

GCTA: A Tool for Genome-wide Complex Trait Analysis

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Nonlinear Instability in Generalized Nonlinear Phase Diffusion Equation. Progress of Theoretical Physics Supplement, 2003, 150, 444-448.	0.2	2
2	Determining Genetic Component of a Disease. , 0, , 91-115.		11
3	Evidence for association of an <i>ACCN1</i> gene variant with response to lithium treatment in Sardinian patients with bipolar disorder. Pharmacogenomics, 2011, 12, 1559-1569.	0.6	82
4	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	4.1	571
5	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
6	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
7	A genome-wide association study on common SNPs and rare CNVs in anorexia nervosa. Molecular Psychiatry, 2011, 16, 949-959.	4.1	186
8	LUPA: A European initiative taking advantage of the canine genome architecture for unravelling complex disorders in both human and dogs. Veterinary Journal, 2011, 189, 155-159.	0.6	95
9	Estimating Missing Heritability for Disease from Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 294-305.	2.6	949
10	Response to Browning and Browning. American Journal of Human Genetics, 2011, 89, 193-195.	2.6	27
11	Population Structure Can Inflate SNP-Based Heritability Estimates. American Journal of Human Genetics, 2011, 89, 191-193.	2.6	83
12	Recent methods for polygenic analysis of genome-wide data implicate an important effect of common variants on cardiovascular disease risk. BMC Medical Genetics, 2011, 12, 146.	2.1	51
13	Evaluation of polygenic risk scores for predicting breast and prostate cancer risk. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	74
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18	Analysis of case-control association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	1.8	36

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19	The Search for Genetic Modifiers of Disease Severity in the $\hat{\text{A}}$ -Hemoglobinopathies. Cold Spring Harbor Perspectives in Medicine, 2012, 2, a015032-a015032.	2.9	48
20	Inbreeding causes early death in a passerine bird. Nature Communications, 2012, 3, 863.	5.8	50
21	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. Translational Psychiatry, 2012, 2, e102-e102.	2.4	156
22	Maximum likelihood estimation of individual inbreeding coefficients and null allele frequencies. Genetical Research, 2012, 94, 151-161.	0.3	18
23	Genome-wide association study of age-related macular degeneration identifies associated variants in the TNXB $\hat{\text{A}}$ FKBPL $\hat{\text{A}}$ NOTCH4 region of chromosome 6p21.3. Human Molecular Genetics, 2012, 21, 4138-4150.	1.4	80
24	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. Bioinformatics, 2012, 28, 2540-2542.	1.8	564
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34	The genetic architecture of economic and political preferences. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8026-8031.	3.3	225
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38	A genome-wide association study of host genetic determinants of the antibody response to Anthrax Vaccine Adsorbed. <i>Vaccine</i> , 2012, 30, 4778-4784.	1.7	24
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43	The Measurement of Local Variation in Shape. <i>Evolutionary Biology</i> , 2012, 39, 419-439.	0.5	48
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56	Genome-wide genetic changes during modern breeding of maize. <i>Nature Genetics</i> , 2012, 44, 812-815.	9.4	352
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91	Genomic study in Mexicans identifies a new locus for triglycerides and refines European lipid loci. <i>Journal of Medical Genetics</i> , 2013, 50, 298-308.	1.5	116

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93	Using Phenotypic Heterogeneity to Increase the Power of Genome-Wide Association Studies: Application to Age at Onset of Ischaemic Stroke Subphenotypes. <i>Genetic Epidemiology</i> , 2013, 37, 495-503.	0.6	10
94	Pharmacogenetics of antidepressant drugs: An update after almost 20 years of research. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 487-520.	1.1	77
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123	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 868-876.	9.4	179
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1003	Reevaluation of SNP heritability in complex human traits. <i>Nature Genetics</i> , 2017, 49, 986-992.	9.4	427
1004	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	5.8	230
1005	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 211-221.	13.9	633
1006	A fast algorithm for Bayesian multi-locus model in genome-wide association studies. <i>Molecular Genetics and Genomics</i> , 2017, 292, 923-934.	1.0	5
1007	Replication and fine-mapping of genetic predictors of lipid traits in African-Americans. <i>Journal of Human Genetics</i> , 2017, 62, 895-901.	1.1	9
1008	Does neighbourhood deprivation affect the genetic influence on body mass?. <i>Social Science and Medicine</i> , 2017, 185, 38-45.	1.8	7

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1010	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.3	615
1011	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132.	9.4	472
1012	Whole-genome sequencing of monozygotic twins discordant for schizophrenia indicates multiple genetic risk factors for schizophrenia. <i>Journal of Genetics and Genomics</i> , 2017, 44, 295-306.	1.7	36
1013	Genome-wide association study of facial emotion recognition in children and association with polygenic risk for mental health disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 701-711.	1.1	26
1014	Genetics of Depression: Progress at Last. <i>Current Psychiatry Reports</i> , 2017, 19, 43.	2.1	101
1015	Insights into the genetic architecture of morphological traits in two passerine bird species. <i>Heredity</i> , 2017, 119, 197-205.	1.2	44
1016	Genetic Determinants of 1,3-Butadiene Metabolism and Detoxification in Three Populations of Smokers with Different Risks of Lung Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1034-1042.	1.1	22
1017	Sequential recruitment of study participants may inflate genetic heritability estimates. <i>Human Genetics</i> , 2017, 136, 743-757.	1.8	20
1018	The impact of structural variation on human gene expression. <i>Nature Genetics</i> , 2017, 49, 692-699.	9.4	334
1019	Genome-Wide Polygenic Scores Predict Reading Performance Throughout the School Years. <i>Scientific Studies of Reading</i> , 2017, 21, 334-349.	1.3	32
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1021	A genome-wide linkage and association analysis of imputed insertions and deletions with cardiometabolic phenotypes in Mexican Americans: The Insulin Resistance Atherosclerosis Family Study. <i>Genetic Epidemiology</i> , 2017, 41, 353-362.	0.6	8
1022	The Relationship between Genes, Personality Traits, and Political Interest. <i>Political Research Quarterly</i> , 2017, 70, 467-479.	1.1	18
1023	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. <i>Nature Genetics</i> , 2017, 49, 789-794.	9.4	259
1024	SeqArray—a storage-efficient high-performance data format for WGS variant calls. <i>Bioinformatics</i> , 2017, 33, 2251-2257.	1.8	127
1025	Genomewide Association Scan of a Mortality Associated Endophenotype for a Long and Healthy Life in the Long Life Family Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, 1411-1416.	1.7	6
1026	Genetic Analysis of Venous Thromboembolism in UK Biobank Identifies the ZFPM2 Locus and Implicates Obesity as a Causal Risk Factor. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	90

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1028	Genetic architecture of bone quality variation in layer chickens revealed by a genome-wide association study. <i>Scientific Reports</i> , 2017, 7, 45317.	1.6	25
1029	Genetics of stroke in a UK African ancestry case-control study. <i>Neurology: Genetics</i> , 2017, 3, e142.	0.9	19
1030	Using Patterns of Genetic Association to Elucidate Shared Genetic Etiologies Across Psychiatric Disorders. <i>Behavior Genetics</i> , 2017, 47, 405-415.	1.4	3
1031	A Preliminary Study of Genetic Variation in the Dopaminergic and Serotonergic Systems and Genome-Wide Additive Genetic Effects on Depression Severity and Treatment Response. <i>Clinical Psychological Science</i> , 2017, 5, 158-165.	2.4	2
1032	Fine-mapping the MHC locus in juvenile idiopathic arthritis (JIA) reveals genetic heterogeneity corresponding to distinct adult inflammatory arthritic diseases. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 765-772.	0.5	88
1033	Genome-wide association mapping and Identification of candidate genes for fatty acid composition in <i>Brassica napus</i> L. using SNP markers. <i>BMC Genomics</i> , 2017, 18, 232.	1.2	105
1034	A cis-acting eQTL in <i>OPRM1</i> is Associated with Subjective Response to Alcohol and Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 929-938.	1.4	13
1035	Identifying candidate positive selection genes in Korean imported pig breeds. <i>Genes and Genomics</i> , 2017, 39, 557-565.	0.5	7
1036	Common variants on 2p16.1, 6p22.1 and 10q24.32 are associated with schizophrenia in Han Chinese population. <i>Molecular Psychiatry</i> , 2017, 22, 954-960.	4.1	74
1037	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. <i>JAMA Psychiatry</i> , 2017, 74, 162.	6.0	82
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1040	Inbreeding depression by environment interactions in a free-living mammal population. <i>Heredity</i> , 2017, 118, 64-77.	1.2	33
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1042	Genetic Variants Associated with Circulating Parathyroid Hormone. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 1553-1565.	3.0	52
1043	Neurogenetics of developmental dyslexia: from genes to behavior through brain neuroimaging and cognitive and sensorial mechanisms. <i>Translational Psychiatry</i> , 2017, 7, e987-e987.	2.4	91
1044	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	2.6	178

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1046	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 82, 312-321.	0.7	26
1047	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 269-273.	9.4	230
1048	Close genetic relationships between a spousal pair with autism-affected children and high minor allele content in cases in autism-associated SNPs. <i>Genomics</i> , 2017, 109, 9-15.	1.3	6
1049	Pudong White pig: a unique genetic resource disclosed by sequencing data. <i>Animal</i> , 2017, 11, 1117-1124.	1.3	11
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1051	SNP-Based Heritability Estimates of Common and Specific Variance in Self- and Informant-Reported Neuroticism Scales. <i>Journal of Personality</i> , 2017, 85, 906-919.	1.8	8
1052	Growth Differentiation Factor 15 as a Novel Biomarker for Metformin. <i>Diabetes Care</i> , 2017, 40, 280-283.	4.3	112
1053	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. <i>Nature Communications</i> , 2017, 8, 1167.	5.8	40
1054	Variation in Position Effect Variegation Within a Natural Population. <i>Genetics</i> , 2017, 207, 1157-1166.	1.2	20
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1056	Single Marker Family-Based Association Analysis Not Conditional on Parental Information. <i>Methods in Molecular Biology</i> , 2017, 1666, 409-439.	0.4	0
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1058	Convergence between biological, behavioural and genetic determinants of obesity. <i>Nature Reviews Genetics</i> , 2017, 18, 731-748.	7.7	83
1059	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. <i>Nature Genetics</i> , 2017, 49, 1576-1583.	9.4	395
1060	Influence of population structure on the compilation of the Bonsmara genomic reference population. <i>Advances in Animal Biosciences</i> , 2017, 8, s45-s47.	1.0	1
1061	A machine-learning heuristic to improve gene score prediction of polygenic traits. <i>Scientific Reports</i> , 2017, 7, 12665.	1.6	69
1062	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2017, 101, 539-551.	2.6	200

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1064	Prediction for Intravenous Immunoglobulin Resistance by Using Weighted Genetic Risk Score Identified From Genome-Wide Association Study in Kawasaki Disease. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	33
1065	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017, 207, 1275-1283.	1.2	19
1066	Genomic Quantitative Genetics to Study Evolution in the Wild. <i>Trends in Ecology and Evolution</i> , 2017, 32, 897-908.	4.2	127
1067	Widespread covariation of early environmental exposures and trait-associated polygenic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11727-11732.	3.3	68
1068	A Comparison of Heritability Estimates by Classical Twin Modeling and Based on Genome-Wide Genetic Relatedness for Cardiac Conduction Traits. <i>Twin Research and Human Genetics</i> , 2017, 20, 489-498.	0.3	14
1069	Recent natural selection causes adaptive evolution of an avian polygenic trait. <i>Science</i> , 2017, 358, 365-368.	6.0	161
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1071	Analysis of Gene-Gene Interactions. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.14.1-1.14.10.	3.5	34
1072	Population Stratification in Genetic Association Studies. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.22.1-1.22.23.	3.5	108
1073	Genomic differentiation and patterns of gene flow between two long-tailed tit species (<i>Aegithalos</i>). <i>Molecular Ecology</i> , 2017, 26, 6654-6665.	2.0	11
1074	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. <i>Molecular Biology and Evolution</i> , 2017, 34, 3148-3153.	3.5	14
1075	Discovery of susceptibility loci associated with tuberculosis in Han Chinese. <i>Human Molecular Genetics</i> , 2017, 26, 4752-4763.	1.4	50
1076	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	9.4	378
1077	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. <i>Scientific Reports</i> , 2017, 7, 11008.	1.6	88
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1079	Iterative hard thresholding for model selection in genome-wide association studies. <i>Genetic Epidemiology</i> , 2017, 41, 756-768.	0.6	6
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1083	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , 2017, 1, 757-765.	6.2	137
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1090	Genome-wide comparative analyses of correlated and uncorrelated phenotypes identify major pleiotropic variants in dairy cattle. <i>Scientific Reports</i> , 2017, 7, 9248.	1.6	34
1091	Convergent and divergent genetic changes in the genome of Chinese and European pigs. <i>Scientific Reports</i> , 2017, 7, 8662.	1.6	13
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1093	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. <i>New England Journal of Medicine</i> , 2017, 377, 1156-1167.	13.9	309
1094	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. <i>Genetics</i> , 2017, 207, 63-73.	1.2	8
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1097	The Evolving Genomic Landscape of Barrettâ€™s Esophagus and Esophageal Adenocarcinoma. <i>Gastroenterology</i> , 2017, 153, 657-673.e1.	0.6	69
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1104	Genotypic variability based association identifies novel non-additive loci DHCR7 and IRF4 in sero-negative rheumatoid arthritis. <i>Scientific Reports</i> , 2017, 7, 5261.	1.6	20
1105	Detection and quantification of inbreeding depression for complex traits from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8602-8607.	3.3	48
1106	Genetic contribution to lipid levels in early life based on 158 loci validated in adults: the FAMILY study. <i>Scientific Reports</i> , 2017, 7, 68.	1.6	4
1107	Low-Frequency Synonymous Coding Variation in CYP2R1 Has Large Effects on Vitamin D Levels and Risk of Multiple Sclerosis. <i>American Journal of Human Genetics</i> , 2017, 101, 227-238.	2.6	112
1108	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112â€‰%117). <i>Molecular Psychiatry</i> , 2017, 22, 1376-1384.	4.1	351
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1112	The pharmacogenetics of metformin. <i>Diabetologia</i> , 2017, 60, 1648-1655.	2.9	65
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1115	Genetic and environmental influences on household financial distress. <i>Journal of Economic Behavior and Organization</i> , 2017, 142, 404-424.	1.0	29
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1125	A large multi-ethnic genome-wide association study identifies novel genetic loci for intraocular pressure. <i>Nature Communications</i> , 2017, 8, 2108.	5.8	80
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1148	Genomic and phenotypic analysis of Vavilov's historic landraces reveals the impact of environment and genomic islands of agronomic traits. <i>Scientific Reports</i> , 2017, 7, 4816.	1.6	24
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1150	Fine-mapping inflammatory bowel disease loci to single-variant resolution. <i>Nature</i> , 2017, 547, 173-178.	13.7	473
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1159	Microbial genome-wide association studies: lessons from human GWAS. Nature Reviews Genetics, 2017, 18, 41-50.	7.7	239
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1305	Systematic analysis of copy number variation associated with congenital diaphragmatic hernia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5247-5252.	3.3	26
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1312	Statistical genetics and its application to neuroimmunology. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 7-12.	0.5	3
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1314	Nineteen and Up study (19Up): understanding pathways to mental health disorders in young Australian twins. <i>BMJ Open</i> , 2018, 8, e018959.	0.8	19
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1322	A Simple Test Identifies Selection on Complex Traits. <i>Genetics</i> , 2018, 209, 321-333.	1.2	18
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1328	Methodological implementation of mixed linear models in multi-locus genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2018, 19, 700-712.	3.2	315
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1351	Genome-wide association study of delay discounting in 23,217 adult research participants of European ancestry. <i>Nature Neuroscience</i> , 2018, 21, 16-18.	7.1	98

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1482	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018, 361, 511-516.	6.0	56
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1488	Genome-Wide Association Studies of 11 Agronomic Traits in Cassava (<i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 2018, 9, 503.	1.7	43
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1490	Genome-wide detection of selection signatures in Chinese indigenous Laiwu pigs revealed candidate genes regulating fat deposition in muscle. <i>BMC Genetics</i> , 2018, 19, 31.	2.7	40
1491	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	5.8	570
1492	<i>Personality Genetics</i> . , 2018, , 185-203.		0
1493	Heritability and genome-wide association study of diffusing capacity of the lung. <i>European Respiratory Journal</i> , 2018, 52, 1800647.	3.1	18
1494	Inferences of genetic architecture of bill morphology in house sparrow using a high-density SNP array point to a polygenic basis. <i>Molecular Ecology</i> , 2018, 27, 3498-3514.	2.0	45
1495	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. <i>PLoS ONE</i> , 2018, 13, e0200486.	1.1	25
1496	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. <i>PLoS Genetics</i> , 2018, 14, e1007501.	1.5	44

