

Common SNPs explain a large proportion of the heritability

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Determining Genetic Component of a Disease. , 0, , 91-115.		11
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3	Genomic selection and complex trait prediction using a fast EM algorithm applied to genome-wide markers. BMC Bioinformatics, 2010, 11, 529.	1.2	43
4	Seeing the forest through the geneâ€trees. Evolutionary Anthropology, 2010, 19, 210-221.	1.7	14
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
6	Investigation of Mendelian forms of obesity holds out the prospect of personalized medicine. Annals of the New York Academy of Sciences, 2010, 1214, 180-189.	1.8	43
7	Genetics tells tall tales. Nature, 2010, 465, 998-998.	13.7	3
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10	Hints of hidden heritability in GWAS. Nature Genetics, 2010, 42, 558-560.	9.4	258
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12	Reconciling the analysis of IBD and IBS in complex trait studies. Nature Reviews Genetics, 2010, 11, 800-805.	7.7	295
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20	Statistical analysis of genetic interactions. <i>Genetical Research</i> , 2010, 92, 443-459.	0.3	25
21	Genetic Association in Multivariate Phenotypic Data: Power in Five Models. <i>Twin Research and Human Genetics</i> , 2010, 13, 525-543.	0.3	23
22	A Genome-Wide Association Study of Self-Rated Health. <i>Twin Research and Human Genetics</i> , 2010, 13, 398-403.	0.3	14
23	Genomic selection in livestock populations. <i>Genetical Research</i> , 2010, 92, 413-421.	0.3	90
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25	Insights from GWAS into the quantitative genetics of transcription in humans. <i>Genetical Research</i> , 2010, 92, 361-369.	0.3	10
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1054	The genome as pharmacopeia: Association of genetic dose with phenotypic response. <i>Biochemical Pharmacology</i> , 2015, 94, 229-240.	2.0	3
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1078	Bayesian semiparametric copula estimation with application to psychiatric genetics. <i>Biometrical Journal</i> , 2015, 57, 468-484.	0.6	7
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1386	Adult height, nutrition, and population health. <i>Nutrition Reviews</i> , 2016, 74, 149-165.	2.6	272
1387	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. <i>Genetics</i> , 2016, 203, 573-581.	1.2	81

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1389	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. <i>American Journal of Human Genetics</i> , 2016, 98, 525-540.	2.6	75
1390	A new method for estimating effect size distribution and heritability from genome-wide association summary results. <i>Human Genetics</i> , 2016, 135, 171-184.	1.8	5
1391	Genome-wide estimate of the heritability of Multiple System Atrophy. <i>Parkinsonism and Related Disorders</i> , 2016, 22, 35-41.	1.1	42
1392	An Equation to Predict the Accuracy of Genomic Values by Combining Data from Multiple Traits, Populations, or Environments. <i>Genetics</i> , 2016, 202, 799-823.	1.2	54
1393	Genetical Genomics of Behavior: A Novel Chicken Genomic Model for Anxiety Behavior. <i>Genetics</i> , 2016, 202, 327-340.	1.2	51
1394	Model-free Estimation of Recent Genetic Relatedness. <i>American Journal of Human Genetics</i> , 2016, 98, 127-148.	2.6	331
1395	Misspecification in Mixed-Model-Based Association Analysis. <i>Genetics</i> , 2016, 202, 363-366.	1.2	4
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1397	The genetics and neurobiology of ESSENCE: The third Birgit Olsson lecture. <i>Nordic Journal of Psychiatry</i> , 2016, 70, 1-9.	0.7	16
1398	Prenatal and early life influences on epigenetic age in children: a study of motherâ€™offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016, 25, 191-201.	1.4	205
1399	Genetic link between family socioeconomic status and childrenâ€™s educational achievement estimated from genome-wide SNPs. <i>Molecular Psychiatry</i> , 2016, 21, 437-443.	4.1	128
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1401	Schizophrenia: A critical view on genetic effects. <i>Psychosis</i> , 2016, 8, 72-84.	0.4	4
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1403	Cohort Effects in the Genetic Influence on Smoking. <i>Behavior Genetics</i> , 2016, 46, 31-42.	1.4	31
1404	The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. <i>Biological Psychiatry</i> , 2016, 79, 988-996.	0.7	44
1405	Pharmacogenomic variants have larger effect sizes than genetic variants associated with other dichotomous complex traits. <i>Pharmacogenomics Journal</i> , 2016, 16, 388-392.	0.9	56

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1408	Efficient Estimation of Realized Kinship from Single Nucleotide Polymorphism Genotypes. <i>Genetics</i> , 2017, 205, 1063-1078.	1.2	55
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1412	Discovery and functional prioritization of Parkinson's disease candidate genes from large-scale whole exome sequencing. <i>Genome Biology</i> , 2017, 18, 22.	3.8	96
1413	Gray matter heritability in family-based and population-based studies using voxel-based morphometry. <i>Human Brain Mapping</i> , 2017, 38, 2408-2423.	1.9	9
1414	Genomic predictions can accelerate selection for resistance against <i>Piscirickettsia salmonis</i> in Atlantic salmon (<i>Salmo salar</i>). <i>BMC Genomics</i> , 2017, 18, 121.	1.2	140
1415	Human Facial Shape and Size Heritability and Genetic Correlations. <i>Genetics</i> , 2017, 205, 967-978.	1.2	70
1416	Association mapping of morphological traits in wild and captive zebra finches: reliable within, but not between populations. <i>Molecular Ecology</i> , 2017, 26, 1285-1305.	2.0	18
1417	A systematic SNP selection approach to identify mechanisms underlying disease aetiology: linking height to post-menopausal breast and colorectal cancer risk. <i>Scientific Reports</i> , 2017, 7, 41034.	1.6	10
1418	Using information of relatives in genomic prediction to apply effective stratified medicine. <i>Scientific Reports</i> , 2017, 7, 42091.	1.6	38
1419	Phenotypic and Genetic Relationship Between BMI and Drinking in a Sample of UK Adults. <i>Behavior Genetics</i> , 2017, 47, 290-297.	1.4	10
1420	A genomic view of short tandem repeats. <i>Current Opinion in Genetics and Development</i> , 2017, 44, 9-16.	1.5	123
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1422	Personalized medicine: Genetic risk prediction of drug response. , 2017, 175, 75-90.		47
1423	Genomic prediction of reproduction traits for Merino sheep. <i>Animal Genetics</i> , 2017, 48, 338-348.	0.6	11

