1708-1725.	2.0	3
2107	Multi-omic association study identifies DNA methylation-mediated genotype and smoking exposure effects on lung function in children living in urban settings. <i>PLoS Genetics</i> , 2023, 19, e1010594.	1.5	2
2108	Exploring the Genetic Association between Obesity and Serum Lipid Levels Using Bivariate Methods. <i>Twin Research and Human Genetics</i> , 0, , 1-11.	0.3	1
2109	The bovine foot skin microbiota is associated with host genotype and the development of infectious digital dermatitis lesions. <i>Microbiome</i> , 2023, 11, .	4.9	4
2110	Genome-wide association study for loin muscle area of commercial crossbred pigs. <i>Animal Bioscience</i> , 0, , .	0.8	1
2111	Modeling the influence of phenotypic plasticity on maize hybrid performance. <i>Plant Communications</i> , 2023, 4, 100548.	3.6	3
2113	Complex genetic architecture underlying the plasticity of maize agronomic traits. <i>Plant Communications</i> , 2023, 4, 100473.	3.6	9
2114	No evidence for sex chromosomes in natural populations of the cichlid fish <i>Astatotilapia burtoni</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	5
2115	Lymphoid enhancer binding factor 1 is associated with nose color in Yunong black pigs. <i>Animal Genetics</i> , 2023, 54, 398-402.	0.6	0
2116	Whole-genome resequencing reveals genetic differences and the genetic basis of parapodium number in Russian and Chinese <i>Apostichopus japonicus</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	3
2117	Natural selection of immune and metabolic genes associated with health in two lowland Bolivian populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	8

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2119	Genetic dissection of fatty acid components in the Chinese peanut (<i>Arachis hypogaea</i> L.) mini-core collection under multi-environments. <i>PLoS ONE</i> , 2022, 17, e0279650.	1.1	4
2120	Genomic footprints of Kam Sweet Rice domestication indicate possible migration routes of the Dong people in China and provide resources for future rice breeding. <i>Molecular Plant</i> , 2023, 16, 415-431.	3.9	4
2121	275. Comparison of genomic prediction methods for residual feed intake in broilers. , 2022, , .		0
2122	378. Investigation of GWAS variants associated with loin depth in commercial pigs. , 2022, , .		0
2124	Genetic approaches to exploit landraces for improvement of <i>Triticum turgidum</i> ssp. <i>durum</i> in the age of climate change. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
2126	Combined population transcriptomic and genomic analysis reveals cis-regulatory differentiation of non-coding RNAs in maize. <i>Theoretical and Applied Genetics</i> , 2023, 136, 1-13.	1.8	0
2127	Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
2128	Genome-wide association study reveals genetic loci and candidate genes for meat quality traits in a four-way crossbred pig population. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
2129	A sheep pangenome reveals the spectrum of structural variations and their effects on tail phenotypes. <i>Genome Research</i> , 2023, 33, 463-477.	2.4	19
2130	Assessing the relationship between the in silico predicted consequences of 97 missense mutations mapping to 68 genes related to lipid metabolism and their association with porcine fatness traits. <i>Genomics</i> , 2023, 115, 110589.	1.3	0
2133	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. <i>Nature Communications</i> , 2023, 14, .	5.8	8
2134	Genome-wide association study reveals candidate genes for pollution excreta traits in pigs. <i>Animal Genetics</i> , 0, , .	0.6	1
2136	Insight into the genetic basis of ammonia tolerance in razor clam <i>Sinonovacula constricta</i> by genome-wide association study. <i>Aquaculture</i> , 2023, 569, 739351.	1.7	2
2137	Genome-wide association study for growth-related traits in golden pompano (<i>Trachinotus ovatus</i>). <i>Aquaculture</i> , 2023, 572, 739549.	1.7	4
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