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1498	Genomic prediction of the polled and horned phenotypes in Merino sheep. <i>Genetics Selection Evolution</i> , 2018, 50, 28.	1.2	12
1499	Decomposing Additive Genetic Variance Revealed Novel Insights into Trait Evolution in Synthetic Hexaploid Wheat. <i>Frontiers in Genetics</i> , 2018, 9, 27.	1.1	17
1500	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. <i>Frontiers in Genetics</i> , 2018, 9, 57.	1.1	45
1501	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. <i>Frontiers in Genetics</i> , 2018, 9, 97.	1.1	26
1502	Genome-Wide Association Analysis of Age-Dependent Egg Weights in Chickens. <i>Frontiers in Genetics</i> , 2018, 9, 128.	1.1	23
1503	Functional Partitioning of Genomic Variance and Genome-Wide Association Study for Carcass Traits in Korean Hanwoo Cattle Using Imputed Sequence Level SNP Data. <i>Frontiers in Genetics</i> , 2018, 9, 217.	1.1	38
1504	Genetic Architecture of Feeding Behavior and Feed Efficiency in a Duroc Pig Population. <i>Frontiers in Genetics</i> , 2018, 9, 220.	1.1	105
1505	Genome-wide association study of developmental dysplasia of the hip identifies an association with GDF5. <i>Communications Biology</i> , 2018, 1, 56.	2.0	45
1506	Genetics of resistance to photobacteriosis in gilthead sea bream (<i>Sparus aurata</i>) using 2b-RAD sequencing. <i>BMC Genetics</i> , 2018, 19, 43.	2.7	35
1507	Genetic Selection to Enhance Animal Welfare Using Meat Inspection Data from Slaughter Plants. <i>Animals</i> , 2018, 8, 16.	1.0	8
1508	Multi-level genomic analyses suggest new genetic variants involved in human memory. <i>European Journal of Human Genetics</i> , 2018, 26, 1668-1678.	1.4	5
1509	Linkage disequilibrium pattern and genome-wide association mapping for meat traits in multiple porcine F_2 crosses. <i>Animal Genetics</i> , 2018, 49, 403-412.	0.6	9
1510	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	9.4	139
1511	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018, 50, 1072-1080.	9.4	106
1512	Genetic diversity, population structure and phylogenetic relationships of three indigenous pig breeds from Jiangxi Province, China, in a worldwide panel of pigs. <i>Animal Genetics</i> , 2018, 49, 275-283.	0.6	20
1513	Strong Association of the HLA-DR/DQ Locus with Childhood Steroid-Sensitive Nephrotic Syndrome in the Japanese Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2189-2199.	3.0	54
1514	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	1.2	34

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1515	Whole-genome sequencing reveals selection signatures associated with important traits in six goat breeds. <i>Scientific Reports</i> , 2018, 8, 10405.	1.6	93
1516	Modeling Schizophrenia with Human Stem Cells. , 2018, , 13-26.		1
1517	Carotid Artery Atherosclerosis: A Review on Heritability and Genetics. <i>Twin Research and Human Genetics</i> , 2018, 21, 333-346.	0.3	25
1518	The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. <i>Nature Communications</i> , 2018, 9, 2690.	5.8	176
1519	Genetic variations for egg quality of chickens at late laying period revealed by genome-wide association study. <i>Scientific Reports</i> , 2018, 8, 10832.	1.6	45
1520	The coexistence of copy number variations (CNVs) and single nucleotide polymorphisms (SNPs) at a locus can result in distorted calculations of the significance in associating SNPs to disease. <i>Human Genetics</i> , 2018, 137, 553-567.	1.8	57
1521	The relationship between serum insulin-like growth factor-1 (IGF-1) concentration and reproductive performance, and genome-wide associations for serum IGF-1 in Holstein cows. <i>Journal of Dairy Science</i> , 2018, 101, 9154-9167.	1.4	16
1522	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018, 19, 451.	1.2	22
1523	Assessing the Genetic Landscape of Animal Behavior. <i>Genetics</i> , 2018, 209, 223-232.	1.2	25
1524	An update on the genetics of hyperuricaemia and gout. <i>Nature Reviews Rheumatology</i> , 2018, 14, 341-353.	3.5	186
1525	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. <i>Scientific Reports</i> , 2018, 8, 7102.	1.6	9
1526	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , 2018, 50, 10.	1.2	32
1527	Analysis of circulating angiopoietin-like protein 3 and genetic variants in lipid metabolism and liver health: the DiOGenes study. <i>Genes and Nutrition</i> , 2018, 13, 7.	1.2	15
1528	WISARD: workbench for integrated superfast association studies for related datasets. <i>BMC Medical Genomics</i> , 2018, 11, 39.	0.7	11
1529	Common genetic variation and novel loci associated with volumetric mammographic density. <i>Breast Cancer Research</i> , 2018, 20, 30.	2.2	18
1530	A systematic review of genome-wide research on psychotic experiences and negative symptom traits: new revelations and implications for psychiatry. <i>Human Molecular Genetics</i> , 2018, 27, R136-R152.	1.4	27
1531	Characterization of Population Genetic Structure of red swamp crayfish, <i>Procambarus clarkii</i> , in China. <i>Scientific Reports</i> , 2018, 8, 5586.	1.6	50
1532	Use of Genotypes of Common Variants for Genome-Wide Regional Association Analysis. <i>Russian Journal of Genetics</i> , 2018, 54, 250-258.	0.2	0

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1533	CETP (Cholesteryl Ester Transfer Protein) Concentration. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002034.	1.6	44
1534	The relationship between serum anti-MÅ¼llerian hormone concentrations and fertility, and genome-wide associations for anti-MÅ¼llerian hormone in Holstein cows. <i>Journal of Dairy Science</i> , 2018, 101, 7563-7574.	1.4	30
1535	Genes associated with anhedonia: a new analysis in a large clinical trial (GENDEP). <i>Translational Psychiatry</i> , 2018, 8, 150.	2.4	19
1536	Statistical properties of simple random-effects models for genetic heritability. <i>Electronic Journal of Statistics</i> , 2018, 12, 321-356.	0.4	10
1537	Genome-Wide Association Study and Selection Signatures Detect Genomic Regions Associated with Seed Yield and Oil Quality in Flax. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2303.	1.8	49
1538	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
1539	Revealing the selection history of adaptive loci using genome-wide scans for selection: an example from domestic sheep. <i>BMC Genomics</i> , 2018, 19, 71.	1.2	95
1540	Joint genome-wide association study of progressive supranuclear palsy identifies novel susceptibility loci and genetic correlation to neurodegenerative diseases. <i>Molecular Neurodegeneration</i> , 2018, 13, 41.	4.4	77
1541	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.	1.5	117
1542	Relatedness disequilibrium regression estimates heritability without environmental bias. <i>Nature Genetics</i> , 2018, 50, 1304-1310.	9.4	147
1543	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018, 50, 1335-1341.	9.4	896
1544	Fine mapping of 2q35 high-risk neuroblastoma locus reveals independent functional risk variants and suggests full-length BARD1 as tumor-suppressor. <i>International Journal of Cancer</i> , 2018, 143, 2828-2837.	2.3	54
1545	Trans-Ethnic Polygenic Analysis Supports Genetic Overlaps of Lumbar Disc Degeneration With Height, Body Mass Index, and Bone Mineral Density. <i>Frontiers in Genetics</i> , 2018, 9, 267.	1.1	8
1546	Cross-genetic determination of maternal and neonatal immune mediators during pregnancy. <i>Genome Medicine</i> , 2018, 10, 67.	3.6	27
1547	Application of the parametric bootstrap for gene-set analysis of gene-environment interactions. <i>European Journal of Human Genetics</i> , 2018, 26, 1679-1686.	1.4	5
1548	Meta-analysis of genome-wide association studies for height and body mass index in 14700000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	1.4	1,541
1549	How to estimate kinship. <i>Molecular Ecology</i> , 2018, 27, 4121-4135.	2.0	87
1550	A Large Multiethnic Genome-Wide Association Study of Adult Body Mass Index Identifies Novel Loci. <i>Genetics</i> , 2018, 210, 499-515.	1.2	131

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1551	An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. <i>Cell Host and Microbe</i> , 2018, 24, 308-323.e6.	5.1	48
1552	A non-coding genetic variant maximally associated with serum urate levels is functionally linked to HNF4A-dependent PDZK1 expression. <i>Human Molecular Genetics</i> , 2018, 27, 3964-3973.	1.4	26
1553	Predicting Growth Traits with Genomic Selection Methods in Zhikong Scallop (<i>Chlamys farreri</i>). <i>Marine Biotechnology</i> , 2018, 20, 769-779.	1.1	32
1554	Late-Onset Crohn's Disease Is A Subgroup Distinct in Genetic and Behavioral Risk Factors With UC-Like Characteristics. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 2413-2422.	0.9	14
1555	Exploring the association of genetic factors with participation in the Avon Longitudinal Study of Parents and Children. <i>International Journal of Epidemiology</i> , 2018, 47, 1207-1216.	0.9	174
1556	Genetic risk prediction using a spatial autoregressive model with adaptive lasso. <i>Statistics in Medicine</i> , 2018, 37, 3764-3775.	0.8	4
1557	Human-Mediated Introgression of Haplotypes in a Modern Dairy Cattle Breed. <i>Genetics</i> , 2018, 209, 1305-1317.	1.2	21
1558	Genetic Epidemiology. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	1
1559	Copy Number Variation. <i>Methods in Molecular Biology</i> , 2018, 1793, 231-258.	0.4	31
1560	Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2018, 1793, 37-49.	0.4	64
1561	Polygenic risk score, genome-wide association, and gene set analyses of cognitive domain deficits in schizophrenia. <i>Schizophrenia Research</i> , 2018, 201, 393-399.	1.1	19
1563	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
1564	A multiethnic genome-wide association study of primary open-angle glaucoma identifies novel risk loci. <i>Nature Communications</i> , 2018, 9, 2278.	5.8	124
1565	Transethnic, Genome-Wide Analysis Reveals Immune-Related Risk Alleles and Phenotypic Correlates in Pediatric Steroid-Sensitive Nephrotic Syndrome. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2000-2013.	3.0	72
1566	Using tree-based methods for detection of gene-gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. <i>Bioinformatics</i> , 2019, 35, 181-188.	1.8	10
1567	What genome-wide association studies reveal about the association between intelligence and mental health. <i>Current Opinion in Psychology</i> , 2019, 27, 25-30.	2.5	36
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1569	Aggressive behaviour in childhood and adolescence: the role of smoking during pregnancy, evidence from four twin cohorts in the EU-ACTION consortium. <i>Psychological Medicine</i> , 2019, 49, 646-654.	2.7	15

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1571	Genetics of alcohol use disorder: a review. <i>Current Opinion in Psychology</i> , 2019, 27, 56-61.	2.5	43
1572	Fine-mapping analysis of a chromosome 2 region linked to resistance to <i>Mycobacterium tuberculosis</i> infection in Uganda reveals potential regulatory variants. <i>Genes and Immunity</i> , 2019, 20, 473-483.	2.2	18
1573	Nuclear-Mitochondrial interactions influence susceptibility to HIV-associated neurocognitive impairment. <i>Mitochondrion</i> , 2019, 46, 247-255.	1.6	5
1574	Heritability estimation and differential analysis of count data with generalized linear mixed models in genomic sequencing studies. <i>Bioinformatics</i> , 2019, 35, 487-496.	1.8	60
1575	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. <i>Cerebral Cortex</i> , 2019, 29, 2904-2914.	1.6	36
1576	Associations between loneliness and personality are mostly driven by a genetic association with Neuroticism. <i>Journal of Personality</i> , 2019, 87, 386-397.	1.8	66
1577	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. <i>PLoS ONE</i> , 2019, 14, e0220827.	1.1	14
1578	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. <i>National Science Review</i> , 2019, 6, 1201-1222.	4.6	30
1579	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. <i>Communications Biology</i> , 2019, 2, 285.	2.0	27
1580	Optimizing the Power to Identify the Genetic Basis of Complex Traits with Evolve and Resequencing Studies. <i>Molecular Biology and Evolution</i> , 2019, 36, 2890-2905.	3.5	14
1581	GWAS of Behavioral Traits. <i>Current Topics in Behavioral Neurosciences</i> , 2019, 42, 1-34.	0.8	0
1582	Genome-wide association analysis of egg production performance in chickens across the whole laying period. <i>BMC Genetics</i> , 2019, 20, 67.	2.7	38
1583	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	4.7	123
1584	In search of a genetic explanation for LDLc variability in an FH family: common SNPs and a rare mutation in MTP explain only part of LDL variability in an FH family. <i>Journal of Lipid Research</i> , 2019, 60, 1733-1740.	2.0	2
1585	GWAS for urinary sodium and potassium excretion highlights pathways shared with cardiovascular traits. <i>Nature Communications</i> , 2019, 10, 3653.	5.8	24
1586	Genome-wide association studies of severe <i>P. falciparum</i> malaria susceptibility: progress, pitfalls and prospects. <i>BMC Medical Genomics</i> , 2019, 12, 120.	0.7	28
1587	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 1402-1413.	2.5	77

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1589	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
1590	Validation of 46 loci associated with female fertility traits in cattle. <i>BMC Genomics</i> , 2019, 20, 576.	1.2	22
1591	Estimating variance components in population scale family trees. <i>PLoS Genetics</i> , 2019, 15, e1008124.	1.5	11
1592	Solving the missing heritability problem. <i>PLoS Genetics</i> , 2019, 15, e1008222.	1.5	164
1593	Clinical and Genome-Wide Analysis of Serum Platinum Levels after Cisplatin-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 5913-5924.	3.2	16
1594	GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. <i>BMC Medicine</i> , 2019, 17, 135.	2.3	110
1595	Genomic Analysis Reveals Pleiotropic Alleles at EDN3 and BMP7 Involved in Chicken Comb Color and Egg Production. <i>Frontiers in Genetics</i> , 2019, 10, 612.	1.1	20
1596	Single-Locus and Multi-Locus Genome-Wide Association Studies for Intramuscular Fat in Duroc Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 619.	1.1	47
1597	Average information residual maximum likelihood in practice. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 262-272.	0.8	13
1598	Desert island papersâ€”A life in variance parameter and quantitative genetic parameter estimation reviewed using 16 papers. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 230-242.	0.8	4
1599	Comparing Within- and Between-Family Polygenic Score Prediction. <i>American Journal of Human Genetics</i> , 2019, 105, 351-363.	2.6	190
1600	Heritability estimation of dichotomous phenotypes using a liability threshold model on ascertained familyâ€”based samples. <i>Genetic Epidemiology</i> , 2019, 43, 761-775.	0.6	2
1601	The project MinE databrowser: bringing large-scale whole-genome sequencing in ALS to researchers and the public. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2019, 20, 432-440.	1.1	60
1602	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	9.4	641
1603	Analysis of the genetic basis of height in large Jewish nuclear families. <i>PLoS Genetics</i> , 2019, 15, e1008082.	1.5	1
1604	Wholeâ€”genome <scp>SNP</scp> data unravel population structure and signatures of selection for black plumage of indigenous chicken breeds from Jiangxi province, China. <i>Animal Genetics</i> , 2019, 50, 475-483.	0.6	10
1605	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	5.8	44

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1607	Genome resequencing of the orange-spotted grouper (<i>Epinephelus coioides</i>) for a genome-wide association study on ammonia tolerance. <i>Aquaculture</i> , 2019, 512, 734332.	1.7	24
1608	Ancestry-specific polygenic scores and SNP heritability of 25(OH)D in African- and European-ancestry populations. <i>Human Genetics</i> , 2019, 138, 1155-1169.	1.8	6
1609	Genetic diversity of the Sichuan snub-nosed monkey (<i>Rhinopithecus roxellana</i>) in Shennongjia National Park, China using RAD-seq analyses. <i>Genetica</i> , 2019, 147, 327-335.	0.5	6
1610	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. <i>Nature Genetics</i> , 2019, 51, 1244-1251.	9.4	69
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1612	“Ghost Introgression” As a Cause of Deep Mitochondrial Divergence in a Bird Species Complex. <i>Molecular Biology and Evolution</i> , 2019, 36, 2375-2386.	3.5	69
1613	Stochastic Lanczos estimation of genomic variance components for linear mixed-effects models. <i>BMC Bioinformatics</i> , 2019, 20, 411.	1.2	5
1614	“Arte et Labore” A Blackburn Rovers fan's legacy in human complex trait genetics. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 273-278.	0.8	1
1615	Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960.	1.5	42
1616	Genetic Diversity of Indigenous Pigs from South China Area Revealed by SNP Array. <i>Animals</i> , 2019, 9, 361.	1.0	19
1617	Functionalization of the TMEM175 p.M393T variant as a risk factor for Parkinson disease. <i>Human Molecular Genetics</i> , 2019, 28, 3244-3254.	1.4	56
1618	An integrative approach to detect epigenetic mechanisms that putatively mediate the influence of lifestyle exposures on disease susceptibility. <i>International Journal of Epidemiology</i> , 2019, 48, 887-898.	0.9	15
1619	A genomic prediction model for racecourse starts in the Thoroughbred horse. <i>Animal Genetics</i> , 2019, 50, 347-357.	0.6	12
1620	Genetic variability and history of a native Finnish horse breed. <i>Genetics Selection Evolution</i> , 2019, 51, 35.	1.2	13
1621	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	4.7	218
1622	Sequence-based GWAS, network and pathway analyses reveal genes co-associated with milk cheese-making properties and milk composition in MontbÃ©liarde cows. <i>Genetics Selection Evolution</i> , 2019, 51, 34.	1.2	46
1623	A Fast and Powerful Empirical Bayes Method for Genome-Wide Association Studies. <i>Animals</i> , 2019, 9, 305.	1.0	3