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1425	Genome-wide analyses identify common variants associated with macular telangiectasia type 2. <i>Nature Genetics</i> , 2017, 49, 559-567.	9.4	105
1426	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 428-443.	2.6	141
1427	An experimental validation of genomic selection in octoploid strawberry. <i>Horticulture Research</i> , 2017, 4, 16070.	2.9	79
1428	A Guide to Genome-Wide Association Mapping in Plants. <i>Current Protocols in Plant Biology</i> , 2017, 2, 22-38.	2.8	75
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1430	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1415-1430.	1.8	99
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1432	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 389-390.	1.0	1
1433	Shared genetic influences between dimensional ASD and ADHD symptoms during child and adolescent development. <i>Molecular Autism</i> , 2017, 8, 18.	2.6	73
1434	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. <i>European Journal of Human Genetics</i> , 2017, 25, 877-885.	1.4	67
1435	Leveraging cell type specific regulatory regions to detect SNPs associated with tissue factor pathway inhibitor plasma levels. <i>Genetic Epidemiology</i> , 2017, 41, 455-466.	0.6	1
1436	The Yin and Yang of Autism Genetics: How Rare De Novo and Common Variations Affect Liability. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 167-187.	2.5	44
1437	Mitigation of inbreeding while preserving genetic gain in genomic breeding programs for outbred plants. <i>Theoretical and Applied Genetics</i> , 2017, 130, 969-980.	1.8	53
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1441	Genetic Characterization of Dog Personality Traits. <i>Genetics</i> , 2017, 206, 1101-1111.	1.2	67

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1443	Heritability of Heart Rate Response to Arousals in Twins. <i>Sleep</i> , 2017, 40, .	0.6	21
1444	Heritability analysis with repeat measurements and its application to resting-state functional connectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5521-5526.	3.3	122
1445	GenoDiver: A combined coalescence and forward-time simulator for populations undergoing selection for complex traits. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 553-563.	0.8	8
1446	Flexible results for quadratic forms with applications to variance components estimation. <i>Annals of Statistics</i> , 2017, 45, .	1.4	14
1447	Animal breeding strategies can improve meat quality attributes within entire populations. <i>Meat Science</i> , 2017, 132, 6-18.	2.7	36
1448	Variable Susceptibility to Cigarette Smoke-Induced Emphysema in 34 Inbred Strains of Mice Implicates <i>Abi3</i> in Emphysema Susceptibility. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 367-375.	1.4	22
1449	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , 2017, 8, 15034.	5.8	40
1450	Analysis of Quantitative Trait Loci. <i>Methods in Molecular Biology</i> , 2017, 1526, 191-203.	0.4	1
1451	An Expanded View of Complex Traits: From Polygenic to Omnigenic. <i>Cell</i> , 2017, 169, 1177-1186.	13.5	2,336
1452	Lipid drug conjugate nanoparticle as a potential nanocarrier for the oral delivery of pemetrexed diacid: Formulation design, characterization, ex vivo , and in vivo assessment. <i>International Journal of Biological Macromolecules</i> , 2017, 103, 139-151.	3.6	34
1453	Genomic variance estimates: With or without disequilibrium covariances?. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 232-241.	0.8	64
1454	A comparison of identity-by-descent and identity-by-state matrices that are used for genetic evaluation and estimation of variance components. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 213-223.	0.8	15
1455	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. <i>Genetics</i> , 2017, 206, 1297-1307.	1.2	125
1456	Cancer is an adaptation that selects in animals against energy dissipation. <i>Medical Hypotheses</i> , 2017, 104, 104-115.	0.8	12
1457	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. <i>Human Genetics</i> , 2017, 136, 963-974.	1.8	11
1458	Why the missing heritability might not be in the DNA. <i>BioEssays</i> , 2017, 39, 1700067.	1.2	43
1460	Composite measures of selection can improve the signal-to-noise ratio in genome scans. <i>Methods in Ecology and Evolution</i> , 2017, 8, 717-727.	2.2	48

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1463	Reevaluation of SNP heritability in complex human traits. <i>Nature Genetics</i> , 2017, 49, 986-992.	9.4	427
1464	Genomics of coloration in natural animal populations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160337.	1.8	54
1465	Polygenic Risk, Personality Dimensions, and Adolescent Alcohol Use Problems: A Longitudinal Study. <i>Journal of Studies on Alcohol and Drugs</i> , 2017, 78, 442-451.	0.6	27
1466	Genetics of rheumatoid arthritis susceptibility, severity, and treatment response. <i>Seminars in Immunopathology</i> , 2017, 39, 395-408.	2.8	73
1467	Invited review: Inbreeding in the genomics era: Inbreeding, inbreeding depression, and management of genomic variability. <i>Journal of Dairy Science</i> , 2017, 100, 6009-6024.	1.4	122
1468	Insights into the genetic architecture of morphological traits in two passerine bird species. <i>Heredity</i> , 2017, 119, 197-205.	1.2	44
1469	Genetic tests in major psychiatric disorders—integrating molecular medicine with clinical psychiatry—why is it so difficult?. <i>Translational Psychiatry</i> , 2017, 7, e1151-e1151.	2.4	44
1470	Genetic Basis of Chronotype in Humans: Insights From Three Landmark GWAS. <i>Sleep</i> , 2017, 40, .	0.6	141
1471	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
1472	The genetic architecture of molecular traits. <i>Current Opinion in Systems Biology</i> , 2017, 1, 25-31.	1.3	6
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1475	The Relationship between Genes, Personality Traits, and Political Interest. <i>Political Research Quarterly</i> , 2017, 70, 467-479.	1.1	18
1476	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. <i>American Journal of Human Genetics</i> , 2017, 100, 605-616.	2.6	76
1477	Inbreeding depression maintained by recessive lethal mutations interacting with stabilizing selection on quantitative characters in a partially self-fertilizing population. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1191-1204.	1.1	13
1479	Exome sequence genotype imputation in globally diverse hexaploid wheat accessions. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1393-1404.	1.8	25

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1482	Using Patterns of Genetic Association to Elucidate Shared Genetic Etiologies Across Psychiatric Disorders. <i>Behavior Genetics</i> , 2017, 47, 405-415.	1.4	3
1483	Assessing connectivity related injury burden in diffuse traumatic brain injury. <i>Human Brain Mapping</i> , 2017, 38, 2913-2922.	1.9	24
1484	Genome-wide estimation of heritability and its functional components for flowering, defense, ionomics, and developmental traits in a geographically diverse population of <i>Arabidopsis thaliana</i> . <i>Genome</i> , 2017, 60, 572-580.	0.9	7
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1487	Mating strategies with genomic information reduce rates of inbreeding in animal breeding schemes without compromising genetic gain. <i>Animal</i> , 2017, 11, 547-555.	1.3	16
1488	Impact of genotyping errors on statistical power of association tests in genomic analyses: A case study. <i>Genetic Epidemiology</i> , 2017, 41, 152-162.	0.6	12
1489	Genome-wide Association Studies in Maize: Praise and Stargaze. <i>Molecular Plant</i> , 2017, 10, 359-374.	3.9	334
1490	Identification of marker-trait associations for morphological descriptors and yield component traits in sugarcane. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 185-196.	1.4	24
1491	Genomic prediction for carcass traits in Japanese Black cattle using single nucleotide polymorphism markers of different densities. <i>Animal Production Science</i> , 2017, 57, 1631.	0.6	15
1492	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
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1494	Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 101, 686-699.	2.6	102
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1497	Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801.	5.8	15