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1625	TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 258-266.	2.6	84
1626	Characterization of DSM-IV Opioid Dependence Among Individuals of European Ancestry. <i>Journal of Studies on Alcohol and Drugs</i> , 2019, 80, 319-330.	0.6	11
1627	The use of mid-infrared spectra to map genes affecting milk composition. <i>Journal of Dairy Science</i> , 2019, 102, 7189-7203.	1.4	12
1628	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019, 9, 15192.	1.6	32
1629	Research on the Construction of Humanistic Airport. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 304, 032029.	0.2	0
1630	Analysis of genetic variation contributing to measured speed in Thoroughbreds identifies genomic regions involved in the transcriptional response to exercise. <i>Animal Genetics</i> , 2019, 50, 670-685.	0.6	15
1631	Cardiovascular Predictive Value and Genetic Basis of Ventricular Repolarization Dynamics. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2019, 12, e007549.	2.1	13
1632	QTLs Associated with Resistance to Cardiomyopathy Syndrome in Atlantic Salmon. <i>Journal of Heredity</i> , 2019, 110, 727-737.	1.0	30
1633	Genetic dissection of complex behaviour traits in German Shepherd dogs. <i>Heredity</i> , 2019, 123, 746-758.	1.2	19
1634	Genome-Wide Association Study Reveals Two Nucleotide Variants Associated with Educational Attainment in Koreans. <i>Russian Journal of Genetics</i> , 2019, 55, 1130-1136.	0.2	0
1635	Theoretical Evaluation of Multi-Breed Genomic Prediction in Chinese Indigenous Cattle. <i>Animals</i> , 2019, 9, 789.	1.0	4
1636	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. <i>Cell</i> , 2019, 179, 750-771.e22.	13.5	174
1637	A variant of the castor zinc finger 1 (CASZ1) gene is differentially associated with the clinical classification of chronic venous disease. <i>Scientific Reports</i> , 2019, 9, 14011.	1.6	5
1638	Single-plant GWAS coupled with bulk segregant analysis allows rapid identification and corroboration of plant-height candidate SNPs. <i>BMC Plant Biology</i> , 2019, 19, 412.	1.6	21
1640	Multivariate genome-wide analysis of stress-related quantitative phenotypes. <i>European Neuropsychopharmacology</i> , 2019, 29, 1354-1364.	0.3	7
1641	A genome-wide association and replication study of blood pressure in Ugandan early adolescents. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00950.	0.6	15
1642	Gene-level genome-wide association analysis of suicide attempt, a preliminary study in a psychiatric Mexican population. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e983.	0.6	13

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1644	Genome-Wide Association Studies. , 2019, , .		7
1645	First genome-wide association study of non-severe malaria in two birth cohorts in Benin. <i>Human Genetics</i> , 2019, 138, 1341-1357.	1.8	14
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1647	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2019, 18, 1091-1102.	4.9	1,414
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1659	Summary statistic analyses can mistake confounding bias for heritability. <i>Genetic Epidemiology</i> , 2019, 43, 930-940.	0.6	8
1660	Gene-by-Sex Interactions in Mitochondrial Functions and Cardio-Metabolic Traits. <i>Cell Metabolism</i> , 2019, 29, 932-949.e4.	7.2	79

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1736	A genome-wide association study for susceptibility and infectivity of Holstein Friesian dairy cattle to digital dermatitis. <i>Journal of Dairy Science</i> , 2019, 102, 6248-6262.	1.4	14
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1790	Genome-Wide Signatures of Selection Detection in Three South China Indigenous Pigs. <i>Genes</i> , 2019, 10, 346.	1.0	29
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1804	FunSPU: A versatile and adaptive multiple functional annotation-based association test of whole-genome sequencing data. <i>PLoS Genetics</i> , 2019, 15, e1008081.	1.5	16

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1805	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	9.4	89
1806	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	9.4	402
1807	Differential effects on neurodevelopment of <i>FTO</i> variants in obesity and bipolar disorder suggested by in silico prediction of functional impact: An analysis in Mexican population. <i>Brain and Behavior</i> , 2019, 9, e01249.	1.0	7
1808	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. <i>Cell</i> , 2019, 177, 1022-1034.e6.	13.5	385
1809	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. <i>Scientific Reports</i> , 2019, 9, 6077.	1.6	21
1810	Overlap between eQTL and QTL associated with production traits and fertility in dairy cattle. <i>BMC Genomics</i> , 2019, 20, 291.	1.2	25
1811	X-chromosome association study reveals genetic susceptibility loci of nasopharyngeal carcinoma. <i>Biology of Sex Differences</i> , 2019, 10, 13.	1.8	12
1812	Selection signatures in four German warmblood horse breeds: Tracing breeding history in the modern sport horse. <i>PLoS ONE</i> , 2019, 14, e0215913.	1.1	41
1813	Effects of input data quantity on genome-wide association studies (GWAS). <i>International Journal of Data Mining and Bioinformatics</i> , 2019, 22, 19.	0.1	5
1814	Data-adaptive multi-locus association testing in subjects with arbitrary genealogical relationships. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.2	1
1815	Genetic components of human pain sensitivity: a protocol for a genome-wide association study of experimental pain in healthy volunteers. <i>BMJ Open</i> , 2019, 9, e025530.	0.8	17
1816	The genomics of schizophrenia: Shortcomings and solutions. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2019, 93, 71-76.	2.5	27
1817	Association between polygenic risk for tobacco or alcohol consumption and liability to licit and illicit substance use in young Australian adults. <i>Drug and Alcohol Dependence</i> , 2019, 197, 271-279.	1.6	20
1818	Genome-wide genotyping uncovers genetic diversity, phylogeny, signatures of selection, and population structure of Chinese Jiangquhai pigs in a global perspective1. <i>Journal of Animal Science</i> , 2019, 97, 1491-1500.	0.2	18
1819	Rainbow trout resistance to bacterial cold water disease: two new quantitative trait loci identified after a natural disease outbreak on a French farm. <i>Animal Genetics</i> , 2019, 50, 293-297.	0.6	28
1820	Deep Genome Resequencing Reveals Artificial and Natural Selection for Visual Deterioration, Plateau Adaptability and High Prolificacy in Chinese Domestic Sheep. <i>Frontiers in Genetics</i> , 2019, 10, 300.	1.1	33
1821	Genome wide analysis for mouth ulcers identifies associations at immune regulatory loci. <i>Nature Communications</i> , 2019, 10, 1052.	5.8	50
1822	Multitrait genome-wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. <i>New Phytologist</i> , 2019, 223, 293-309.	3.5	85

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1823	Genome-wide association meta-analysis and Mendelian randomization analysis confirm the influence of ALDH2 on sleep duration in the Japanese population. <i>Sleep</i> , 2019, 42, .	0.6	16
1824	A pathway-driven predictive model of tramadol pharmacogenetics. <i>European Journal of Human Genetics</i> , 2019, 27, 1143-1156.	1.4	4
1825	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. <i>Cell</i> , 2019, 177, 162-183.	13.5	331
1826	Genome-wide association analysis reveals KCTD12 and miR-383-binding genes in the background of rumination. <i>Translational Psychiatry</i> , 2019, 9, 119.	2.4	18
1827	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37
1828	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	9.4	154
1829	The Origin of a Coastal Indigenous Horse Breed in China Revealed by Genome-Wide SNP Data. <i>Genes</i> , 2019, 10, 241.	1.0	11
1831	Fast Model-Fitting of Bayesian Variable Selection Regression Using the Iterative Complex Factorization Algorithm. <i>Bayesian Analysis</i> , 2019, 14, 573-594.	1.6	5
1832	Genome-wide association study in frontal fibrosing alopecia identifies four susceptibility loci including HLA-B*07:02. <i>Nature Communications</i> , 2019, 10, 1150.	5.8	82
1833	VIMCO: variational inference for multiple correlated outcomes in genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 3693-3700.	1.8	9
1834	Animal models with group-specific additive genetic variances: extending genetic group models. <i>Genetics Selection Evolution</i> , 2019, 51, 7.	1.2	15
1835	Multi-population GWAS and enrichment analyses reveal novel genomic regions and promising candidate genes underlying bovine milk fatty acid composition. <i>BMC Genomics</i> , 2019, 20, 178.	1.2	26
1836	Genomewide association study for C-reactive protein in Indians replicates known associations of common variants. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	9
1837	Identification of genetic heterogeneity of Alzheimer's disease across age. <i>Neurobiology of Aging</i> , 2019, 84, 243.e1-243.e9.	1.5	34
1838	Regulation of MFGE8 by the intergenic coronary artery disease locus on 15q26.1. <i>Atherosclerosis</i> , 2019, 284, 11-17.	0.4	26
1839	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. <i>Communications Biology</i> , 2019, 2, 89.	2.0	14
1840	Fast and flexible linear mixed models for genome-wide genetics. <i>PLoS Genetics</i> , 2019, 15, e1007978.	1.5	54
1841	Combinations of single nucleotide polymorphisms identified in genome-wide association studies determine risk for colorectal cancer. <i>International Journal of Cancer</i> , 2019, 145, 2661-2669.	2.3	25

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1842	Whole-genome resequencing of 472 <i>Vitis</i> accessions for grapevine diversity and demographic history analyses. <i>Nature Communications</i> , 2019, 10, 1190.	5.8	155
1843	Population genomics reveals that refugial isolation and habitat change lead to incipient speciation in the Ground tit. <i>Zoologica Scripta</i> , 2019, 48, 277-288.	0.7	4
1844	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear (<i>P. pyrifolia</i>) Fruit. <i>Plant Physiology</i> , 2019, 180, 435-452.	2.3	33
1845	Genomic and Transcriptomic Analysis of Amoebic Gill Disease Resistance in Atlantic Salmon (<i>Salmo</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	52
1846	Protocols, Methods, and Tools for Genome-Wide Association Studies (GWAS) of Dental Traits. <i>Methods in Molecular Biology</i> , 2019, 1922, 493-509.	0.4	14
1847	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. <i>Clinical Cancer Research</i> , 2019, 25, 4104-4116.	3.2	27
1848	Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and α -synuclein mechanisms. <i>Movement Disorders</i> , 2019, 34, 866-875.	2.2	258
1849	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019, 3, 576-586.	6.2	47
1850	Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits. <i>Nature Human Behaviour</i> , 2019, 3, 513-525.	6.2	511
1851	Reverse GWAS: Using genetics to identify and model phenotypic subtypes. <i>PLoS Genetics</i> , 2019, 15, e1008009.	1.5	34
1852	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	1.2	99
1853	Global signal regression strengthens association between resting-state functional connectivity and behavior. <i>NeuroImage</i> , 2019, 196, 126-141.	2.1	292
1854	Genome-wide association study of suicide attempt in a Mexican population: a study protocol. <i>BMJ Open</i> , 2019, 9, e025335.	0.8	2
1855	Genome-wide associations and functional gene analyses for endoparasite resistance in an endangered population of native German Black Pied cattle. <i>BMC Genomics</i> , 2019, 20, 277.	1.2	17
1856	A QTL for Number of Teats Shows Breed Specific Effects on Number of Vertebrae in Pigs: Bridging the Gap Between Molecular and Quantitative Genetics. <i>Frontiers in Genetics</i> , 2019, 10, 272.	1.1	28
1857	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2019, , .	1.0	0
1858	Unravelling the genetic basis of schizophrenia and bipolar disorder with GWAS: A systematic review. <i>Journal of Psychiatric Research</i> , 2019, 114, 178-207.	1.5	81
1859	Computational Approaches for Identification of Pleiotropic Biomarker Profiles in Psychiatry. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1134, 111-128.	0.8	0

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1860	Pharmacogenomic Variants and Drug Interactions Identified Through the Genetic Analysis of Clozapine Metabolism. <i>American Journal of Psychiatry</i> , 2019, 176, 477-486.	4.0	54
1861	Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. <i>PLoS Genetics</i> , 2019, 15, e1007973.	1.5	5
1862	Genome-wide association studies targeting the yield of extraembryonic fluid and production traits in Russian White chickens. <i>BMC Genomics</i> , 2019, 20, 270.	1.2	22
1863	Prioritizing candidate genes for fertility in dairy cows using gene-based analysis, functional annotation and differential gene expression. <i>BMC Genomics</i> , 2019, 20, 255.	1.2	30
1864	Concordance of genetic variation that increases risk for Tourette Syndrome and that influences its underlying neurocircuitry. <i>Translational Psychiatry</i> , 2019, 9, 120.	2.4	24
1865	Comparative population genomics identified genomic regions and candidate genes associated with fruit domestication traits in peach. <i>Plant Biotechnology Journal</i> , 2019, 17, 1954-1970.	4.1	52
1866	Heritability and genetic variance of dementia with Lewy bodies. <i>Neurobiology of Disease</i> , 2019, 127, 492-501.	2.1	29
1867	Contribution of Genetic Background and Data Collection on Adverse Events of Anti-HIV Drugs (D:A:D) Clinical Risk Score to Chronic Kidney Disease in Swiss HIV-infected Persons With Normal Baseline Estimated Glomerular Filtration Rate. <i>Clinical Infectious Diseases</i> , 2019, 70, 890-897.	2.9	7
1868	Neuropsychiatric Genetics of African Populations-Psychosis (NeuroGAP-Psychosis): a case-control study protocol and GWAS in Ethiopia, Kenya, South Africa and Uganda. <i>BMJ Open</i> , 2019, 9, e025469.	0.8	65
1869	Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. <i>PLoS ONE</i> , 2019, 14, e0208217.	1.1	84
1870	Meta-Analysis of Genome-Wide Association Studies Identifies Three Loci Associated With Stiffness Index of the Calcaneus. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1275-1283.	3.1	8
1871	Association of Genetic Variants in <i>NUDT15</i> With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease. <i>JAMA - Journal of the American Medical Association</i> , 2019, 321, 773.	3.8	129
1872	The gut microbiota is largely independent of host genetics in regulating fat deposition in chickens. <i>ISME Journal</i> , 2019, 13, 1422-1436.	4.4	146
1873	The genomics of major psychiatric disorders in a large pedigree from Northern Sweden. <i>Translational Psychiatry</i> , 2019, 9, 60.	2.4	15
1874	Genome wide association study of body weight and feed efficiency traits in a commercial broiler chicken population, a re-visitation. <i>Scientific Reports</i> , 2019, 9, 922.	1.6	28
1875	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. <i>Human Genomics</i> , 2019, 13, 6.	1.4	25
1876	OCMA: Fast, Memory-Efficient Factorization of Prohibitively Large Relationship Matrices. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 13-19.	0.8	6
1877	Predicting the effect of reference population on the accuracy of within, across, and multibreed genomic prediction. <i>Journal of Dairy Science</i> , 2019, 102, 3155-3174.	1.4	29

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1878	Association Study Reveals Genetic Loci Responsible for Arsenic, Cadmium and Lead Accumulation in Rice Grain in Contaminated Farmlands. <i>Frontiers in Plant Science</i> , 2019, 10, 61.	1.7	29
1879	Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. <i>Genetics Selection Evolution</i> , 2019, 51, 4.	1.2	33
1880	Dissecting closely linked association signals in combination with the mammalian phenotype database can identify candidate genes in dairy cattle. <i>BMC Genetics</i> , 2019, 20, 15.	2.7	20
1881	Analysis of the genetic architecture of energy balance and its major determinants dry matter intake and energy-corrected milk yield in primiparous Holstein cows. <i>Journal of Dairy Science</i> , 2019, 102, 3241-3253.	1.4	26
1882	Association analysis of the major histocompatibility complex region in psoriasis vulgaris. <i>British Journal of Dermatology</i> , 2019, 180, 1553-1554.	1.4	0
1883	Analysis of Genetic Diversity and Population Structure in Three Forest Musk Deer Captive Populations with Different Origins. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1037-1044.	0.8	14
1884	Overlapping genetic effects between suicidal ideation and neurocognitive functioning. <i>Journal of Affective Disorders</i> , 2019, 249, 104-111.	2.0	10
1885	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	9.4	201
1886	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
1887	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
1888	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. <i>Human Genetics</i> , 2019, 138, 307-326.	1.8	44
1889	The genetic underpinnings of callous-unemotional traits: A systematic research review. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 100, 85-97.	2.9	56
1890	Prioritizing Parkinson's disease genes using population-scale transcriptomic data. <i>Nature Communications</i> , 2019, 10, 994.	5.8	130
1891	Candidate gene analyses for acute pain and morphine analgesia after pediatric day surgery: African American versus European Caucasian ancestry and dose prediction limits. <i>Pharmacogenomics Journal</i> , 2019, 19, 570-581.	0.9	17
1892	Polygenic and sex specific architecture for two maturation traits in farmed Atlantic salmon. <i>BMC Genomics</i> , 2019, 20, 139.	1.2	25
1893	Comparative population genomics unveils candidate genes for athletic performance in Hanoverians. <i>Genome</i> , 2019, 62, 279-285.	0.9	10
1894	Fine-mapping sequence mutations with a major effect on oligosaccharide content in bovine milk. <i>Scientific Reports</i> , 2019, 9, 2137.	1.6	13
1895	Genomic analyses of an extensive collection of wild and cultivated accessions provide new insights into peach breeding history. <i>Genome Biology</i> , 2019, 20, 36.	3.8	120

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1896	Genome-wide analysis of genetic predisposition to Alzheimer's disease and related sex disparities. <i>Alzheimer's Research and Therapy</i> , 2019, 11, 5.	3.0	61
1897	Fine mapping and subphenotyping implicates <i>ADRA1B</i> gene variants in psoriasis susceptibility in a Chinese population. <i>Epigenomics</i> , 2019, 11, 455-467.	1.0	10
1898	Editorial: The Applications of New Multi-Locus GWAS Methodologies in the Genetic Dissection of Complex Traits. <i>Frontiers in Plant Science</i> , 2019, 10, 100.	1.7	121
1899	Functional Urate-Associated Genetic Variants Influence Expression of lincRNAs LINC01229 and MAFTRR. <i>Frontiers in Genetics</i> , 2018, 9, 733.	1.1	18
1900	The genetic and environmental etiology of child maltreatment in a parent-based extended family design. <i>Development and Psychopathology</i> , 2019, 31, 157-172.	1.4	23
1901	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. <i>Nature Communications</i> , 2019, 10, 790.	5.8	98
1902	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations. <i>Genetics</i> , 2019, 213, 759-770.	1.2	17
1903	GWAS for Meat and Carcass Traits Using Imputed Sequence Level Genotypes in Pooled F2-Designs in Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2823-2834.	0.8	46
1904	CLARITE Facilitates the Quality Control and Analysis Process for EWAS of Metabolic-Related Traits. <i>Frontiers in Genetics</i> , 2019, 10, 1240.	1.1	12
1905	Identification of <i>TYW3/CRYZ</i> and <i>FGD4</i> as susceptibility genes for amyotrophic lateral sclerosis. <i>Neurology: Genetics</i> , 2019, 5, e375.	0.9	16
1906	On the genomic regions associated with milk lactose in Fleckvieh cattle. <i>Journal of Dairy Science</i> , 2019, 102, 10088-10099.	1.4	17
1907	Combining multi-population datasets for joint genome-wide association and meta-analyses: The case of bovine milk fat composition traits. <i>Journal of Dairy Science</i> , 2019, 102, 11124-11141.	1.4	12
1908	Best Prediction of the Additive Genomic Variance in Random-Effects Models. <i>Genetics</i> , 2019, 213, 379-394.	1.2	8
1909	Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. <i>Genetics</i> , 2019, 213, 1237-1253.	1.2	27
1910	Genomic pedigree reconstruction identifies predictors of mating and reproductive success in an invasive vertebrate. <i>Ecology and Evolution</i> , 2019, 9, 11863-11877.	0.8	11
1911	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	5.8	291
1912	Comprehensive genome and transcriptome analyses reveal genetic relationship, selection signature, and transcriptome landscape of small-sized Korean native Jeju horse. <i>Scientific Reports</i> , 2019, 9, 16672.	1.6	18
1913	Genomic Patterns of Homozygosity in Chinese Local Cattle. <i>Scientific Reports</i> , 2019, 9, 16977.	1.6	40

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1914	Anti-Allergenic hormone in grazing dairy cows: Identification of factors affecting plasma concentration, relationship with phenotypic fertility, and genome-wide associations. <i>Journal of Dairy Science</i> , 2019, 102, 11622-11635.	1.4	19
1915	A meta-analysis of genome-wide association studies of epigenetic age acceleration. <i>PLoS Genetics</i> , 2019, 15, e1008104.	1.5	83
1916	Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. <i>Genome Biology</i> , 2019, 20, 243.	3.8	65
1917	Oral Mucosal Immunity and Microbiome. <i>Advances in Experimental Medicine and Biology</i> , 2019, , .	0.8	2
1918	Associations between polygenic risk for tobacco and alcohol use and liability to tobacco and alcohol use, and psychiatric disorders in an independent sample of 13,999 Australian adults. <i>Drug and Alcohol Dependence</i> , 2019, 205, 107704.	1.6	19
1919	Genome-wide analysis of Cushion willow provides insights into alpine plant divergence in a biodiversity hotspot. <i>Nature Communications</i> , 2019, 10, 5230.	5.8	75
1920	Insights into malaria susceptibility using genome-wide data on 17,000 individuals from Africa, Asia and Oceania. <i>Nature Communications</i> , 2019, 10, 5732.	5.8	126
1921	Genetic correlations of psychiatric traits with body composition and glycemic traits are sex- and age-dependent. <i>Nature Communications</i> , 2019, 10, 5765.	5.8	59
1922	Comparative genome analyses reveal the unique genetic composition and selection signals underlying the phenotypic characteristics of three Chinese domestic goat breeds. <i>Genetics Selection Evolution</i> , 2019, 51, 70.	1.2	26
1923	Genomic Analysis of Spontaneous Abortion in Holstein Heifers and Primiparous Cows. <i>Genes</i> , 2019, 10, 954.	1.0	6
1924	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. <i>Molecular Psychiatry</i> , 2021, 26, 4344-4354.	4.1	10
1925	Three genetic-environmental networks for human personality. <i>Molecular Psychiatry</i> , 2021, 26, 3858-3875.	4.1	58
1926	Identification of loci associated with conception rate in primiparous Holstein cows. <i>BMC Genomics</i> , 2019, 20, 840.	1.2	16
1927	Genetic Risk Scores. <i>Current Protocols in Human Genetics</i> , 2019, 104, e95.	3.5	69
1928	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. <i>Nature Communications</i> , 2019, 10, 5508.	5.8	17
1929	Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. <i>Frontiers in Plant Science</i> , 2019, 10, 1570.	1.7	24
1930	Exome resequencing and GWAS for growth, ecophysiology, and chemical and metabolomic composition of wood of <i>Populus trichocarpa</i> . <i>BMC Genomics</i> , 2019, 20, 875.	1.2	19
1931	A Mechanogenetic Model of Exercise-Induced Pulmonary Haemorrhage in the Thoroughbred Horse. <i>Genes</i> , 2019, 10, 880.	1.0	5

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1932	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019, 51, 1749-1755.	9.4	294
1933	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. <i>Communications Biology</i> , 2019, 2, 435.	2.0	22
1934	Genetic risk for major depressive disorder and loneliness in sex-specific associations with coronary artery disease. <i>Molecular Psychiatry</i> , 2021, 26, 4254-4264.	4.1	26
1935	Genetics of cognitive trajectory in Brazilians: 15 years of follow-up from the BambuÃ-Epigen Cohort Study of Aging. <i>Scientific Reports</i> , 2019, 9, 18085.	1.6	6
1936	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. <i>Nature Communications</i> , 2019, 10, 5741.	5.8	110
1937	Analysis of genome-wide DNA arrays reveals the genomic population structure and diversity in autochthonous Greek goat breeds. <i>PLoS ONE</i> , 2019, 14, e0226179.	1.1	17
1938	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	9.4	192
1939	Genetic Diversity and Signatures of Selection in 15 Chinese Indigenous Dog Breeds Revealed by Genome-Wide SNPs. <i>Frontiers in Genetics</i> , 2019, 10, 1174.	1.1	12
1940	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	2.0	37
1941	Combining information from genome-wide association and multi-tissue gene expression studies to elucidate factors underlying genetic variation for residual feed intake in Australian Angus cattle. <i>BMC Genomics</i> , 2019, 20, 939.	1.2	19
1942	Supervised Classification of CYP2D6 Genotype and Metabolizer Phenotype With Postmortem Tramadol-Exposed Finns. <i>American Journal of Forensic Medicine and Pathology</i> , 2019, 40, 8-18.	0.4	8
1943	Efficient Signal Inclusion With Genomic Applications. <i>Journal of the American Statistical Association</i> , 2019, 114, 1787-1799.	1.8	4
1944	Pair Matcher (<i>PaM</i>): fast model-based optimization of treatment/case-control matches. <i>Bioinformatics</i> , 2019, 35, 2243-2250.	1.8	10
1945	Genome-wide meta-analysis reveals shared new <i>loci</i> in systemic seropositive rheumatic diseases. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 311-319.	0.5	81
1946	A genome-wide association study of sodium levels and drug metabolism in an epilepsy cohort treated with carbamazepine and oxcarbazepine. <i>Epilepsia Open</i> , 2019, 4, 102-109.	1.3	9
1947	Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect. <i>DNA Research</i> , 2019, 26, 119-130.	1.5	21
1948	Evidence for Weak Selective Constraint on Human Gene Expression. <i>Genetics</i> , 2019, 211, 757-772.	1.2	48
1949	Association of Genetic Risk Factors for Psychiatric Disorders and Traits of These Disorders in a Swedish Population Twin Sample. <i>JAMA Psychiatry</i> , 2019, 76, 280.	6.0	114

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1950	Moderate-to-severe asthma in individuals of European ancestry: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , 2019, 7, 20-34.	5.2	183
1951	An atlas of genetic influences on osteoporosis in humans and mice. <i>Nature Genetics</i> , 2019, 51, 258-266.	9.4	557
1952	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
1953	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. <i>American Journal of Physical Anthropology</i> , 2019, 168, 4-26.	2.1	45
1954	Progression of diabetic kidney disease and trajectory of kidney function decline in Chinese patients with Type 2 diabetes. <i>Kidney International</i> , 2019, 95, 178-187.	2.6	105
1955	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	9.4	1,594
1956	Heritability of metabolic traits associated with equine metabolic syndrome in Welsh ponies and Morgan horses. <i>Equine Veterinary Journal</i> , 2019, 51, 475-480.	0.9	24
1957	Concordance of genetic variation that increases risk for anxiety disorders and posttraumatic stress disorders and that influences their underlying neurocircuitry. <i>Journal of Affective Disorders</i> , 2019, 245, 885-896.	2.0	21
1958	Semiautomated Feature Extraction from RGB Images for Sorghum Panicle Architecture GWAS. <i>Plant Physiology</i> , 2019, 179, 24-37.	2.3	53
1959	Population genetic analyses of seven Chinese indigenous chicken breeds in a context of global breeds. <i>Animal Genetics</i> , 2019, 50, 82-86.	0.6	27
1960	Detailed insights into pan-European population structure and inbreeding in wild and hatchery Pacific oysters (<i>Crassostrea gigas</i>) revealed by genome-wide SNP data. <i>Evolutionary Applications</i> , 2019, 12, 519-534.	1.5	39
1961	Genomic analyses in African populations identify novel risk loci for cleft palate. <i>Human Molecular Genetics</i> , 2019, 28, 1038-1051.	1.4	61
1962	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
1963	Sex differences in the genetic architecture of obsessive-compulsive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 351-364.	1.1	41
1964	A powerful and data-adaptive test for rare variant-based gene-environment interaction analysis. <i>Statistics in Medicine</i> , 2019, 38, 1230-1244.	0.8	15
1965	Genome-wide association study of anti-Müllerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. <i>Human Molecular Genetics</i> , 2019, 28, 1392-1401.	1.4	22
1966	Genetic diversity analysis of French goat populations reveals selective sweeps involved in their differentiation. <i>Animal Genetics</i> , 2019, 50, 54-63.	0.6	22
1967	The contribution of myostatin (<i>MSTN</i>) and additional modifying genetic loci to race distance aptitude in Thoroughbred horses racing in different geographic regions. <i>Equine Veterinary Journal</i> , 2019, 51, 625-633.	0.9	14

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1968	Genome-wide association study of birth weight in sheep. <i>Animal</i> , 2019, 13, 1797-1803.	1.3	37
1969	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (<i>Sorghum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1.2 51		
1970	Association Mapping Analysis of Fatty Acid Content in Different Ecotypic Rapeseed Using mrMLM. <i>Frontiers in Plant Science</i> , 2018, 9, 1872.	1.7	44
1971	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. <i>Current Biology</i> , 2019, 29, 340-349.e7.	1.8	94
1972	A rapid and efficient linear mixed model approach using the score test and its application to GWAS. <i>Livestock Science</i> , 2019, 220, 37-45.	0.6	4
1973	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	9.4	1,307
1974	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019, 51, 245-257.	9.4	536
1975	A genome-wide association study in individuals of African ancestry reveals the importance of the Duffy-null genotype in the assessment of clozapine-related neutropenia. <i>Molecular Psychiatry</i> , 2019, 24, 328-337.	4.1	42
1976	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , 2019, 133, 967-977.	0.6	34
1977	A pan-transcriptome analysis shows that disease resistance genes have undergone more selection pressure during barley domestication. <i>BMC Genomics</i> , 2019, 20, 12.	1.2	31
1978	The relationship between anogenital distance and fertility, and genome-wide associations for anogenital distance in Irish Holstein-Friesian cows. <i>Journal of Dairy Science</i> , 2019, 102, 1702-1711.	1.4	13
1979	Genome-Wide Association Study Meta-Analysis of the Alcohol Use Disorders Identification Test (AUDIT) in Two Population-Based Cohorts. <i>American Journal of Psychiatry</i> , 2019, 176, 107-118.	4.0	326
1980	A Mendelian Randomization-Based Approach to Identify Early and Sensitive Diagnostic Biomarkers of Disease. <i>Clinical Chemistry</i> , 2019, 65, 427-436.	1.5	16
1981	Translating Alzheimer's disease-associated polymorphisms into functional candidates: a survey of IGAP genes and SNPs. <i>Neurobiology of Aging</i> , 2019, 74, 135-146.	1.5	25
1982	SNP -based heritability and genetic architecture of tarsal osteochondrosis in North American Standardbred horses. <i>Animal Genetics</i> , 2019, 50, 78-81.	0.6	9
1983	The Role of Emergence in Genetically Informed Relationships Research: A Methodological Analysis. <i>Behavior Genetics</i> , 2019, 49, 211-220.	1.4	1
1984	Cigarette smoking and personality: interrogating causality using Mendelian randomisation. <i>Psychological Medicine</i> , 2019, 49, 2197-2205.	2.7	13
1985	Gene-environment correlations in parental emotional warmth and intolerance: genome-wide analysis over two generations of the Young Finns Study. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2019, 60, 277-285.	3.1	11

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1986	Generalized multifactor dimensionality reduction approaches to identification of genetic interactions underlying ordinal traits. <i>Genetic Epidemiology</i> , 2019, 43, 24-36.	0.6	11
1987	Genome-wide association study for carcass traits in spent hens at 72 weeks old. <i>Italian Journal of Animal Science</i> , 2019, 18, 261-266.	0.8	5
1988	eQTL analysis from co-localization of 2739 GWAS loci detects associated genes across 14 human cancers. <i>Journal of Theoretical Biology</i> , 2019, 462, 240-246.	0.8	1
1989	Myopia: is the nature-nurture debate finally over?. <i>Australasian journal of optometry, The</i> , 2019, 102, 3-17.	0.6	77
1990	Non-genetic and genetic predictors of a superficial first basal cell carcinoma. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2019, 33, 533-540.	1.3	5
1991	Multifactorial Inheritance and Complex Diseases. , 2019, , 323-358.		3
1992	eQTL of KCNK2 regionally influences the brain sulcal widening: evidence from 15,597 UK Biobank participants with neuroimaging data. <i>Brain Structure and Function</i> , 2019, 224, 847-857.	1.2	21
1993	SumHer better estimates the SNP heritability of complex traits from summary statistics. <i>Nature Genetics</i> , 2019, 51, 277-284.	9.4	181
1994	Multivariate genomic predictions for age at puberty in tropically adapted beef heifers1. <i>Journal of Animal Science</i> , 2019, 97, 90-100.	0.2	10
1995	Joint analysis of individual-level and summary-level GWAS data by leveraging pleiotropy. <i>Bioinformatics</i> , 2019, 35, 1729-1736.	1.8	3
1996	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019, 28, 166-174.	1.4	752
1997	The Shared Genetic Basis of Educational Attainment and Cerebral Cortical Morphology. <i>Cerebral Cortex</i> , 2019, 29, 3471-3481.	1.6	23
1998	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. <i>Bioinformatics</i> , 2019, 35, 1644-1652.	1.8	36
1999	Nonequivalent lethal equivalents: Models and inbreeding metrics for unbiased estimation of inbreeding load. <i>Evolutionary Applications</i> , 2019, 12, 266-279.	1.5	43
2000	Independent and Joint GWAS for growth traits in Eucalyptus by assembling genome-wide data for 3373 individuals across four breeding populations. <i>New Phytologist</i> , 2019, 221, 818-833.	3.5	62
2001	Genome-wide meta-analysis identifies <i>BARX1</i> and <i>EML4-MTA3</i> as new loci associated with infantile hypertrophic pyloric stenosis. <i>Human Molecular Genetics</i> , 2019, 28, 332-340.	1.4	18
2002	Genetic contributors to serum uric acid levels in Mexicans and their effect on premature coronary artery disease. <i>International Journal of Cardiology</i> , 2019, 279, 168-173.	0.8	15
2003	Integrating regulatory features data for prediction of functional disease-associated SNPs. <i>Briefings in Bioinformatics</i> , 2019, 20, 26-32.	3.2	11