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1499	A novel haplotype of low-frequency variants in the aldosterone synthase gene among northern Han Chinese with essential hypertension. <i>Medicine (United States)</i> , 2017, 96, e8150.	0.4	7
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1502	Genome-wide association studies of cancer: current insights and future perspectives. <i>Nature Reviews Cancer</i> , 2017, 17, 692-704.	12.8	285
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1504	Polygenic Risk Scores in Psychiatry. <i>Biological Psychiatry</i> , 2017, 82, 698-699.	0.7	14
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1508	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
1509	Loci Contributing to Boric Acid Toxicity in Two Reference Populations of <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1631-1641.	0.8	24
1510	Population Stratification in Genetic Association Studies. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.22.1-1.22.23.	3.5	108
1511	Invited review: A perspective on the future of genomic selection in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 8633-8644.	1.4	75
1512	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	9.4	378
1513	Accuracies of breeding values for dry matter intake using nongenotyped animals and predictor traits in different lactations. <i>Journal of Dairy Science</i> , 2017, 100, 9103-9114.	1.4	10
1514	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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1522	Genomic Relationships and GBLUP. , 2017, , 311-354.		3
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1527	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. <i>New England Journal of Medicine</i> , 2017, 377, 1156-1167.	13.9	309
1528	Body Height and Incident Risk of Venous Thromboembolism. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	9
1529	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. <i>Genetics</i> , 2017, 207, 63-73.	1.2	8
1530	Short communication: Implementation of a breeding value for heat tolerance in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 7362-7367.	1.4	50
1531	A genome-wide association study suggests that <i>MAPK14</i> is associated with diabetic foot ulcers. <i>British Journal of Dermatology</i> , 2017, 177, 1664-1670.	1.4	30
1532	A Unified Characterization of Population Structure and Relatedness. <i>Genetics</i> , 2017, 206, 2085-2103.	1.2	135
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1535	A robust DF-REML framework for variance components estimation in genetic studies. <i>Bioinformatics</i> , 2017, 33, 3584-3594.	1.8	11
1536	The infinitesimal model: Definition, derivation, and implications. <i>Theoretical Population Biology</i> , 2017, 118, 50-73.	0.5	250
1537	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
1538	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147
1539	Common variants of T-cells contribute differently to phenotypic variation in sarcoidosis. <i>Scientific Reports</i> , 2017, 7, 5623.	1.6	9
1540	Whole exome sequencing reveals inherited and de novo variants in autism spectrum disorder: a trio study from Saudi families. <i>Scientific Reports</i> , 2017, 7, 5679.	1.6	70
1541	Endocrinology Meets Metabolomics: Achievements, Pitfalls, and Challenges. <i>Trends in Endocrinology and Metabolism</i> , 2017, 28, 705-721.	3.1	29
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1543	EigenPrism: Inference for High Dimensional Signal-to-Noise Ratios. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2017, 79, 1037-1065.	1.1	37
1544	Glittering gold and the quest for Isla de Muerta. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1509-1511.	0.8	19
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1709	A Simple Test Identifies Selection on Complex Traits. <i>Genetics</i> , 2018, 209, 321-333.	1.2	18
1710	Functional Validation of Candidate Genes Detected by Genomic Feature Models. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1659-1668.	0.8	14
1711	Using the <i>Mus musculus</i> hybrid zone to assess covariation and genetic architecture of limb bone lengths. <i>Molecular Ecology Resources</i> , 2018, 18, 908-921.	2.2	8
1712	Genome, transcriptome and proteome: the rise of omics data and their integration in biomedical sciences. <i>Briefings in Bioinformatics</i> , 2018, 19, 286-302.	3.2	498
1713	Determination and regulation of body composition in elite athletes. <i>British Journal of Sports Medicine</i> , 2018, 52, 219-229.	3.1	15
1714	ASD and schizophrenia show distinct developmental profiles in common genetic overlap with population-based social communication difficulties. <i>Molecular Psychiatry</i> , 2018, 23, 263-270.	4.1	107
1715	INVOLVEMENT OF MULTIPLE MOLECULAR PATHWAYS IN THE GENETICS OF OCULAR REFRACTION AND MYOPIA. <i>Retina</i> , 2018, 38, 91-101.	1.0	25
1716	Largest GWAS of PTSD (N=20,070) yields genetic overlap with schizophrenia and sex differences in heritability. <i>Molecular Psychiatry</i> , 2018, 23, 666-673.	4.1	374

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1718	Genetic contributions to self-reported tiredness. <i>Molecular Psychiatry</i> , 2018, 23, 609-620.	4.1	45
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1720	Genes, Personality Traits, and the Sense of Civic Duty. <i>American Politics Research</i> , 2018, 46, 47-76.	0.9	19
1721	Proper joint analysis of summary association statistics requires the adjustment of heterogeneity in SNP coverage pattern. <i>Briefings in Bioinformatics</i> , 2018, 19, 1337-1343.	3.2	2
1722	Protective Factors in Risk Assessment Schemes for Adolescents in Mental Health and Criminal Justice Populations: A Systematic Review and Meta-Analysis of their Predictive Efficacy. <i>Adolescent Research Review</i> , 2018, 3, 95-112.	2.3	15
1723	Quantitative trait locus mapping and analysis of heritable variation in affiliative social behavior and co-occurring traits. <i>Genes, Brain and Behavior</i> , 2018, 17, e12431.	1.1	46
1724	Developmental Changes Within the Genetic Architecture of Social Communication Behavior: A Multivariate Study of Genetic Variance in Unrelated Individuals. <i>Biological Psychiatry</i> , 2018, 83, 598-606.	0.7	30
1725	Maternal and fetal genetic contribution to gestational weight gain. <i>International Journal of Obesity</i> , 2018, 42, 775-784.	1.6	36
1726	Identification of autism spectrum disorder using deep learning and the ABIDE dataset. <i>NeuroImage: Clinical</i> , 2018, 17, 16-23.	1.4	594
1727	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. <i>Psychological Medicine</i> , 2018, 48, 1055-1067.	2.7	66
1728	Charting the genotype-phenotype map: lessons from the <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2018, 7, e289.	5.9	121
1729	Variants in chondroitin sulfate metabolism genes in thrombotic storm. <i>Thrombosis Research</i> , 2018, 161, 43-51.	0.8	5
1730	Gene expression profiles indicate tissue-specific obesity regulation changes and strong obesity relevant tissues. <i>International Journal of Obesity</i> , 2018, 42, 363-369.	1.6	12
1731	Collective effects of common single nucleotide polymorphisms and genetic risk prediction in type 1 diabetes. <i>Clinical Genetics</i> , 2018, 93, 1069-1074.	1.0	8
1732	Obesity and obesogenic growth are both highly heritable and modified by diet in a nonhuman primate model, the African green monkey (<i>Chlorocebus aethiops sabaeus</i>). <i>International Journal of Obesity</i> , 2018, 42, 765-774.	1.6	41
1733	Metabolome-wide association studies for agronomic traits of rice. <i>Heredity</i> , 2018, 120, 342-355.	1.2	33
1734	Genomic prediction and GWAS of <i>Gibberella</i> ear rot resistance traits in dent and flint lines of a public maize breeding program. <i>Euphytica</i> , 2018, 214, 1.	0.6	32