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2004	Genome-wide association study of alcohol use disorder identification test (AUDIT) scores in 20,328 research participants of European ancestry. <i>Addiction Biology</i> , 2019, 24, 121-131.	1.4	84
2005	Shared additive genetic variation for alcohol dependence among subjects of African and European ancestry. <i>Addiction Biology</i> , 2019, 24, 132-144.	1.4	18
2006	Polygenic risk for psychiatric disorders correlates with executive function in typical development. <i>Genes, Brain and Behavior</i> , 2019, 18, e12480.	1.1	16
2007	A genome-wide association study of coping behaviors suggests <i>FBXO45</i> is associated with emotional expression. <i>Genes, Brain and Behavior</i> , 2019, 18, e12481.	1.1	13
2008	Detecting epistasis within chromatin regulatory circuitry reveals <i>CAND2</i> as a novel susceptibility gene for obesity. <i>International Journal of Obesity</i> , 2019, 43, 450-456.	1.6	4
2009	An Exome-Wide Association Study Identifies New Susceptibility Loci for Age of Smoking Initiation in African- and European-American Populations. <i>Nicotine and Tobacco Research</i> , 2019, 21, 707-713.	1.4	6
2010	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence. <i>Molecular Psychiatry</i> , 2019, 24, 169-181.	4.1	238
2011	Beyond genome-wide significance: integrative approaches to the interpretation and extension of GWAS findings for alcohol use disorder. <i>Addiction Biology</i> , 2019, 24, 275-289.	1.4	15
2012	Brain scans from 21,297 individuals reveal the genetic architecture of hippocampal subfield volumes. <i>Molecular Psychiatry</i> , 2020, 25, 3053-3065.	4.1	80
2014	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. <i>International Journal of Epidemiology</i> , 2020, 49, 233-243.	0.9	18
2015	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. <i>Pharmacogenomics Journal</i> , 2020, 20, 329-341.	0.9	45
2016	Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. <i>Human Genetics</i> , 2020, 139, 5-21.	1.8	37
2017	Whole-genome resequencing reveals selection signatures associated with milk production traits in African Kenana dairy zebu cattle. <i>Genomics</i> , 2020, 112, 880-885.	1.3	19
2018	Genome-Wide Association Study of Cerebral Microbleeds on MRI. <i>Neurotoxicity Research</i> , 2020, 37, 146-155.	1.3	13
2019	Missing heritability of complex diseases: case solved?. <i>Human Genetics</i> , 2020, 139, 103-113.	1.8	109
2020	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life. <i>Molecular Psychiatry</i> , 2020, 25, 3034-3052.	4.1	60
2021	Genome-wide association study of the level of blood components in Pekin ducks. <i>Genomics</i> , 2020, 112, 379-387.	1.3	10
2022	OpenMendel: a cooperative programming project for statistical genetics. <i>Human Genetics</i> , 2020, 139, 61-71.	1.8	29

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2023	Comparison of ancestral, partial, and genomic inbreeding in a local pig breed to achieve genetic diversity. <i>Conservation Genetics Resources</i> , 2020, 12, 77-86.	0.4	19
2024	Genetics of suicide attempts in individuals with and without mental disorders: a population-based genome-wide association study. <i>Molecular Psychiatry</i> , 2020, 25, 2410-2421.	4.1	124
2025	Identification of novel loci associated with infant cognitive ability. <i>Molecular Psychiatry</i> , 2020, 25, 3010-3019.	4.1	6
2026	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz009.	1.5	2
2027	Epigenetic Age Acceleration and Cognitive Function in African American Adults in Midlife: The Atherosclerosis Risk in Communities Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 473-480.	1.7	15
2028	The fine-scale genetic structure and selection signals of Chinese indigenous pigs. <i>Evolutionary Applications</i> , 2020, 13, 458-475.	1.5	30
2029	Transethnic meta-analysis of metabolic syndrome in a multiethnic study. <i>Genetic Epidemiology</i> , 2020, 44, 16-25.	0.6	8
2030	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. <i>Molecular Psychiatry</i> , 2020, 25, 2455-2467.	4.1	82
2031	An Allele-Specific Functional SNP Associated with Two Systemic Autoimmune Diseases Modulates IRF5 Expression by Long-Range Chromatin Loop Formation. <i>Journal of Investigative Dermatology</i> , 2020, 140, 348-360.e11.	0.3	25
2032	Sex-specific SNP-SNP interaction analyses within topologically associated domains reveals ANGPT1 as a novel tumor suppressor gene for lung cancer. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 13-22.	1.5	6
2033	RICOPILI: Rapid Imputation for Consortias Pipeline. <i>Bioinformatics</i> , 2020, 36, 930-933.	1.8	201
2034	Exploratory analysis of genetic variants influencing molecular traits in cerebral cortex of suicide completers. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 26-37.	1.1	6
2035	Genome-wide association studies of the self-rating of effects of ethanol (SRE). <i>Addiction Biology</i> , 2020, 25, e12800.	1.4	20
2036	BIVAS: A Scalable Bayesian Method for Bi-Level Variable Selection With Applications. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 40-52.	0.9	6
2037	Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. <i>Human Genetics</i> , 2020, 139, 23-41.	1.8	72
2038	Pharmacogenomic genotypes define genetic ancestry in patients and enable population-specific genomic implementation. <i>Pharmacogenomics Journal</i> , 2020, 20, 126-135.	0.9	14
2039	Elevated risk of invasive group A streptococcal disease and host genetic variation in the human leucocyte antigen locus. <i>Genes and Immunity</i> , 2020, 21, 63-70.	2.2	5
2040	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. <i>Molecular Biology and Evolution</i> , 2020, 37, 134-148.	3.5	23

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2041	The TMEM106B FTLN-protective variant, rs1990621, is also associated with increased neuronal proportion. <i>Acta Neuropathologica</i> , 2020, 139, 45-61.	3.9	51
2042	Introducing M-GCTA a Software Package to Estimate Maternal (or Paternal) Genetic Effects on Offspring Phenotypes. <i>Behavior Genetics</i> , 2020, 50, 51-66.	1.4	18
2043	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
2044	The interaction between ABCA1 polymorphism and physical activity on the HDL-cholesterol levels in a Japanese population. <i>Journal of Lipid Research</i> , 2020, 61, 86-94.	2.0	11
2045	Genome-wide association study of vitamin E in sweet corn kernels. <i>Crop Journal</i> , 2020, 8, 341-350.	2.3	20
2046	Genotype imputation and reference panel: a systematic evaluation on haplotype size and diversity. <i>Briefings in Bioinformatics</i> , 2020, 21, 1806-1817.	3.2	27
2047	Genome-wide heritability analysis of severe malaria resistance reveals evidence of polygenic inheritance. <i>Human Molecular Genetics</i> , 2020, 29, 168-176.	1.4	8
2048	Restriction site-associated DNA sequencing reveals the molecular genetic diversity of grapevine and genes related to white rot disease. <i>Scientia Horticulturae</i> , 2020, 261, 108907.	1.7	8
2049	Identifying biological markers for improved precision medicine in psychiatry. <i>Molecular Psychiatry</i> , 2020, 25, 243-253.	4.1	40
2050	Brain Imaging Genomics: Integrated Analysis and Machine Learning. <i>Proceedings of the IEEE</i> , 2020, 108, 125-162.	16.4	100
2051	Genomic analyses reveal selection footprints in rice landraces grown under on-farm conservation conditions during a short-term period of domestication. <i>Evolutionary Applications</i> , 2020, 13, 290-302.	1.5	9
2052	Identification of genetic loci for leaf hair development in rice through genome-wide association study. <i>Plant Growth Regulation</i> , 2020, 90, 101-108.	1.8	1
2054	Evaluating genomic data for management of local adaptation in a changing climate: A lodgepole pine case study. <i>Evolutionary Applications</i> , 2020, 13, 116-131.	1.5	61
2055	Individualized mating system estimation using genomic data. <i>Molecular Ecology Resources</i> , 2020, 20, 333-347.	2.2	17
2056	Genetic correlations between pain phenotypes and depression and neuroticism. <i>European Journal of Human Genetics</i> , 2020, 28, 358-366.	1.4	52
2057	Bivariate genome-wide association analyses of the broad depression phenotype combined with major depressive disorder, bipolar disorder or schizophrenia reveal eight novel genetic loci for depression. <i>Molecular Psychiatry</i> , 2020, 25, 1420-1429.	4.1	68
2058	Genetic meta-analysis of obsessive-compulsive disorder and self-report compulsive symptoms. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 208-216.	1.1	30
2059	Population structure of indigenous southern African goats based on the Illumina Goat50K SNP panel. <i>Tropical Animal Health and Production</i> , 2020, 52, 1795-1802.	0.5	11

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2060	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
2061	Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <i>Animal</i> , 2020, 14, 910-920.	1.3	36
2062	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020, 6, 34-45.	4.7	449
2063	Genetic risk for dengue hemorrhagic fever and dengue fever in multiple ancestries. <i>EBioMedicine</i> , 2020, 51, 102584.	2.7	10
2064	Heritability estimates for 361 blood metabolites across 40 genome-wide association studies. <i>Nature Communications</i> , 2020, 11, 39.	5.8	64
2065	Genetic modifiers of risk and age at onset in GBA associated Parkinson's disease and Lewy body dementia. <i>Brain</i> , 2020, 143, 234-248.	3.7	149
2066	The genetics of bipolar disorder. <i>Molecular Psychiatry</i> , 2020, 25, 544-559.	4.1	161
2067	Resequencing of 683 common bean genotypes identifies yield component trait associations across a north-south cline. <i>Nature Genetics</i> , 2020, 52, 118-125.	9.4	81
2068	Genome-wide association study reveals two novel risk alleles for incident obstructive sleep apnea in the EPISONO cohort. <i>Sleep Medicine</i> , 2020, 66, 24-32.	0.8	25
2069	Heritability of the Fibromyalgia Phenotype Varies by Age. <i>Arthritis and Rheumatology</i> , 2020, 72, 815-823.	2.9	15
2070	Statistical genetic concepts in psychiatric genomics. , 2020, , 103-116.		0
2071	Genetics of alcohol use disorder. , 2020, , 147-159.		1
2072	A Robust Method Uncovers Significant Context-Specific Heritability in Diverse Complex Traits. <i>American Journal of Human Genetics</i> , 2020, 106, 71-91.	2.6	54
2073	The Psychiatric Genomics Consortium: History, development, and the future. , 2020, , 91-101.		6
2074	Genome-wide association study for growth and fatness traits in Chinese Sujiang pigs. <i>Animal Genetics</i> , 2020, 51, 314-318.	0.6	19
2075	Infant Neuromotor Development: An Early Indicator of Genetic Liability for Neurodevelopmental Disorders. <i>Biological Psychiatry</i> , 2020, 87, 93-94.	0.7	2
2076	Specific domains of early parenting, their heritability and differential association with adolescent behavioural and emotional disorders and academic achievement. <i>European Child and Adolescent Psychiatry</i> , 2020, 29, 1401-1409.	2.8	9
2077	A review of studies examining the association between genetic biomarkers (short tandem repeats and) Tj ETQq1 1 0.784314 rgBT /Over biomarkers. <i>Prostate International</i> , 2020, 8, 135-145.	1.2	2

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2078	Assessing the developmental trajectory of mouse models of neurodevelopmental disorders: Social and communication deficits in mice with Neurexin 1 \pm deletion. <i>Genes, Brain and Behavior</i> , 2020, 19, e12630.	1.1	25
2079	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. <i>European Journal of Human Genetics</i> , 2020, 28, 253-263.	1.4	29
2080	Accuracy of selection for omega-3 fatty acid content in Atlantic salmon fillets. <i>Aquaculture</i> , 2020, 519, 734767.	1.7	11
2081	Genomic evidence of population genetic differentiation in deep-sea squat lobster <i>Shinkaiia crosnieri</i> (crustacea: Decapoda: Anomura) from Northwestern Pacific hydrothermal vent and cold seep. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 156, 103188.	0.6	15
2082	Insights into the genetic basis of retinal detachment. <i>Human Molecular Genetics</i> , 2020, 29, 689-702.	1.4	26
2083	Association of missense variants in <i>GDF9</i> with litter size in Entlebucher Mountain dogs. <i>Animal Genetics</i> , 2020, 51, 78-86.	0.6	3
2084	A road map for understanding molecular and genetic determinants of osteoporosis. <i>Nature Reviews Endocrinology</i> , 2020, 16, 91-103.	4.3	200
2085	The Causal Relationship of Circulating Triglyceride and Glycated Hemoglobin: A Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 908-919.	1.8	10
2086	Integrating a genome-wide association study with transcriptomic analysis to detect genes controlling grain drying rate in maize (<i>Zea mays</i> , L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 623-634.	1.8	16
2087	Genomic prediction for disease resistance to Hepatopancreatic parvovirus and growth, carcass and quality traits in Banana shrimp <i>Fenneropenaeus merguensis</i> . <i>Genomics</i> , 2020, 112, 2021-2027.	1.3	26
2088	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , 2020, 294, 188-204.	2.8	23
2089	The impact of disregarding family structure on genome-wide association analysis of complex diseases in cohorts with simple pedigrees. <i>Journal of Applied Genetics</i> , 2020, 61, 75-86.	1.0	3
2090	Familial Influences on Neuroticism and Education in the UK Biobank. <i>Behavior Genetics</i> , 2020, 50, 84-93.	1.4	9
2091	ADDO: a comprehensive toolkit to detect, classify and visualize additive and non-additive quantitative trait loci. <i>Bioinformatics</i> , 2020, 36, 1517-1521.	1.8	2
2092	Genome-wide association study and genomic evaluation of feed efficiency traits in Japanese Black cattle using single-step genomic best linear unbiased prediction method. <i>Animal Science Journal</i> , 2020, 91, e13316.	0.6	10
2093	Genome-wide association study provides insights into the genetic architecture of bone size and mass in chickens. <i>Genome</i> , 2020, 63, 133-143.	0.9	20
2094	Genome-wide association study reveals genes associated with the absence of intermuscular bones in tambaqui (<i>Colossoma macropomum</i>). <i>Animal Genetics</i> , 2020, 51, 899-909.	0.6	16
2095	Genetic signature of hybridization between Chinese spot-billed ducks and domesticated ducks. <i>Animal Genetics</i> , 2020, 51, 866-875.	0.6	6

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2096	Genomic Phylogeography of <i>Gymnocarpus przewalskii</i> (Caryophyllaceae): Insights into Habitat Fragmentation in Arid Northwestern China. <i>Diversity</i> , 2020, 12, 335.	0.7	12
2097	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	5.8	32
2098	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
2099	Quantitative trait loci (QTL) associated with resistance of rainbow trout <i>Oncorhynchus mykiss</i> against the parasitic ciliate <i>Ichthyophthirius multifiliis</i> . <i>Journal of Fish Diseases</i> , 2020, 43, 1591-1602.	0.9	30
2100	Confirmed effects of candidate variants for milk production, udder health, and udder morphology in dairy cattle. <i>Genetics Selection Evolution</i> , 2020, 52, 55.	1.2	32
2101	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61
2102	Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. <i>Genome Research</i> , 2020, 30, 1379-1392.	2.4	35
2103	Neurological disorder-associated genetic variants in individuals with psychogenic nonepileptic seizures. <i>Scientific Reports</i> , 2020, 10, 15205.	1.6	12
2104	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
2105	The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism. <i>Nature Genetics</i> , 2020, 52, 1099-1110.	9.4	61
2106	Combined approaches to reveal genes associated with litter size in Yunshang black goats. <i>Animal Genetics</i> , 2020, 51, 924-934.	0.6	24
2107	Wide variation in the suboptimal distribution of photosynthetic capacity in relation to light across genotypes of wheat. <i>AoB PLANTS</i> , 2020, 12, plaa039.	1.2	8
2108	Use of gene expression and whole-genome sequence information to improve the accuracy of genomic prediction for carcass traits in Hanwoo cattle. <i>Genetics Selection Evolution</i> , 2020, 52, 54.	1.2	24
2109	Validation and association of candidate markers for adult migration timing and fitness in Chinook Salmon. <i>Evolutionary Applications</i> , 2020, 13, 2316-2332.	1.5	19
2110	Rapid prediction of head rice yield and grain shape for genome-wide association study in indica rice. <i>Journal of Cereal Science</i> , 2020, 96, 103091.	1.8	12
2111	The <i>FAM171A2</i> gene is a key regulator of progranulin expression and modifies the risk of multiple neurodegenerative diseases. <i>Science Advances</i> , 2020, 6, .	4.7	9
2112	Genome-Wide Association Study in Two Cohorts from a Multi-generational Mouse Advanced Intercross Line Highlights the Difficulty of Replication Due to Study-Specific Heterogeneity. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 951-965.	0.8	9
2113	Screening of Microbes Associated With Swine Growth and Fat Deposition Traits Across the Intestinal Tract. <i>Frontiers in Microbiology</i> , 2020, 11, 586776.	1.5	47

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2114	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , 2020, 8, 145.	4.9	77
2115	Inferring Gene-by-Environment Interactions with a Bayesian Whole-Genome Regression Model. <i>American Journal of Human Genetics</i> , 2020, 107, 698-713.	2.6	32
2116	Genome-wide association study of bone quality and feed efficiency-related traits in Pekin ducks. <i>Genomics</i> , 2020, 112, 5021-5028.	1.3	7
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2167	Breeding history and candidate genes responsible for black skin of Xichuan black-bone chicken. <i>BMC Genomics</i> , 2020, 21, 511.	1.2	32
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2252	Temperament and Brain Networks of Attention. , 2020, , 155-168.		2
2253	Personality in Nonhuman Animals. , 2020, , 235-246.		0
2254	Genetics of Personality. , 2020, , 247-258.		0
2255	Approach to Avoidance Theories of Personality. , 2020, , 259-272.		1
2256	Cognitive Processes and Models. , 2020, , 295-315.		0
2257	Basic Needs, Goals and Motivation. , 2020, , 330-338.		1
2258	Personality and the Self. , 2020, , 339-351.		6

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2260	Personality and Politics. , 2020, , 413-424.		1
2261	Personality at Work. , 2020, , 427-438.		2
2263	Personality in Clinical Psychology. , 2020, , 451-462.		0
2266	Conceptual and Historical Perspectives. , 2020, , 13-30.		3
2267	Personality and the Unconscious. , 2020, , 69-80.		0
2268	Personality and Emotion. , 2020, , 81-100.		8
2269	Personality Assessment Methods. , 2020, , 103-114.		0
2270	Personality and Intelligence. , 2020, , 142-152.		0
2271	Development of Personality across the Life Span. , 2020, , 169-182.		3
2272	Personality Traits and Mental Disorders. , 2020, , 183-192.		0
2273	Attachment Theory. , 2020, , 208-220.		0
2274	Evolutionary Personality Psychology. , 2020, , 223-234.		4
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2276	Self-Regulation and Control in Personality Functioning. , 2020, , 316-329.		0
2277	Traits and Dynamic Processes. , 2020, , 352-363.		0
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2306	Bayesian modeling reveals host genetics associated with rumen microbiota jointly influence methane emission in dairy cows. <i>ISME Journal</i> , 2020, 14, 2019-2033.	4.4	48
2307	Genome-wide association study of emotional empathy in children. <i>Scientific Reports</i> , 2020, 10, 7469.	1.6	8
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2316	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. <i>Molecular Psychiatry</i> , 2021, 26, 2056-2069.	4.1	79
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2334	Interactions between season of birth, chronological age and genetic polymorphisms in determining later-life chronotype. <i>Mechanisms of Ageing and Development</i> , 2020, 188, 111253.	2.2	5
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2407	An Integrated Genomic and Transcriptomic Analysis Reveals Candidates of Susceptibility Genes for Crohn's Disease in Japanese Populations. <i>Scientific Reports</i> , 2020, 10, 10236.	1.6	8
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2435	Efficient Estimation and Applications of Cross-Validated Genetic Predictions to Polygenic Risk Scores and Linear Mixed Models. <i>Journal of Computational Biology</i> , 2020, 27, 599-612.	0.8	19
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2451	Methylation quantitative trait loci analysis in Korean exposome study. <i>Molecular and Cellular Toxicology</i> , 2020, 16, 175-183.	0.8	12
2452	Influence of Genetic Ancestry on Human Serum Proteome. <i>American Journal of Human Genetics</i> , 2020, 106, 303-314.	2.6	19
2453	Functional validity, role, and implications of heavy alcohol consumption genetic loci. <i>Science Advances</i> , 2020, 6, eaay5034.	4.7	47
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2465	Genomic regions associated with muscularity in beef cattle differ in five contrasting cattle breeds. <i>Genetics Selection Evolution</i> , 2020, 52, 2.	1.2	26
2466	Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: II: carcass merit traits. <i>BMC Genomics</i> , 2020, 21, 38.	1.2	33
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2470	Genome-Wide Association Study Identifies Genetic Associations with Perceived Age. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2380-2385.	0.3	13
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2475	Is atypical rhythm a risk factor for developmental speech and language disorders?. <i>Wiley Interdisciplinary Reviews: Cognitive Science</i> , 2020, 11, e1528.	1.4	83
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2479	Estimating narrow-sense heritability using family data from admixed populations. <i>Heredity</i> , 2020, 124, 751-762.	1.2	6
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2492	Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations. <i>Journal of Dairy Science</i> , 2020, 103, 5183-5199.	1.4	85
2493	Genetic Contributions to Multivariate Data-Driven Brain Networks Constructed via Source-Based Morphometry. <i>Cerebral Cortex</i> , 2020, 30, 4899-4913.	1.6	7
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2495	Genome-wide association mapping and accuracy of predictions for amoebic gill disease in Atlantic salmon (<i>Salmo salar</i>). <i>Scientific Reports</i> , 2020, 10, 6435.	1.6	20
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2497	Genes acting in synapses and neuron projections are early targets of selection during urban colonization. <i>Molecular Ecology</i> , 2020, 29, 3403-3412.	2.0	31
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2502	Discovery of novel hepatocyte eQTLs in African Americans. <i>PLoS Genetics</i> , 2020, 16, e1008662.	1.5	21
2503	Fast Algorithms for Conducting Large-Scale GWAS of Age-at-Onset Traits Using Cox Mixed-Effects Models. <i>Genetics</i> , 2020, 215, 41-58.	1.2	29
2504	Association Analysis of Driver Gene-Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1423-1429.	1.1	6
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2513	Common genetic substrates of alcohol and substance use disorder severity revealed by pleiotropy detection against GWAS catalog in two populations. <i>Addiction Biology</i> , 2021, 26, e12877.	1.4	7
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2515	Genome-wide association study of six quality-related traits in common wheat (<i>Triticum aestivum</i> L.) under two sowing conditions. <i>Theoretical and Applied Genetics</i> , 2021, 134, 399-418.	1.8	22
2516	Genome-wide association study of non-tuberculous mycobacterial pulmonary disease. <i>Thorax</i> , 2021, 76, 169-177.	2.7	6

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2518	Genetic predictors of educational attainment and intelligence test performance predict voter turnout. <i>Nature Human Behaviour</i> , 2021, 5, 281-291.	6.2	15
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2524	Genomic analyses reveal the genetic basis of early maturity and identification of loci and candidate genes in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 109-123.	4.1	42
2525	Investigating asthma heterogeneity through shared and distinct genetics: Insights from genome-wide cross-trait analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 796-807.	1.5	53
2526	Genome-wide association studies reveal QTL hotspots for grain brightness and black point traits in barley. <i>Crop Journal</i> , 2021, 9, 154-167.	2.3	10
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2532	The developmental origins of genetic factors influencing language and literacy: Associations with early-childhood vocabulary. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2021, 62, 728-738.	3.1	14
2533	Experimental validation of genetic selection for resistance against <i>Streptococcus agalactiae</i> via different routes of infection in the commercial Nile tilapia breeding programme. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 338-348.	0.8	9
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2539	No Evidence for Passive Gene-Environment Correlation or the Influence of Genetic Risk for Psychiatric Disorders on Adult Body Composition via the Adoption Design. <i>Behavior Genetics</i> , 2021, 51, 58-67.	1.4	2
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2541	Genome-wide association study identifies 7q11.22 and 7q36.3 associated with noise-induced hearing loss among Chinese population. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 411-420.	1.6	11
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2543	A genome-wide association study for highly sensitive cardiac troponin T levels identified a novel genetic variation near a RBAK-ZNF890P locus in the Japanese general population. <i>International Journal of Cardiology</i> , 2021, 329, 186-191.	0.8	3
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2566	Genome-Wide Association Study on Resistance to Rice Black-Streaked Dwarf Disease Caused by Rice black-streaked dwarf virus. <i>Plant Disease</i> , 2021, 105, 607-615.	0.7	11
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2569	Explore the genetics of weedy traits using rice 3K database. , 2021, 62, 2.		6
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2577	Genome-wide association study of patients with a severe major depressive episode treated with electroconvulsive therapy. <i>Molecular Psychiatry</i> , 2021, 26, 2429-2439.	4.1	32
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2580	Direct and Indirect Effects of Maternal, Paternal, and Offspring Genotypes: Trio-GCTA. <i>Behavior Genetics</i> , 2021, 51, 154-161.	1.4	27
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2593	Combining twin-family designs with measured genetic variants to study the causes of epigenetic variation. , 2021, , 239-259.		0
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2605	Whole-genome resequencing of Japanese whiting (<i>Sillago japonica</i>) provide insights into local adaptations. <i>Zoological Research</i> , 2021, 42, 548-561.	0.9	5
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2611	Alterations observed in the interferon β and γ signaling pathway in MDD patients are marginally influenced by cis-acting alleles. <i>Scientific Reports</i> , 2021, 11, 727.	1.6	1

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2613	Population Structure and Genetic Diversity of Seven Chinese Indigenous Chicken Populations in Guizhou Province. <i>Journal of Poultry Science</i> , 2021, 58, 211-215.	0.7	4
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2617	Estimation of Parental Effects Using Polygenic Scores. <i>Behavior Genetics</i> , 2021, 51, 264-278.	1.4	34
2619	Genetic variability and genome-wide association analysis of flavor and texture in cooked beans (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 959-978.	1.8	11
2620	Genetic parameter estimates for male and female fertility traits using genomic data to improve fertility in Australian beef cattle. <i>Animal Production Science</i> , 2021, , .	0.6	7
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2623	Genome-Wide Association Study of Korean Asthmatics: A Comparison With UK Asthmatics. <i>Allergy, Asthma and Immunology Research</i> , 2021, 13, 609.	1.1	4
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2629	Genome-wide association study of pediatric obsessive-compulsive traits: shared genetic risk between traits and disorder. <i>Translational Psychiatry</i> , 2021, 11, 91.	2.4	23
2630	An evaluation of approaches for rare variant association analyses of binary traits in related samples. <i>Scientific Reports</i> , 2021, 11, 3145.	1.6	5
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2633	GWAS of peptic ulcer disease implicates <i>Helicobacter pylori</i> infection, other gastrointestinal disorders and depression. <i>Nature Communications</i> , 2021, 12, 1146.	5.8	93
2634	Genome-wide association studies detects candidate genes for wool traits by re-sequencing in Chinese fine-wool sheep. <i>BMC Genomics</i> , 2021, 22, 127.	1.2	17

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2638	Multi-omic and multi-species meta-analyses of nicotine consumption. <i>Translational Psychiatry</i> , 2021, 11, 98.	2.4	13
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2644	E-MAGMA: an eQTL-informed method to identify risk genes using genome-wide association study summary statistics. <i>Bioinformatics</i> , 2021, 37, 2245-2249.	1.8	34
2645	Genome-wide association improves genomic selection for ammonia tolerance in the orange-spotted grouper (<i>Epinephelus coioides</i>). <i>Aquaculture</i> , 2021, 533, 736214.	1.7	19
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2656	Genome-wide association studies for sperm traits in Assaf sheep breed. <i>Animal</i> , 2021, 15, 100065.	1.3	17

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2659	Distinguishing HapMap Accessions Through Recursive Set Partitioning in Hierarchical Decision Trees. <i>Frontiers in Plant Science</i> , 2021, 12, 628421.	1.7	0
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2675	Novel risk factors for craniofacial microsomia and assessment of their utility in clinic diagnosis. <i>Human Molecular Genetics</i> , 2021, 30, 1045-1056.	1.4	3
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2678	Multi-trait association studies discover pleiotropic loci between Alzheimer's disease and cardiometabolic traits. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 34.	3.0	15

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2684	Divergent improvement of two cultivated allotetraploid cotton species. <i>Plant Biotechnology Journal</i> , 2021, 19, 1325-1336.	4.1	26
2685	Genetics of Behçet's Disease: Functional Genetic Analysis and Estimating Disease Heritability. <i>Frontiers in Medicine</i> , 2021, 8, 625710.	1.2	18
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2688	Development of a 76k Alpaca (<i>Vicugna pacos</i>) Single Nucleotide Polymorphisms (SNPs) Microarray. <i>Genes</i> , 2021, 12, 291.	1.0	8
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2690	Donor genetic variants as risk factors for thrombosis after liver transplantation: A genome-wide association study. <i>American Journal of Transplantation</i> , 2021, 21, 3133-3147.	2.6	4
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2708	Identification of genetic factors influencing metabolic dysregulation and retinal support for MacTel, a retinal disorder. <i>Communications Biology</i> , 2021, 4, 274.	2.0	26
2709	VTRNA2-1: Genetic Variation, Heritable Methylation and Disease Association. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2535.	1.8	15
2710	Resequencing and SNP discovery of Amur ide (<i>Leuciscus waleckii</i>) provides insights into local adaptations to extreme environments. <i>Scientific Reports</i> , 2021, 11, 5064.	1.6	15
2711	Genome-wide association study identifies new loci associated with risk of HBV infection and disease progression. <i>BMC Medical Genomics</i> , 2021, 14, 84.	0.7	11
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2719	Genomic Signature for Stem Swollen of Kohlrabi Morphotype in <i>Brassica oleracea</i> . <i>Plant Breeding and Biotechnology</i> , 2021, 9, 45-54.	0.3	0
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2724	Polygenic risk scores for major psychiatric and neurodevelopmental disorders contribute to sleep disturbance in childhood: Adolescent Brain Cognitive Development (ABCD) Study. <i>Translational Psychiatry</i> , 2021, 11, 187.	2.4	20
2725	Genetic and clinical characteristics of treatment-resistant depression using primary care records in two UK cohorts. <i>Molecular Psychiatry</i> , 2021, 26, 3363-3373.	4.1	66
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2732	Quantifying genetic heterogeneity between continental populations for human height and body mass index. <i>Scientific Reports</i> , 2021, 11, 5240.	1.6	19
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2734	Evaluation of genetic diversity and management of disease in Border Collie dogs. <i>Scientific Reports</i> , 2021, 11, 6243.	1.6	9
2735	Revealing New Candidate Genes for Teat Number Relevant Traits in Duroc Pigs Using Genome-Wide Association Studies. <i>Animals</i> , 2021, 11, 806.	1.0	11
2737	Identification of deleterious recessive haplotypes and candidate deleterious recessive mutations in Japanese Black cattle. <i>Scientific Reports</i> , 2021, 11, 6687.	1.6	5
2738	Identification of novel locus associated with coronary artery aneurysms and validation of loci for susceptibility to Kawasaki disease. <i>European Journal of Human Genetics</i> , 2021, 29, 1734-1744.	1.4	10
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2740	Whole-milk consumption decreases the risk of inflammatory bowel disease: a two-sample Mendelian randomization analysis. <i>Journal of Bio-X Research</i> , 2021, 4, 114-119.	0.3	0
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2742	Transcriptome-wide association study reveals two genes that influence mismatch negativity. <i>Cell Reports</i> , 2021, 34, 108868.	2.9	8
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2751	Genome-wide association and whole exome sequencing studies reveal a novel candidate locus for restless legs syndrome. <i>European Journal of Medical Genetics</i> , 2021, 64, 104186.	0.7	8
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2767	Comprehensive analysis of the major histocompatibility complex in systemic sclerosis identifies differential HLA associations by clinical and serological subtypes. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 1040-1047.	0.5	24
2769	Whole-genome resequencing of 445 <i>Lactuca</i> accessions reveals the domestication history of cultivated lettuce. <i>Nature Genetics</i> , 2021, 53, 752-760.	9.4	64
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2772	Genome wide association study identifies four loci for early onset schizophrenia. <i>Translational Psychiatry</i> , 2021, 11, 248.	2.4	15
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2777	Comprehensive Analysis of Multiple Cohort Datasets Deciphers the Utility of Germline Single-Nucleotide Polymorphisms in Prostate Cancer Diagnosis. <i>Cancer Prevention Research</i> , 2021, 14, 741-752.	0.7	4
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2782	Proofs for genotype by environment interactions considering pedigree and genomic data from organic and conventional cow reference populations. <i>Journal of Dairy Science</i> , 2021, 104, 4452-4466.	1.4	10
2784	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. <i>BMC Genomics</i> , 2021, 22, 294.	1.2	11
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2791	Single-Cell RNA Sequencing in Parkinson's Disease. <i>Biomedicines</i> , 2021, 9, 368.	1.4	20
2792	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits. <i>American Journal of Human Genetics</i> , 2021, 108, 632-655.	2.6	73
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2796	MARS: leveraging allelic heterogeneity to increase power of association testing. <i>Genome Biology</i> , 2021, 22, 128.	3.8	2
2797	Systematic Review: Molecular Studies of Common Genetic Variation in Child and Adolescent Psychiatric Disorders. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2022, 61, 227-242.	0.3	15
2799	The copy number variation and stroke (CaNVAS) risk and outcome study. <i>PLoS ONE</i> , 2021, 16, e0248791.	1.1	2
2800	Variation in <i>VKORC1</i> Is Associated with Vascular Dementia. <i>Journal of Alzheimer's Disease</i> , 2021, 80, 1329-1337.	1.2	5
2801	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
2802	On polygenic risk scores for complex traits prediction. <i>Biometrics</i> , 2022, 78, 499-511.	0.8	2