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1736	The SNP rs4252548 (R112H) which is associated with reduced human height compromises the stability of IL-11. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 496-506.	1.9	21
1737	The genetic architecture of ecological adaptation: intraspecific variation in host plant use by the lepidopteran crop pest <i>Chloridea virescens</i> . <i>Heredity</i> , 2018, 120, 234-250.	1.2	7
1738	Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos. <i>Journal of Psychiatric Research</i> , 2018, 99, 167-176.	1.5	15
1739	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	0.6	17
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1741	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , 2018, 101, 1292-1296.	1.4	35
1742	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. <i>Circulation</i> , 2018, 137, 1027-1038.	1.6	196
1743	PCA-Based Multiple-Trait GWAS Analysis: A Powerful Model for Exploring Pleiotropy. <i>Animals</i> , 2018, 8, 239.	1.0	23
1744	An ensemble-based likelihood ratio approach for family-based genomic risk prediction. <i>Journal of Zhejiang University: Science B</i> , 2018, 19, 935-947.	1.3	0
1745	Accounting for heteroscedasticity and censoring in chromosome partitioning analyses. <i>Evolution Letters</i> , 2018, 2, 599-609.	1.6	5
1746	Genomic Prediction Using Prior Quantitative Trait Loci Information Reveals a Large Reservoir of Underutilised Blackleg Resistance in Diverse Canola (<i>Brassica napus</i> L.) Lines. <i>Plant Genome</i> , 2018, 11, 170100.	1.6	40
1747	Replication and discovery of musculoskeletal QTLs in LG/J and SM/J advanced intercross lines. <i>Physiological Reports</i> , 2018, 6, e13561.	0.7	10
1750	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. <i>Frontiers in Genetics</i> , 2018, 9, 455.	1.1	26
1751	The genetic basis of size in pet dogs: The study of quantitative genetic variation in an undergraduate laboratory practical. <i>Biochemistry and Molecular Biology Education</i> , 2018, 46, 623-629.	0.5	1
1752	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. <i>Nature Communications</i> , 2018, 9, 4919.	5.8	6
1753	A scalable estimator of SNP heritability for biobank-scale data. <i>Bioinformatics</i> , 2018, 34, i187-i194.	1.8	37
1754	Heritability informed power optimization (HIPO) leads to enhanced detection of genetic associations across multiple traits. <i>PLoS Genetics</i> , 2018, 14, e1007549.	1.5	36

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1756	Detecting the dominance component of heritability in isolated and outbred human populations. <i>Scientific Reports</i> , 2018, 8, 18048.	1.6	3
1757	GWAS identifies 14 loci for device-measured physical activity and sleep duration. <i>Nature Communications</i> , 2018, 9, 5257.	5.8	241
1758	Widespread Cumulative Influence of Small Effect Size Mutations on Yeast Quantitative Traits. <i>Cell Systems</i> , 2018, 7, 590-600.e6.	2.9	7
1759	Required properties for markers used to calculate unbiased estimates of the genetic correlation between populations. <i>Genetics Selection Evolution</i> , 2018, 50, 65.	1.2	11
1760	The Genetic Diagnosis of Neurodegenerative Diseases and Therapeutic Perspectives. <i>Brain Sciences</i> , 2018, 8, 222.	1.1	23
1761	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <i>Nature Communications</i> , 2018, 9, 5407.	5.8	65
1762	Detection and evaluation of selection signatures in sheep. <i>Pesquisa Agropecuaria Brasileira</i> , 2018, 53, 527-539.	0.9	7
1763	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	5.8	331
1764	Genome-wide study of hair colour in UK Biobank explains most of the SNP heritability. <i>Nature Communications</i> , 2018, 9, 5271.	5.8	96
1765	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. <i>Nature Genetics</i> , 2018, 50, 1600-1607.	9.4	132
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1767	The Small World of Adult Hippocampal Neurogenesis. <i>Frontiers in Neuroscience</i> , 2018, 12, 641.	1.4	7
1768	Analysis of porcine body size variation using re-sequencing data of miniature and large pigs. <i>BMC Genomics</i> , 2018, 19, 687.	1.2	12
1769	Genomic Analyses of Visual Cognition: Perceptual Rivalry and Top-Down Control. <i>Journal of Neuroscience</i> , 2018, 38, 9668-9678.	1.7	11
1770	Genome-wide association study and prediction of genomic breeding values for fatty-acid composition in Korean Hanwoo cattle using a high-density single-nucleotide polymorphism array1. <i>Journal of Animal Science</i> , 2018, 96, 4063-4075.	0.2	13
1771	Reliability of genomic predictions of complex human phenotypes. <i>BMC Proceedings</i> , 2018, 12, 51.	1.8	7
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1774	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , 2018, 9, 4182.	5.8	15
1775	Imputation-Based Whole-Genome Sequence Association Study Reveals Constant and Novel Loci for Hematological Traits in a Large-Scale Swine F2 Resource Population. <i>Frontiers in Genetics</i> , 2018, 9, 401.	1.1	28
1776	Association analysis for seed yield, forage yield and traits related to drought tolerance in orchardgrass (<i>Dactylis glomerata</i>). <i>Crop and Pasture Science</i> , 2018, 69, 1150.	0.7	7
1777	Recovery of novel association loci in <i>Arabidopsis thaliana</i> and <i>Drosophila melanogaster</i> through leveraging INDELs association and integrated burden test. <i>PLoS Genetics</i> , 2018, 14, e1007699.	1.5	16
1778	Genetic Architecture of Adaptive Immune System Identifies Key Immune Regulators. <i>Cell Reports</i> , 2018, 25, 798-810.e6.	2.9	36
1779	Personalized Approach to Statin Selection in Primary Prevention: Genetic Risk Scores Vs Imaging Risk Scores. <i>Current Cardiovascular Risk Reports</i> , 2018, 12, 1.	0.8	0
1780	An atlas of genetic associations in UK Biobank. <i>Nature Genetics</i> , 2018, 50, 1593-1599.	9.4	499
1781	Shared Genomic Regions Underlie Natural Variation in Diverse Toxin Responses. <i>Genetics</i> , 2018, 210, 1509-1525.	1.2	39
1782	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. <i>Nature Communications</i> , 2018, 9, 3522.	5.8	13
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1784	Accurate Genomic Prediction of Human Height. <i>Genetics</i> , 2018, 210, 477-497.	1.2	120
1785	Sustaining the Future of Plant Breeding: The Critical Role of the USDA-ARS National Plant Germplasm System. <i>Crop Science</i> , 2018, 58, 451-468.	0.8	91
1786	Common DNA Variants Accurately Rank an Individual of Extreme Height. <i>International Journal of Genomics</i> , 2018, 2018, 1-7.	0.8	5
1787	Effect of genomic prediction on response to selection in forest tree breeding. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	12
1788	Challenges and Strategies for Breeding Resistance in <i>Capsicum annuum</i> to the Multifarious Pathogen, <i>Phytophthora capsici</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 628.	1.7	83
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1790	Independent erosion of conserved transcription factor binding sites points to shared hindlimb, vision and external testes loss in different mammals. <i>Nucleic Acids Research</i> , 2018, 46, 9299-9308.	6.5	15