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2806	The intermediary role of adolescent temperamental and behavioral traits on the prospective associations between polygenic risk and cannabis use among young adults of European Ancestry. <i>Addiction</i> , 2021, 116, 2779-2789.	1.7	2
2807	Are psychiatric disorders risk factors for COVID-19 susceptibility and severity? a two-sample, bidirectional, univariable, and multivariable Mendelian Randomization study. <i>Translational Psychiatry</i> , 2021, 11, 210.	2.4	21
2808	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100025.	1.0	9
2809	Genome-Wide Variation in DNA Methylation Predicts Variation in Leaf Traits in an Ecosystem-Foundational Oak Species. <i>Forests</i> , 2021, 12, 569.	0.9	8
2810	Whole-genome resequencing provides insights into the population structure and domestication signatures of ducks in eastern China. <i>BMC Genomics</i> , 2021, 22, 401.	1.2	13
2811	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
2812	Similar Genetic Architecture of Alzheimer's Disease and Differential APOE Effect Between Sexes. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 674318.	1.7	8
2813	Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	0.9	3
2814	Sources of Resistance to Common Bacterial Blight and Charcoal Rot Disease for the Production of Mesoamerican Common Beans in the Southern United States. <i>Plants</i> , 2021, 10, 998.	1.6	7
2816	Genomic structural equation modelling provides a whole-system approach for the future crop breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2875-2889.	1.8	3
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2819	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
2820	Population transcriptomic sequencing reveals allopatric divergence and local adaptation in <i>Pseudotaxus chienii</i> (Taxaceae). <i>BMC Genomics</i> , 2021, 22, 388.	1.2	11
2821	Estimating colocalization probability from limited summary statistics. <i>BMC Bioinformatics</i> , 2021, 22, 254.	1.2	4
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2824	Genetic basis of lacunar stroke: a pooled analysis of individual patient data and genome-wide association studies. <i>Lancet Neurology</i> , The, 2021, 20, 351-361.	4.9	95
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2826	Genomic Association of Chronic Idiopathic Anhidrosis to a Potassium Channel Subunit in a Large Animal Model. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2639-2645.e3.	0.3	2
2827	Genome-wide association study-based identification genes influencing agronomic traits in rice (<i>Oryza</i>) Tj ETQq0 0 0 qgBT /Ovgrlock 10 T	1.3	3
2828	Genome-wide association study of cardiac troponin I in the general population. <i>Human Molecular Genetics</i> , 2021, 30, 2027-2039.	1.4	11
2830	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. <i>American Journal of Human Genetics</i> , 2021, 108, 786-798.	2.6	70
2831	Quantifying the contribution of dominance deviation effects to complex trait variation in biobank-scale data. <i>American Journal of Human Genetics</i> , 2021, 108, 799-808.	2.6	23
2832	Genome-wide association study of seed coat color in sesame (<i>Sesamum indicum</i> L.). <i>PLoS ONE</i> , 2021, 16, e0251526.	1.1	23
2833	Exploring the genetic features and signatures of selection in South China indigenous pigs. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1359-1371.	1.7	9
2834	Genome-wide association analysis reveals that <i>EDNRB2</i> causes a dose-dependent loss of pigmentation in ducks. <i>BMC Genomics</i> , 2021, 22, 381.	1.2	20
2837	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. <i>Communications Biology</i> , 2021, 4, 519.	2.0	15
2838	Statistical Learning Methods Applicable to Genome-Wide Association Studies on Unbalanced Case-Control Disease Data. <i>Genes</i> , 2021, 12, 736.	1.0	5
2839	Exploring genetic resistance to infectious salmon anaemia virus in Atlantic salmon by genome-wide association and RNA sequencing. <i>BMC Genomics</i> , 2021, 22, 345.	1.2	11
2840	Genetic Influences on Hippocampal Subfields. <i>Neurology: Genetics</i> , 2021, 7, e591.	0.9	8
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2843	Pharmacogenomic Effects of β -Blocker Use on Femoral Neck Bone Mineral Density. <i>Journal of the Endocrine Society</i> , 2021, 5, bvab092.	0.1	0
2844	Detection of genomic regions underlying milk production traits in Valle del Belice dairy sheep using regional heritability mapping. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 552-561.	0.8	6

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2849	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. <i>Nature Communications</i> , 2021, 12, 2579.	5.8	51
2850	Identification of genes associated with litter size combining genomic approaches in Luzhong mutton sheep. <i>Animal Genetics</i> , 2021, 52, 545-549.	0.6	20
2851	Genetic factors affect the susceptibility to bacterial infections in diabetes. <i>Scientific Reports</i> , 2021, 11, 9464.	1.6	2
2852	Relationship between resistance and tolerance of crown rot in bread wheat. <i>Field Crops Research</i> , 2021, 265, 108106.	2.3	13
2853	Genome-wide association study reveals novel loci associated with feeding behavior in Pekin ducks. <i>BMC Genomics</i> , 2021, 22, 334.	1.2	2
2854	Whole-genome resequencing of <i>Osmanthus fragrans</i> provides insights into flower color evolution. <i>Horticulture Research</i> , 2021, 8, 98.	2.9	35
2855	Genetic diversity and evolutionary patterns of <i>Taraxacum kok-saghyz</i> Rodin. <i>Ecology and Evolution</i> , 2021, 11, 7917-7926.	0.8	7
2857	Penalized linear mixed models for structured genetic data. <i>Genetic Epidemiology</i> , 2021, 45, 427-444.	0.6	3
2858	Gene-environment correlations and causal effects of childhood maltreatment on physical and mental health: a genetically informed approach. <i>Lancet Psychiatry</i> , 2021, 8, 373-386.	3.7	84
2860	Genetics of symptom remission in outpatients with COVID-19. <i>Scientific Reports</i> , 2021, 11, 10847.	1.6	7
2861	Multi-Polygenic Analysis of Nicotine Dependence in Individuals of European Ancestry. <i>Nicotine and Tobacco Research</i> , 2021, 23, 2102-2109.	1.4	2
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2866	Genetic Association of a Gain-of-Function <i>IFNGR1</i> Polymorphism and the Intergenic Region <i>LNCAROD/DKK1</i> With Behçet's Disease. <i>Arthritis and Rheumatology</i> , 2021, 73, 1244-1252.	2.9	21
2867	The value of genomic relationship matrices to estimate levels of inbreeding. <i>Genetics Selection Evolution</i> , 2021, 53, 42.	1.2	31
2868	Genomic selection for resistance to Francisellosis in commercial Nile tilapia population: Genetic and genomic parameters, correlation with growth rate and predictive ability. <i>Aquaculture</i> , 2021, 537, 736515.	1.7	13

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2870	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	1.3	10
2872	An atlas of alternative polyadenylation quantitative trait loci contributing to complex trait and disease heritability. <i>Nature Genetics</i> , 2021, 53, 994-1005.	9.4	85
2873	Genome-Wide Analysis of Sex Disparities in the Genetic Architecture of Lung and Colorectal Cancers. <i>Genes</i> , 2021, 12, 686.	1.0	4
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2880	Genome wide association study of response to interval and continuous exercise training: the Predict-HIIT study. <i>Journal of Biomedical Science</i> , 2021, 28, 37.	2.6	15
2881	Identification of COL3A1 variants associated with sporadic thoracic aortic dissection: a case-control study. <i>Frontiers of Medicine</i> , 2021, 15, 438-447.	1.5	3
2882	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. <i>Epilepsia</i> , 2021, 62, 1518-1527.	2.6	5
2883	Rapid sequence evolution driven by transposable elements at a virulence locus in a fungal wheat pathogen. <i>BMC Genomics</i> , 2021, 22, 393.	1.2	18
2884	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
2885	A Robust and Rapid Candidate Gene Mapping Pipeline Based on M2 Populations. <i>Frontiers in Plant Science</i> , 2021, 12, 681816.	1.7	6
2886	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. <i>Human Genomics</i> , 2021, 15, 34.	1.4	7
2887	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
2888	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. <i>Frontiers in Genetics</i> , 2021, 12, 554948.	1.1	8

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2890	Leveraging both individual-level genetic data and GWAS summary statistics increases polygenic prediction. <i>American Journal of Human Genetics</i> , 2021, 108, 1001-1011.	2.6	22
2891	Divergence of a genomic island leads to the evolution of melanization in a halophyte root fungus. <i>ISME Journal</i> , 2021, 15, 3468-3479.	4.4	9
2892	Human genomics of the humoral immune response against polyomaviruses. <i>Virus Evolution</i> , 2021, 7, veab058.	2.2	9
2893	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab060.	1.5	1
2894	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	2.0	40
2895	Integrative analysis of histomorphology, transcriptome and whole genome resequencing identified DIO2 gene as a crucial gene for the protuberant knob located on forehead in geese. <i>BMC Genomics</i> , 2021, 22, 487.	1.2	5
2898	A further survey of the quantitative trait loci affecting swine body size and carcass traits in five related pig populations. <i>Animal Genetics</i> , 2021, 52, 621-632.	0.6	16
2899	<i>FAT4</i> identified as a potential modifier of orofacial cleft laterality. <i>Genetic Epidemiology</i> , 2021, 45, 721-735.	0.6	14
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2901	Genotype-by-environment interactions for reproduction, body composition, and growth traits in maternal-line pigs based on single-step genomic reaction norms. <i>Genetics Selection Evolution</i> , 2021, 53, 51.	1.2	16
2902	Genetic and plastic rewiring of food webs under climate change. <i>Journal of Animal Ecology</i> , 2021, 90, 1814-1830.	1.3	18
2904	Genome-wide association study and transcriptome analysis discover new genes for bacterial leaf blight resistance in rice (<i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 255.	1.6	14
2905	Genetic diversity and effective population sizes of thirteen Indian cattle breeds. <i>Genetics Selection Evolution</i> , 2021, 53, 47.	1.2	18
2906	Identification of new semen trait-related candidate genes in Duroc boars through genome-wide association and weighted gene co-expression network analyses. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	4
2907	A genome-wide association study suggests correlations of common genetic variants with peritoneal solute transfer rates in patients with kidney failure receiving peritoneal dialysis. <i>Kidney International</i> , 2021, 100, 1101-1111.	2.6	13
2909	Familial aggregation and heritability: a nationwide family-based study of idiopathic inflammatory myopathies. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, annrheumdis-2021-219914.	0.5	9
2910	Parental Transmission Plays the Major Role in High Aggregation of Type 2 Diabetes in Iranian Families: Tehran Lipid and Glucose Study. <i>Canadian Journal of Diabetes</i> , 2022, 46, 60-68.	0.4	3

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2916	Common genetic variation influencing human white matter microstructure. <i>Science</i> , 2021, 372, .	6.0	106
2917	Type 2 Diabetes Is Causally Associated With Reduced Serum Osteocalcin: A Genomewide Association and Mendelian Randomization Study. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1694-1707.	3.1	23
2918	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. <i>Molecular Psychiatry</i> , 2021, 26, 5797-5811.	4.1	30
2919	Role of Common Genetic Variants for Drug-Resistance to Specific Anti-Seizure Medications. <i>Frontiers in Pharmacology</i> , 2021, 12, 688386.	1.6	6
2921	Genome-Wide Association Studies Identifying Multiple Loci Associated With Alfalfa Forage Quality. <i>Frontiers in Plant Science</i> , 2021, 12, 648192.	1.7	7
2922	Effect of genomic X-chromosome regions on Nelore bull fertility. <i>Journal of Applied Genetics</i> , 2021, 62, 655-659.	1.0	2
2923	Estimating Genetic Similarity Matrices Using Phylogenies. <i>Journal of Computational Biology</i> , 2021, 28, 587-600.	0.8	6
2924	Association between STAT4 gene polymorphism and type 2 diabetes risk in Chinese Han population. <i>BMC Medical Genomics</i> , 2021, 14, 169.	0.7	7
2925	Joint contributions of the gut microbiota and host genetics to feed efficiency in chickens. <i>Microbiome</i> , 2021, 9, 126.	4.9	58
2926	Resource profile and user guide of the Polygenic Index Repository. <i>Nature Human Behaviour</i> , 2021, 5, 1744-1758.	6.2	63
2928	Genome wide study of tardive dyskinesia in schizophrenia. <i>Translational Psychiatry</i> , 2021, 11, 351.	2.4	13
2930	The Distribution and Origins of <i>Pyrus hopeiensis</i> —Wild Plant With Tiny Population—Using Whole Genome Resequencing. <i>Frontiers in Plant Science</i> , 2021, 12, 668796.	1.7	3
2931	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
2932	GxEsum: a novel approach to estimate the phenotypic variance explained by genome-wide GxE interaction based on GWAS summary statistics for biobank-scale data. <i>Genome Biology</i> , 2021, 22, 183.	3.8	14
2933	The Analytic Identification of Variance Component Models Common to Behavior Genetics. <i>Behavior Genetics</i> , 2021, 51, 425-437.	1.4	10

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2935	New Polygenic Risk Score to Predict High Myopia in Singapore Chinese Children. <i>Translational Vision Science and Technology</i> , 2021, 10, 26.	1.1	11
2936	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	5.8	24
2938	Genomic Prediction for Whole Weight, Body Shape, Meat Yield, and Color Traits in the Portuguese Oyster <i>Crassostrea angulata</i> . <i>Frontiers in Genetics</i> , 2021, 12, 661276.	1.1	5
2939	The Evolutionary Biology of Religious Behavior. <i>Interdisciplinary Journal for Religion and Transformation in Contemporary Society</i> , 2021, 7, 303-334.	0.1	0
2941	A panel of miRNAs as prognostic markers for African-American patients with triple negative breast cancer. <i>BMC Cancer</i> , 2021, 21, 861.	1.1	8
2942	Recessive/dominant model: Alternative choice in case-control-based genome-wide association studies. <i>PLoS ONE</i> , 2021, 16, e0254947.	1.1	14
2943	X-chromosome influences on neuroanatomical variation in humans. <i>Nature Neuroscience</i> , 2021, 24, 1216-1224.	7.1	26
2944	Genome-wide association screening and verification of potential genes associated with root architectural traits in maize (<i>Zea mays</i> L.) at multiple seedling stages. <i>BMC Genomics</i> , 2021, 22, 558.	1.2	16
2945	Novel genetic variants associated with brain functional networks in 18,445 adults from the UK Biobank. <i>Scientific Reports</i> , 2021, 11, 14633.	1.6	4
2947	Distinction between the effects of parental and fetal genomes on fetal growth. <i>Nature Genetics</i> , 2021, 53, 1135-1142.	9.4	41
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2949	Association Between <i>NEDD4L</i> Variation and the Genetic Risk of Acute Appendicitis. <i>JAMA Surgery</i> , 2021, 156, 917.	2.2	6
2950	Genomic analysis of field pennycress (<i>Thlaspi arvense</i>) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021, 19, 143.	1.7	23
2951	Genome-Wide Heritability Estimates for Family Life Course Complexity. <i>Demography</i> , 2021, 58, 1575-1602.	1.2	2
2952	Genetic association study of childhood aggression across raters, instruments, and age. <i>Translational Psychiatry</i> , 2021, 11, 413.	2.4	31
2953	Data imputation and machine learning improve association analysis and genomic prediction for resistance to fish photobacteriosis in the gilthead sea bream. <i>Aquaculture Reports</i> , 2021, 20, 100661.	0.7	11
2955	Genetic overlap and causal associations between smoking behaviours and mental health. <i>Scientific Reports</i> , 2021, 11, 14871.	1.6	19

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2958	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	1.5	23
2959	Repeatability and heritability of social reaction norms in a wild agamid lizard. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 1953-1965.	1.1	12
2961	Exploring the genomic resources and analysing the genetic diversity and population structure of Chinese indigenous rabbit breeds by RAD-seq. <i>BMC Genomics</i> , 2021, 22, 573.	1.2	3
2962	Genetic prediction of complex traits with polygenic scores: a statistical review. <i>Trends in Genetics</i> , 2021, 37, 995-1011.	2.9	55
2964	Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. <i>Bioinformatics</i> , 2021, 37, 4737-4743.	1.8	3
2967	Accelerated discovery of functional genomic variation in pigs. <i>Genomics</i> , 2021, 113, 2229-2239.	1.3	16
2968	Putting Psychology to the Test: Rethinking Model Evaluation Through Benchmarking and Prediction. <i>Advances in Methods and Practices in Psychological Science</i> , 2021, 4, 251524592110268.	5.4	20
2969	Application of a novel 50K SNP genotyping array to assess the genetic diversity and linkage disequilibrium in a farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>) population. <i>Aquaculture Reports</i> , 2021, 20, 100691.	0.7	6
2970	Accelerated deciphering of the genetic architecture of agricultural economic traits in pigs using a low-coverage whole-genome sequencing strategy. <i>GigaScience</i> , 2021, 10, .	3.3	34
2972	Chromosome-level genome assembly and population genetic analysis of a critically endangered rhododendron provide insights into its conservation. <i>Plant Journal</i> , 2021, 107, 1533-1545.	2.8	35
2973	A fast and robust Bayesian nonparametric method for prediction of complex traits using summary statistics. <i>PLoS Genetics</i> , 2021, 17, e1009697.	1.5	34
2974	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
2975	Compared Heritability of Chronotype Instruments in a Single Population Sample. <i>Journal of Biological Rhythms</i> , 2021, 36, 483-490.	1.4	6
2976	A major quantitative trait locus affecting resistance to Tilapia lake virus in farmed Nile tilapia (<i>Oreochromis niloticus</i>). <i>Heredity</i> , 2021, 127, 334-343.	1.2	29
2977	Contextualizing genetic risk score for disease screening and rare variant discovery. <i>Nature Communications</i> , 2021, 12, 4418.	5.8	11
2979	Genome-Wide Association Study Identifies 12 Loci Associated with Body Weight at Age 8 Weeks in Korean Native Chickens. <i>Genes</i> , 2021, 12, 1170.	1.0	13

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2981	Ridgeâ€penalized adaptive Mantel test and its application in imaging genetics. <i>Statistics in Medicine</i> , 2021, 40, 5313-5332.	0.8	1
2982	Genome-wide scan for selection signatures based on whole-genome re-sequencing in Landrace and Yorkshire pigs. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1898-1906.	1.7	6
2984	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. <i>Npj Genomic Medicine</i> , 2021, 6, 64.	1.7	7
2985	Genomeâ€wide association study and polygenic risk score analysis for hearing measures in children. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 318-328.	1.1	6
2986	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. <i>PLoS Genetics</i> , 2021, 17, e1009331.	1.5	25
2987	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.0	6
2988	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. <i>Plant Biotechnology Journal</i> , 2021, 19, 2206-2220.	4.1	23
2989	Breed identification of meat using machine learning and breed tag SNPs. <i>Food Control</i> , 2021, 125, 107971.	2.8	10
2990	Genome-Wide Association Study Using Whole-Genome Sequence Data for Fertility, Health Indicator, and Endoparasite Infection Traits in German Black Pied Cattle. <i>Genes</i> , 2021, 12, 1163.	1.0	10
2991	Multi-omics integration analysis identifies novel genes for alcoholism with potential overlap with neurodegenerative diseases. <i>Nature Communications</i> , 2021, 12, 5071.	5.8	34
2992	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
2994	Predicting moisture content during maize nixtamalization using machine learning with NIR spectroscopy. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3743-3757.	1.8	3
2997	Genome-wide SNP data unravel the ancestry and signatures of divergent selection in Churrah pigs of India. <i>Livestock Science</i> , 2021, 250, 104587.	0.6	6
2998	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	1.7	14
2999	Phylogeography Reveals Geographic and Environmental Factors Driving Genetic Differentiation of <i>Populus sect. Turanga</i> in Northwest China. <i>Frontiers in Plant Science</i> , 2021, 12, 705083.	1.7	10
3000	Genomeâ€wide analysis of butterfly bush (<i>Buddleja alternifolia</i>) in three uplands provides insights into biogeography, demography and speciation. <i>New Phytologist</i> , 2021, 232, 1463-1476.	3.5	21
3001	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. <i>Nature Neuroscience</i> , 2021, 24, 1367-1376.	7.1	137

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3003	Genetically Predicted Glucose-Dependent Insulinotropic Polypeptide (GIP) Levels and Cardiovascular Disease Risk Are Driven by Distinct Causal Variants in the <i>GIPR</i> Region. <i>Diabetes</i> , 2021, 70, 2706-2719.	0.3	12
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3005	Detecting methylation quantitative trait loci using a methylation random field method. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
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3009	Is Mammographic Breast Density an Endophenotype for Breast Cancer?. <i>Cancers</i> , 2021, 13, 3916.	1.7	4
3010	Genomic partitioning of inbreeding depression in humans. <i>American Journal of Human Genetics</i> , 2021, 108, 1488-1501.	2.6	6
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3014	Opportunities and limits of combining microbiome and genome data for complex trait prediction. <i>Genetics Selection Evolution</i> , 2021, 53, 65.	1.2	17
3016	Integration analysis of GWAS and expression quantitative trait loci to identify candidate genes and pathways for clozapine-related neutropaenia. <i>British Journal of Clinical Pharmacology</i> , 2022, 88, 1904-1912.	1.1	2
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4151	Genome-wide run of homozygosity analysis reveals candidate genomic regions associated with environmental adaptations of Tibetan native chickens. <i>BMC Genomics</i> , 2022, 23, 91.	1.2	16
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4317	Statistical models and computational tools for predicting complex traits and diseases. <i>Genomics and Informatics</i> , 2021, 19, e36.	0.4	8
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4332	<i>Bos taurus</i> haplotypes segregating in Nellore (<i>Bos indicus</i>) cattle. <i>Animal Genetics</i> , 2022, 53, 58-67.	0.6	4
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4335	Mining massive genomic data of two Swiss Braunvieh cattle populations reveals six novel candidate variants that impair reproductive success. <i>Genetics Selection Evolution</i> , 2021, 53, 95.	1.2	5
4336	Genome-Wide Association Mapping of Crown and Brown Rust Resistance in Perennial Ryegrass. <i>Genes</i> , 2022, 13, 20.	1.0	1
4337	Genome-Wide Association Analysis of Salt-Tolerant Traits in Terrestrial Cotton at Seedling Stage. <i>Plants</i> , 2022, 11, 97.	1.6	11
4338	Genome-wide association study and genomic heritabilities for blood protein levels in Lori-Bakhtiari sheep. <i>Scientific Reports</i> , 2021, 11, 23771.	1.6	2
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4340	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
4342	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. <i>Breast Cancer Research</i> , 2022, 24, 27.	2.2	15
4343	Genomic insights on the contribution of introgressions from Xian/Indica to the genetic improvement of Geng/Japonica rice cultivars. <i>Plant Communications</i> , 2022, 3, 100325.	3.6	8
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4345	Genome-wide elucidation of CNV regions and their association with production and reproduction traits in composite Vrindavani cattle. <i>Gene</i> , 2022, 830, 146510.	1.0	5
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4351	Inbreeding is associated with shorter early-life telomere length in a wild passerine. <i>Conservation Genetics</i> , 2022, 23, 639-651.	0.8	5
4352	Linear Mixed-Effect Models Through the Lens of Hardy-Weinberg Disequilibrium. <i>Frontiers in Genetics</i> , 2022, 13, 856872.	1.1	2

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4354	Genome-wide association studies dissect the G \times E interaction for agronomic traits in a worldwide collection of safflowers (<i>Carthamus tinctorius</i> L.). <i>Molecular Breeding</i> , 2022, 42, 1.	1.0	4
4355	Genome-wide association studies for egg quality traits in White Leghorn layers using low-pass sequencing and SNP chip data. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 380-397.	0.8	8
4356	Using mid-infrared spectroscopy to increase GWAS power to detect QTL associated with blood urea nitrogen. <i>Genetics Selection Evolution</i> , 2022, 54, 27.	1.2	2
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4362	Genetic solutions through breeding counteract climate change and secure barley production in Australia. , 2022, 1, 100001.		4
4363	Genomic insights into genetic improvement of upland cotton in the world's largest growing region. <i>Industrial Crops and Products</i> , 2022, 183, 114929.	2.5	7
4653	From Genotype to Phenotype: Polygenic Prediction of Complex Human Traits. <i>Methods in Molecular Biology</i> , 2022, 2467, 421-446.	0.4	2
4654	Overview of Major Computer Packages for Genomic Prediction of Complex Traits. <i>Methods in Molecular Biology</i> , 2022, 2467, 157-187.	0.4	0
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4656	High-throughput characterization, correlation, and mapping of leaf photosynthetic and functional traits in the soybean (<i>Glycine max</i>) nested association mapping population. <i>Genetics</i> , 2022, , .	1.2	8
4658	GenePlexus: a web-server for gene discovery using network-based machine learning. <i>Nucleic Acids Research</i> , 2022, 50, W358-W366.	6.5	3
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4660	A large-scale population based organelle pan-genomes construction and phylogeny analysis reveal the genetic diversity and the evolutionary origins of chloroplast and mitochondrion in <i>Brassica napus</i> L.. <i>BMC Genomics</i> , 2022, 23, 339.	1.2	7
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4667	Gene-environment interaction in type 2 diabetes in Korean cohorts: Interaction of a type 2 diabetes polygenic risk score with triglyceride and cholesterol on fasting glucose levels. <i>Genetic Epidemiology</i> , 2022, 46, 285-302.	0.6	0
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4673	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	6.0	77
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4675	Genome-wide association study revealed <i>TaHXK3</i> as a candidate gene controlling stomatal index in wheat seedlings. <i>Plant, Cell and Environment</i> , 2022, 45, 2306-2323.	2.8	7
4676	Genome-wide association study of three litter traits in Yorkshire pigs. <i>Animal Genetics</i> , 2022, , .	0.6	0
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4678	Investigating how the accuracy of teacher expectations of pupil performance relate to socioeconomic and genetic factors. <i>Scientific Reports</i> , 2022, 12, 7120.	1.6	1
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4681	Evaluating the power and limitations of genome-wide association studies in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	17
4682	Idiosyncratic epistasis leads to global fitness-related correlated trends. <i>Science</i> , 2022, 376, 630-635.	6.0	36
4683	Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. <i>Heredity</i> , 2022, 129, 103-112.	1.2	3
4684	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

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4686	Genomic inbreeding coefficients using imputed genotypes: Assessing different estimators in Holstein-Friesian dairy cows. <i>Journal of Dairy Science</i> , 2022, 105, 5926-5945.	1.4	12
4687	Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. <i>Nature Genetics</i> , 2022, 54, 593-602.	9.4	98
4688	The Genetic Architecture of Nitrogen Use Efficiency in Switchgrass (<i>Panicum virgatum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 893610.	1.7	0
4690	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
4692	Single Nucleotide Polymorphism Effects on Lamb Fecal Egg Count Estimated Breeding Values in Progeny-Tested Katahdin Sires. <i>Frontiers in Genetics</i> , 2022, 13, 866176.	1.1	2
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4694	Three legs of the missing heritability problem. <i>Studies in History and Philosophy of Science Part A</i> , 2022, 93, 183-191.	0.6	13
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4701	Sex differences in the genetic architecture of cognitive resilience to Alzheimer's disease. <i>Brain</i> , 2022, 145, 2541-2554.	3.7	26
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4703	Genome-wide association studies for Alzheimer's disease: bigger is not always better. <i>Brain Communications</i> , 2022, 4, .	1.5	44
4704	Genome-wide detection of genetic structure and runs of homozygosity analysis in Anhui indigenous and Western commercial pig breeds using PorcineSNP80k data. <i>BMC Genomics</i> , 2022, 23, 373.	1.2	6
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4710	Genetic Diversity and Genome-Wide Association Study of Architectural Traits of Spray Cut Chrysanthemum Varieties. <i>Horticulturae</i> , 2022, 8, 458.	1.2	4
4711	Genetic variants associated with two major bovine milk fatty acids offer opportunities to breed for altered milk fat composition. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	5
4712	Genetic Determinants of Survival in Parkinson's Disease in the Asian Population. <i>Movement Disorders</i> , 2022, 37, 1624-1633.	2.2	4
4714	Genome-Wide Association Study of Resistance to <i>Phytophthora capsici</i> in the Pepper (<i>Capsicum</i> spp.) Collection. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	12
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4716	PanaxGDB: A Comprehensive Platform for Panax. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
4717	Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
4721	A parallel survey on the fatty acid composition in backfat and longissimus lumborum and comparison of their associations with growth and carcass traits in pigs. <i>Livestock Science</i> , 2022, 263, 104984.	0.6	0
4722	Asian Swamp eel <i>Monopterus albus</i> Population Structure and Genetic Diversity in China. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
4724	Extensive simulations assess the performance of genome-wide association mapping in various <i>Saccharomyces cerevisiae</i> subpopulations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	3
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4728	Identification of sex determination locus in sea cucumber <i>Apostichopus japonicus</i> using genome-wide association study. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
4730	The missing heritability in type 1 diabetes. <i>Diabetes, Obesity and Metabolism</i> , 2022, 24, 1901-1911.	2.2	4
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4732	Genome-wide SNP analysis reveals the selection signatures of two indigenous buffalo breeds in Sichuan. <i>Conservation Genetics Resources</i> , 0, , .	0.4	0

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4735	An automated multi-modal graph-based pipeline for mouse genetic discovery. <i>Bioinformatics</i> , 0, , .	1.8	3
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4738	Genomic Analyses of Wild and Cultivated Bacanora Agave (<i>Agave angustifolia</i> var. <i>pacifica</i>) Reveal Inbreeding, Few Signs of Cultivation History and Shallow Population Structure. <i>Plants</i> , 2022, 11, 1426.	1.6	6
4740	Investigating the genetic architecture of eye colour in a Canadian cohort. <i>IScience</i> , 2022, 25, 104485.	1.9	2
4741	A phenome-wide association study identifies effects of copy-number variation of VNTRs and multicopy genes on multiple human traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1065-1076.	2.6	12
4742	How genetic risk contributes to autoimmune liver disease. <i>Seminars in Immunopathology</i> , 2022, 44, 397-410.	2.8	11
4743	Genetic correlates of phenotypic heterogeneity in autism. <i>Nature Genetics</i> , 2022, 54, 1293-1304.	9.4	51
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4745	Genome, genetic evolution, and environmental adaptation mechanisms of <i>Schizophyllum commune</i> in deep subseafloor coal-bearing sediments. <i>IScience</i> , 2022, 25, 104417.	1.9	8
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4755	Genetic characterization of outbred Sprague Dawley rats and utility for genome-wide association studies. <i>PLoS Genetics</i> , 2022, 18, e1010234.	1.5	27
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4759	Conserved QTL and chromosomal inversion affect resistance to columnaris disease in 2 rainbow trout (<i>Oncorhynchus mykiss</i>) populations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5

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4761	Genetic diversity and population structure of <i>Caryopteris mongholica</i> revealed by reduced representation sequencing. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
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4766	Sparse block signal detection and identification for shared cross-trait association analysis. <i>Annals of Applied Statistics</i> , 2022, 16, .	0.5	0
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4769	Distributed genetic architecture across the hippocampal formation implies common neuropathology across brain disorders. <i>Nature Communications</i> , 2022, 13, .	5.8	12
4770	Dissecting the limited genetic overlap of Parkinson's and Alzheimer's disease. <i>Annals of Clinical and Translational Neurology</i> , 2022, 9, 1289-1295.	1.7	8
4771	Moment estimators of relatedness from low-depth whole-genome sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
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4773	Genetic Architecture of Powdery Mildew Resistance Revealed by a Genome-Wide Association Study of a Worldwide Collection of Flax (<i>Linum usitatissimum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
4774	Comparing heritability estimators under alternative structures of linkage disequilibrium. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
4775	Genome wide association study identifies novel candidate genes for growth and body conformation traits in goats. <i>Scientific Reports</i> , 2022, 12, .	1.6	15
4776	Clinical autism subscales have common genetic liabilities that are heritable, pleiotropic, and generalizable to the general population. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	11
4777	A 13.42-kb tandem duplication at the ASIP locus is strongly associated with the depigmentation phenotype of non-classic Swiss markings in goats. <i>BMC Genomics</i> , 2022, 23, .	1.2	4

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4788	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	13.7	131
4790	Considering hormone-sensitive cancers as a single disease in the UK biobank reveals shared aetiology. <i>Communications Biology</i> , 2022, 5, .	2.0	3
4791	Pinpointing novel risk loci for Lewy body dementia and the shared genetic etiology with Alzheimer's disease and Parkinson's disease: a large-scale multi-trait association analysis. <i>BMC Medicine</i> , 2022, 20, .	2.3	10
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4795	Genome-Wide Association Study for Chronic Hepatitis B Infection in the Thai Population. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
4796	Pervasive Downward Bias in Estimates of Liability-Scale Heritability in Genome-wide Association Study Meta-analysis: A Simple Solution. <i>Biological Psychiatry</i> , 2023, 93, 29-36.	0.7	28
4797	Mixed model-based eQTL analysis reveals lncRNAs associated with regulation of genes involved in sex determination and spermatogenesis: The key to understanding human gender imbalance. <i>Computational Biology and Chemistry</i> , 2022, 99, 107713.	1.1	0
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4801	Preserving Privacy for Distributed Genome-Wide Analysis Against Identity Tracing Attacks. <i>IEEE Transactions on Dependable and Secure Computing</i> , 2023, 20, 3341-3357.	3.7	3
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4999	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3468-3484.	1.3	4
5000	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
5001	Tissue-specific impacts of aging and genetics on gene expression patterns in humans. <i>Nature Communications</i> , 2022, 13, .	5.8	23
5002	Identify novel, shared and disorder-specific genetic architecture of major depressive disorder, insomnia and chronic pain. <i>Journal of Psychiatric Research</i> , 2022, 155, 511-517.	1.5	5
5003	Genome-wide association study of brain tau deposition as measured by 18F-flortaucipir positron emission tomography imaging. <i>Neurobiology of Aging</i> , 2022, 120, 128-136.	1.5	2

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5027	Microevolutionary mechanism of high-altitude adaptation in Tibetan chicken populations from an elevation gradient. Evolutionary Applications, 2022, 15, 2100-2112.	1.5	3

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5076	Evidence that the pituitary gland connects type 2 diabetes mellitus and schizophrenia based on large-scale trans-ethnic genetic analyses. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	2
5077	Mendelian randomization analysis of factors related to ovulation and reproductive function and endometrial cancer risk. <i>BMC Medicine</i> , 2022, 20, .	2.3	4
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5099	Privacy-aware estimation of relatedness in admixed populations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
5100	Conservation genomics of <i>Agave tequilana</i> Weber var. azul: low genetic differentiation and heterozygote excess in the tequila agave from Jalisco, Mexico. <i>PeerJ</i> , 0, 10, e14398.	0.9	4
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5104	Elucidating breed-specific variants of native pigs in Korea: insights into pig breeds' genomic characteristics. <i>Animal Cells and Systems</i> , 0, , 1-10.	0.8	1
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5126	A genomic assessment of the correlation between milk production traits and claw and udder health traits in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2023, 106, 1190-1205.	1.4	4
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5128	Genome-wide association study reveals novel candidate genes for litter size in Markhoz goats. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	6
5129	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
5130	Structural variation and eQTL analysis in two experimental populations of chickens divergently selected for feather-pecking behavior. <i>Neurogenetics</i> , 0, , .	0.7	1
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5162	Variation and genetic control of individual recombination rates in Norwegian Red dairy cattle. <i>Journal of Dairy Science</i> , 2023, 106, 1130-1141.	1.4	4
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5173	Genetic and microbiome analysis of feed efficiency in laying hens. <i>Poultry Science</i> , 2023, 102, 102393.	1.5	3
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5175	Mega-scale Bayesian Regression methods for genome-wide prediction and association studies with thousands of traits. <i>Genetics</i> , 0, , .	1.2	0
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5197	Maize cytolines as models to study the impact of different cytoplasm on gene expression under heat stress conditions. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
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5201	Genome-Wide Analysis of Left Ventricular Maximum Wall Thickness in the UK Biobank Cohort Reveals a Shared Genetic Background With Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2023, 16, .	1.6	3
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