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1793	MHC-Dependent Mate Selection within 872 Spousal Pairs of European Ancestry from the Health and Retirement Study. Genes, 2018, 9, 53.	1.0	8
1794	Large-effect loci affect survival in Tasmanian devils (<i>Sarcophilus harrisi</i>) infected with a transmissible cancer. Molecular Ecology, 2018, 27, 4189-4199.	2.0	45
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1797	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
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1802	GWAS on family history of Alzheimer's disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
1803	The impact of using old germplasm on genetic merit and diversity—A cattle breed case study. Journal of Animal Breeding and Genetics, 2018, 135, 311-322.	0.8	17
1804	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	5.8	70
1805	GWAS by GBLUP: Single and Multimarker EMMAX and Bayes Factors, with an Example in Detection of a Major Gene for Horse Gait. G3: Genes, Genomes, Genetics, 2018, 8, 2301-2308.	0.8	35
1806	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493.	0.6	23
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1810	Association between Growth Hormone-Insulin-Like Growth Factor-1 Axis Gene Polymorphisms and Short Stature in Chinese Children. <i>BioMed Research International</i> , 2018, 2018, 1-6.	0.9	2
1811	Genome-wide association analysis links multiple psychiatric liability genes to oscillatory brain activity. <i>Human Brain Mapping</i> , 2018, 39, 4183-4195.	1.9	50
1812	Using Stochastic Approximation Techniques to Efficiently Construct Confidence Intervals for Heritability. <i>Journal of Computational Biology</i> , 2018, 25, 794-808.	0.8	11
1813	Genome-wide pleiotropy and shared biological pathways for resistance to bovine pathogens. <i>PLoS ONE</i> , 2018, 13, e0194374.	1.1	4
1814	Massive variation of short tandem repeats with functional consequences across strains of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2018, 28, 1169-1178.	2.4	34
1815	Weak effects of common genetic variation in oxytocin and vasopressin receptor genes on rhesus macaque social behavior. <i>American Journal of Primatology</i> , 2018, 80, e22873.	0.8	16
1816	Genome-Wide Association Studies. , 2018, , 33-41.		3
1817	Mitogenome phylogeographic analysis of a planktonic crustacean. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 138-148.	1.2	36
1818	Consortium-based genome-wide meta-analysis for childhood dental caries traits. <i>Human Molecular Genetics</i> , 2018, 27, 3113-3127.	1.4	32
1819	Estimating realized heritability for growth in Zhikong scallop (<i>Chlamys farreri</i>) using genome-wide complex trait analysis. <i>Aquaculture</i> , 2018, 497, 103-108.	1.7	15
1820	The Behavioral Genetics of Aggression and Violent Behavior. , 0, , 83-105.		1
1821	Population structure and genetic diversity of 25 Russian sheep breeds based on whole-genome genotyping. <i>Genetics Selection Evolution</i> , 2018, 50, 29.	1.2	76
1822	Using whole genome scores to compare three clinical phenotyping methods in complex diseases. <i>Scientific Reports</i> , 2018, 8, 11360.	1.6	9
1823	Landscape Genomic Conservation Assessment of a Narrow-Endemic and a Widespread Morning Glory From Amazonian Savannas. <i>Frontiers in Plant Science</i> , 2018, 9, 532.	1.7	48
1824	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
1825	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. <i>Nature Genetics</i> , 2018, 50, 1067-1071.	9.4	152
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1828	Using Multi-Scale Genetic, Neuroimaging and Clinical Data for Predicting Alzheimer's Disease and Reconstruction of Relevant Biological Mechanisms. <i>Scientific Reports</i> , 2018, 8, 11173.	1.6	59
1829	Genomic Prediction Using Individual-Level Data and Summary Statistics from Multiple Populations. <i>Genetics</i> , 2018, 210, 53-69.	1.2	15
1830	Family-Based Genome-Wide Association Study of South Indian Pedigrees Supports <i>WNT7B</i> as a Central Corneal Thickness Locus. , 2018, 59, 2495.		11
1831	Genomic prediction of the polled and horned phenotypes in Merino sheep. <i>Genetics Selection Evolution</i> , 2018, 50, 28.	1.2	12
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1836	Genetic Architecture of Feeding Behavior and Feed Efficiency in a Duroc Pig Population. <i>Frontiers in Genetics</i> , 2018, 9, 220.	1.1	105
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1838	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
1839	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. <i>ELife</i> , 2018, 7, .	2.8	94
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1843	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
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1849	Genetic risk for Alzheimer's disease is concentrated in specific macrophage and microglial transcriptional networks. Genome Medicine, 2018, 10, 14.	3.6	83
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1858	Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies across 32 complex traits. Nature Genetics, 2018, 50, 1318-1326.	9.4	225
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1860	Reduced-representation sequencing identifies small effective population sizes of Anopheles gambiae in the north-western Lake Victoria basin, Uganda. Malaria Journal, 2018, 17, 285.	0.8	7
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1866	Exploitation of data from breeding programs supports rapid implementation of genomic selection for key agronomic traits in perennial ryegrass. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1891-1902.	1.8	49
1867	Heritability and longitudinal outcomes of spelling skills in individuals with histories of early speech and language disorders. <i>Learning and Individual Differences</i> , 2018, 65, 1-11.	1.5	18
1868	Host genetics and microbiome associations through the lens of genome wide association studies. <i>Current Opinion in Microbiology</i> , 2018, 44, 9-19.	2.3	33
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1870	Williams Syndrome neuroanatomical score associates with GTF2IRD1 in large-scale magnetic resonance imaging cohorts: a proof of concept for multivariate endophenotypes. <i>Translational Psychiatry</i> , 2018, 8, 114.	2.4	6
1871	Population genetics and GWAS: A primer. <i>PLoS Biology</i> , 2018, 16, e2005485.	2.6	36
1872	Germline Variation and Breast Cancer Incidence: A Gene-Based Association Study and Whole-Genome Prediction of Early-Onset Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1057-1064.	1.1	9
1873	The genetic architecture of type 1 diabetes mellitus. <i>Molecular and Cellular Endocrinology</i> , 2018, 477, 70-80.	1.6	51
1874	GWASinlps: non-local prior based iterative SNP selection tool for genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 1-11.	1.8	26
1875	What genome-wide association studies reveal about the association between intelligence and physical health, illness, and mortality. <i>Current Opinion in Psychology</i> , 2019, 27, 6-12.	2.5	45
1876	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
1877	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
1878	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
1879	Genome-Wide Association Study of Metabolic Syndrome Reveals Primary Genetic Variants at CETP Locus in Indians. <i>Biomolecules</i> , 2019, 9, 321.	1.8	16
1880	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. <i>American Journal of Human Genetics</i> , 2019, 105, 456-476.	2.6	175

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1881	To clean or not to clean phenotypic datasets for outlier plants in genetic analyses?. <i>Journal of Experimental Botany</i> , 2019, 70, 3693-3698.	2.4	7
1882	GWAS of Behavioral Traits. <i>Current Topics in Behavioral Neurosciences</i> , 2019, 42, 1-34.	0.8	0
1883	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
1886	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
1887	Estimating variance components in population scale family trees. <i>PLoS Genetics</i> , 2019, 15, e1008124.	1.5	11
1888	Solving the missing heritability problem. <i>PLoS Genetics</i> , 2019, 15, e1008222.	1.5	164
1889	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. <i>Science</i> , 2019, 365, .	6.0	152
1890	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
1891	Heritability estimation of dichotomous phenotypes using a liability threshold model on ascertained family-based samples. <i>Genetic Epidemiology</i> , 2019, 43, 761-775.	0.6	2
1892	Reconciling S-LDSC and LDK functional enrichment estimates. <i>Nature Genetics</i> , 2019, 51, 1202-1204.	9.4	77
1893	Thinking About the Evolution of Complex Traits in the Era of Genome-Wide Association Studies. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 461-493.	2.5	186
1894	A Guide for Using Deep Learning for Complex Trait Genomic Prediction. <i>Genes</i> , 2019, 10, 553.	1.0	116
1895	A Random Forests Framework for Modeling Haplotypes as Mosaics of Reference Haplotypes. <i>Frontiers in Genetics</i> , 2019, 10, 562.	1.1	4
1896	Multiple auto- and allopolyploidisations marked the Pleistocene history of the widespread Eurasian steppe plant <i>Astragalus onobrychis</i> (Fabaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106572.	1.2	27
1897	Realized Genome Sharing in Heritability Estimation Using Random Effects Models. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1385-1391.	0.8	3
1898	Non-coding variability at the APOE locus contributes to the Alzheimer's risk. <i>Nature Communications</i> , 2019, 10, 3310.	5.8	91
1899	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. <i>Nature Genetics</i> , 2019, 51, 1244-1251.	9.4	69
1900	Heritability of human visual contour integration—an integrated genomic study. <i>European Journal of Human Genetics</i> , 2019, 27, 1867-1875.	1.4	2

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1901	“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
1902	Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960.	1.5	42
1903	Frequentist p-values for large-scale-single step genome-wide association, with an application to birth weight in American Angus cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 28.	1.2	97
1904	A subset of topologically associating domains fold into mesoscale core-periphery networks. <i>Scientific Reports</i> , 2019, 9, 9526.	1.6	9
1905	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	4.7	218
1906	Association Mapping and Disease: Evolutionary Perspectives. <i>Methods in Molecular Biology</i> , 2019, 1910, 533-553.	0.4	0
1907	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. <i>Nature Communications</i> , 2019, 10, 4558.	5.8	363
1908	Genomic prediction of serum biomarkers of health in early lactation. <i>Journal of Dairy Science</i> , 2019, 102, 11142-11152.	1.4	13
1909	Genetic interaction networks mediate individual statin drug response in <i>Saccharomyces cerevisiae</i> . <i>Npj Systems Biology and Applications</i> , 2019, 5, 35.	1.4	11
1910	Autosomal and X-linked additive genetic effects on body weight, body measurements and efficiency-related traits in sheep. <i>Small Ruminant Research</i> , 2019, 180, 21-26.	0.6	7
1911	Analysis of pooled genome sequences from Djallonke and Sahelian sheep of Ghana reveals co-localisation of regions of reduced heterozygosity with candidate genes for disease resistance and adaptation to a tropical environment. <i>BMC Genomics</i> , 2019, 20, 816.	1.2	10
1912	Genome-wide association analysis of 19,629 individuals identifies variants influencing regional brain volumes and refines their genetic co-architecture with cognitive and mental health traits. <i>Nature Genetics</i> , 2019, 51, 1637-1644.	9.4	186
1913	Impact of merging commercial breeding lines on the genetic diversity of Landrace pigs. <i>Genetics Selection Evolution</i> , 2019, 51, 60.	1.2	18
1914	Effect of F1 and F2 generations on genetic variability and working steps of doubled haploid production in maize. <i>PLoS ONE</i> , 2019, 14, e0224631.	1.1	11
1915	Natural Variation Reveals a Key Role for Rhamnogalacturonan I in Seed Outer Mucilage and Underlying Genes. <i>Plant Physiology</i> , 2019, 181, 1498-1518.	2.3	23
1916	A mating advice system in dairy cattle incorporating genomic information. <i>Journal of Dairy Science</i> , 2019, 102, 8210-8220.	1.4	21
1917	The Pathogenesis of Endometriosis: Molecular and Cell Biology Insights. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5615.	1.8	270
1918	Gene-based association analysis of survival traits via functional regression-based mixed effect cox models for related samples. <i>Genetic Epidemiology</i> , 2019, 43, 952-965.	0.6	4

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1919	Genetic Contributions to Health Literacy. <i>Twin Research and Human Genetics</i> , 2019, 22, 131-139.	0.3	0
1920	Complex Phenotypes: Mechanisms Underlying Variation in Human Stature. <i>Current Osteoporosis Reports</i> , 2019, 17, 301-323.	1.5	11
1921	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. <i>Nature Communications</i> , 2019, 10, 3765.	5.8	43
1922	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
1923	Gene-set association and epistatic analyses reveal complex gene interaction networks affecting flowering time in a worldwide barley collection. <i>Journal of Experimental Botany</i> , 2019, 70, 5603-5616.	2.4	49
1924	An overview of myopia genetics. <i>Experimental Eye Research</i> , 2019, 188, 107778.	1.2	79
1925	Ultrarare variants drive substantial cis heritability of human gene expression. <i>Nature Genetics</i> , 2019, 51, 1349-1355.	9.4	98
1926	Functional disease architectures reveal unique biological role of transposable elements. <i>Nature Communications</i> , 2019, 10, 4054.	5.8	14
1927	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19398-19408.	3.3	99
1928	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
1929	Natural variation in <i>Arabidopsis</i> shoot branching plasticity in response to nitrate supply affects fitness. <i>PLoS Genetics</i> , 2019, 15, e1008366.	1.5	29
1930	Evaluation of the Genetic Variance of Alzheimer's Disease Explained by the Disease-Associated Chromosomal Regions. <i>Journal of Alzheimer's Disease</i> , 2019, 70, 907-915.	1.2	3
1931	Quantitative analyses of adiposity dynamics in zebrafish. <i>Adipocyte</i> , 2019, 8, 330-338.	1.3	5
1932	Classifying the fertility of dairy cows using milk mid-infrared spectroscopy. <i>Journal of Dairy Science</i> , 2019, 102, 10460-10470.	1.4	24
1933	Genome-Wide Association and Gene Co-expression Network Analyses Reveal Complex Genetics of Resistance to Goss's Wilt of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3139-3152.	0.8	6
1934	Atrial Fibrillation Genetics Update: Toward Clinical Implementation. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 127.	1.1	26
1935	Predicting women's height from their socioeconomic status: A machine learning approach. <i>Social Science and Medicine</i> , 2019, 238, 112486.	1.8	19
1936	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	6.0	710

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1937	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. <i>Scientific Reports</i> , 2019, 9, 13556.	1.6	3
1938	Evaluation of Genomic Prediction for Pasmus Resistance in Flax. <i>International Journal of Molecular Sciences</i> , 2019, 20, 359.	1.8	45
1939	Assessment of breeding programs sustainability: application of phenotypic and genomic indicators to a North European grain maize program. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1321-1334.	1.8	26
1940	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
1941	Prioritizing Crohn's disease genes by integrating association signals with gene expression implicates monocyte subsets. <i>Genes and Immunity</i> , 2019, 20, 577-588.	2.2	16
1942	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. <i>Nature Neuroscience</i> , 2019, 22, 353-361.	7.1	173
1943	Reducing inbreeding rates with a breeding circle: Theory and practice in Veluws Heideschaap. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 51-62.	0.8	6
1944	Multiple QTL underlie milk phenotypes at the CSF2RB locus. <i>Genetics Selection Evolution</i> , 2019, 51, 3.	1.2	18
1945	Co-inheritance of sea age at maturity and iteroparity in the Atlantic salmon <i>vgl3</i> genomic region. <i>Journal of Evolutionary Biology</i> , 2019, 32, 343-355.	0.8	20
1946	Population structure of human gut bacteria in a diverse cohort from rural Tanzania and Botswana. <i>Genome Biology</i> , 2019, 20, 16.	3.8	66
1947	Systematic identification and characterization of candidate genes for the regulation of plant height in maize. <i>Euphytica</i> , 2019, 215, 1.	0.6	4
1948	Disentangling polygenic associations between attention-deficit/hyperactivity disorder, educational attainment, literacy and language. <i>Translational Psychiatry</i> , 2019, 9, 35.	2.4	25
1949	SNP variable selection by generalized graph domination. <i>PLoS ONE</i> , 2019, 14, e0203242.	1.1	7
1950	Heritability of fetal hemoglobin, white cell count, and other clinical traits from a sickle cell disease family cohort. <i>American Journal of Hematology</i> , 2019, 94, 522-527.	2.0	6
1951	Phenotype and Environment Matter: Discovering the Genetic and Epigenetic Architecture of Alcohol Use Disorders. <i>American Journal of Psychiatry</i> , 2019, 176, 92-95.	4.0	3
1952	Quantifying between-cohort and between-sex genetic heterogeneity in major depressive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 439-447.	1.1	35
1953	The Effects of Epistasis and Pleiotropy on Genome-Wide Scans for Adaptive Outlier Loci. <i>Journal of Heredity</i> , 2019, 110, 494-513.	1.0	3
1954	A genome-wide association study reveals specific transferases as candidate loci for bovine milk oligosaccharides synthesis. <i>BMC Genomics</i> , 2019, 20, 404.	1.2	14

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1955	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	1.2	23
1957	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002481.	1.6	59
1958	The etiology of DSM-5 alcohol use disorder: Evidence of shared and non-shared additive genetic effects. <i>Drug and Alcohol Dependence</i> , 2019, 201, 147-154.	1.6	7
1959	The Genome-Wide Study of Human Social Behavior and Its Application in Sociology. <i>Frontiers in Sociology</i> , 2019, 4, 53.	1.0	2
1960	Heritability analysis of nontraditional glycemic biomarkers in the Atherosclerosis Risk in Communities Study. <i>Genetic Epidemiology</i> , 2019, 43, 776-785.	0.6	8
1961	A comprehensive overview of the developmental basis and adaptive significance of a textbook polymorphism: head asymmetry in the cichlid fish <i>Perissodus microlepis</i> . <i>Hydrobiologia</i> , 2019, 832, 65-84.	1.0	13
1962	Use of a Bayesian model including QTL markers increases prediction reliability when test animals are distant from the reference population. <i>Journal of Dairy Science</i> , 2019, 102, 7237-7247.	1.4	13
1963	Germline variants and somatic mutation signatures of breast cancer across populations of African and European ancestry in the US and Nigeria. <i>International Journal of Cancer</i> , 2019, 145, 3321-3333.	2.3	16
1964	Gene and environment interplay in cognition: Evidence from twin and molecular studies, future directions and suggestions for effective candidate gene x environment (cGxE) research. <i>Multiple Sclerosis and Related Disorders</i> , 2019, 33, 121-130.	0.9	3
1965	Comprehensive analysis of coding variants highlights genetic complexity in developmental and epileptic encephalopathy. <i>Nature Communications</i> , 2019, 10, 2506.	5.8	46
1966	Association of taller stature with lower cardiovascular disease mortality in Asian people: a systematic review. <i>Journal of Physiological Anthropology</i> , 2019, 38, 6.	1.0	5
1967	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2946-2957.	1.2	45
1968	Genetic correlations of polygenic disease traits: from theory to practice. <i>Nature Reviews Genetics</i> , 2019, 20, 567-581.	7.7	236
1969	Gene Regulatory Networks to Explain Coronary Artery Disease Heritability. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2958-2960.	1.2	0
1970	A local score approach improves GWAS resolution and detects minor QTL: application to <i>Medicago truncatula</i> quantitative disease resistance to multiple <i>Aphanomyces euteiches</i> isolates. <i>Heredity</i> , 2019, 123, 517-531.	1.2	36
1971	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019, 20, 107.	3.8	105
1972	Inferring the Nature of Missing Heritability in Human Traits Using Data from the GWAS Catalog. <i>Genetics</i> , 2019, 212, 891-904.	1.2	34
1973	The Fallacy of Equating the Hereditarian Hypothesis with Racism. <i>Psych</i> , 2019, 1, 262-278.	0.7	7

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1974	Estimation of metabolic syndrome heritability in three large populations including full pedigree and genomic information. <i>Human Genetics</i> , 2019, 138, 739-748.	1.8	4
1975	Genome Wide Association Study and Next Generation Sequencing: A Glimmer of Light Toward New Possible Horizons in Frontotemporal Dementia Research. <i>Frontiers in Neuroscience</i> , 2019, 13, 506.	1.4	23
1976	Systemic Sclerosis. <i>Rare Diseases of the Immune System</i> , 2019, , 19-35.	0.1	0
1978	Genome-wide association study reveals candidate genes associated with body measurement traits in Chinese Wagyu beef cattle. <i>Animal Genetics</i> , 2019, 50, 386-390.	0.6	32
1979	What Is the Heritability of Periodontitis? A Systematic Review. <i>Journal of Dental Research</i> , 2019, 98, 632-641.	2.5	63
1980	Accelerated estimation and permutation inference for ACE modeling. <i>Human Brain Mapping</i> , 2019, 40, 3488-3507.	1.9	19
1981	Genomic selection on breeding time in a wild bird population. <i>Evolution Letters</i> , 2019, 3, 142-151.	1.6	40
1982	Benefits and limitations of genome-wide association studies. <i>Nature Reviews Genetics</i> , 2019, 20, 467-484.	7.7	1,226
1983	Genomic evidence of genetic variation with pleiotropic effects on caterpillar fitness and plant traits in a model legume. <i>Molecular Ecology</i> , 2019, 28, 2967-2985.	2.0	19
1984	Genetics of Vascular Diseases. <i>Learning Materials in Biosciences</i> , 2019, , 245-269.	0.2	0
1985	RAD-seq for estimating genomic relatedness matrix-based heritability in the wild: A case study in roe deer. <i>Molecular Ecology Resources</i> , 2019, 19, 1205-1217.	2.2	18
1986	Genetic and phenotypic analyses indicate that resistance to flooding stress is uncoupled from performance in cultivated sunflower. <i>New Phytologist</i> , 2019, 223, 1657-1670.	3.5	14
1987	Translational Potential of Neuroimaging Genomic Analyses to Diagnosis and Treatment in Mental Disorders. <i>Proceedings of the IEEE</i> , 2019, 107, 912-927.	16.4	4
1988	Reliable heritability estimation using sparse regularization in ultrahigh dimensional genome-wide association studies. <i>BMC Bioinformatics</i> , 2019, 20, 219.	1.2	7
1989	Analysis of Heritability and Genetic Architecture of Pancreatic Cancer: A PanC4 Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1238-1245.	1.1	48
1990	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	2.8	276
1991	Polygenic prediction via Bayesian regression and continuous shrinkage priors. <i>Nature Communications</i> , 2019, 10, 1776.	5.8	832
1992	Correlations between relatives: From Mendelian theory to complete genome sequence. <i>Genetic Epidemiology</i> , 2019, 43, 577-591.	0.6	3

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1993	Genetic architecture of socioeconomic outcomes: Educational attainment, occupational status, and wealth. <i>Social Science Research</i> , 2019, 82, 137-147.	1.1	8
1994	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. <i>Cell</i> , 2019, 177, 1022-1034.e6.	13.5	385
1995	Reconstructing recent population history while mapping rare variants using haplotypes. <i>Scientific Reports</i> , 2019, 9, 5849.	1.6	4
1996	The evolution of microendemism in a reef fish (<i>Hypoplectrus maya</i>). <i>Molecular Ecology</i> , 2019, 28, 2872-2885.	2.0	10
1997	Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. <i>PLoS Biology</i> , 2019, 17, e3000244.	2.6	82
1998	The genetics of depression: successful genome-wide association studies introduce new challenges. <i>Translational Psychiatry</i> , 2019, 9, 114.	2.4	75
1999	Genetics of Axial Spondyloarthritis. , 2019, , 67-85.		0
2001	Efficient Implementation of Penalized Regression for Genetic Risk Prediction. <i>Genetics</i> , 2019, 212, 65-74.	1.2	51
2002	Genomic Medicine—Progress, Pitfalls, and Promise. <i>Cell</i> , 2019, 177, 45-57.	13.5	143
2003	Genome-wide association study of blood lipids in Indians confirms universality of established variants. <i>Journal of Human Genetics</i> , 2019, 64, 573-587.	1.1	22
2004	SummaryAUC: a tool for evaluating the performance of polygenic risk prediction models in validation datasets with only summary level statistics. <i>Bioinformatics</i> , 2019, 35, 4038-4044.	1.8	15
2005	Idiopathic short stature and growth hormone sensitivity in prepubertal children. <i>Clinical Endocrinology</i> , 2019, 91, 110-117.	1.2	6
2006	Landscape genomics to the rescue of a tropical bee threatened by habitat loss and climate change. <i>Evolutionary Applications</i> , 2019, 12, 1164-1177.	1.5	41
2008	Restriction-site associated DNA sequencing supports a sister group relationship of <i>Nigritella</i> and <i>Gymnadenia</i> (Orchidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 21-28.	1.2	24
2009	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
2010	Identification of genetic heterogeneity of Alzheimer's disease across age. <i>Neurobiology of Aging</i> , 2019, 84, 243.e1-243.e9.	1.5	34
2011	Dissection of Complex, Fitness-Related Traits in Multiple <i>Drosophila</i> Mapping Populations Offers Insight into the Genetic Control of Stress Resistance. <i>Genetics</i> , 2019, 211, 1449-1467.	1.2	22
2012	Integrating Gene Expression Data Into Genomic Prediction. <i>Frontiers in Genetics</i> , 2019, 10, 126.	1.1	57

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2013	2018 William Allan Award: Discovering the Genes for Common Disease: From Families to Populations. <i>American Journal of Human Genetics</i> , 2019, 104, 375-383.	2.6	0
2014	Heritability estimates of individual psychological distress symptoms from genetic variation. <i>Journal of Affective Disorders</i> , 2019, 252, 413-420.	2.0	9
2015	Reverse GWAS: Using genetics to identify and model phenotypic subtypes. <i>PLoS Genetics</i> , 2019, 15, e1008009.	1.5	34
2016	Transcriptome profiling of four candidate milk genes in milk and tissue samples of temperate and tropical cattle. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	3
2017	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
2018	Heritability and individuality of the plasma sodium concentration: a twin study in the United States veteran population. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, F1114-F1123.	1.3	5
2019	Genome-wide association study reveals sex-specific genetic architecture of facial attractiveness. <i>PLoS Genetics</i> , 2019, 15, e1007973.	1.5	5
2020	Predicting male fertility in dairy cattle using markers with large effect and functional annotation data. <i>BMC Genomics</i> , 2019, 20, 258.	1.2	44
2021	Estimating the purebred-crossbred genetic correlation of body weight in broiler chickens with pedigree or genomic relationships. <i>Genetics Selection Evolution</i> , 2019, 51, 6.	1.2	16
2022	Genetic redundancy fuels polygenic adaptation in <i>Drosophila</i> . <i>PLoS Biology</i> , 2019, 17, e3000128.	2.6	212
2023	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
2024	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
2025	Exposing the Causal Effect of Body Mass Index on the Risk of Type 2 Diabetes Mellitus: A Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2019, 10, 94.	1.1	55
2026	Haplotype and Haplotype-Environment Interaction Analysis Revealed Roles of <i>SPRY2</i> for NSCL/P among Chinese Populations. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 557.	1.2	4
2027	Genomewide association study of C-peptide surfaces key regulatory genes in Indians. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	7
2028	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. <i>Nature Communications</i> , 2019, 10, 569.	5.8	50
2029	Design of training populations for selective phenotyping in genomic prediction. <i>Scientific Reports</i> , 2019, 9, 1446.	1.6	70
2030	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538

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2031	A Multivariate Genome-Wide Association Study of Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2019, 211, 1429-1447.	1.2	54
2032	Genomic Predictors of Asthma Phenotypes and Treatment Response. <i>Frontiers in Pediatrics</i> , 2019, 7, 6.	0.9	61
2033	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
2034	Genomic Selection with Allele Dosage in <i>Panicum maximum</i> Jacq.. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2463-2475.	0.8	57
2035	Graph-structured Sparse Mixed Models for Genetic Association with Confounding Factors Correction. , 2019, , .		0
2036	Best Prediction of the Additive Genomic Variance in Random-Effects Models. <i>Genetics</i> , 2019, 213, 379-394.	1.2	8
2037	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
2038	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	5.8	291
2039	Optimal sequencing depth design for whole genome re-sequencing in pigs. <i>BMC Bioinformatics</i> , 2019, 20, 556.	1.2	28
2040	Anti-Allergic 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
2041	Habitat Loss Does Not Always Entail Negative Genetic Consequences. <i>Frontiers in Genetics</i> , 2019, 10, 1011.	1.1	32
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2047	Genome-Wide identification of doublesex and Mab-3-Related transcription factor (DMRT) genes in Nile tilapia (<i>Oreochromis niloticus</i>). <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2019, 24, e00398.	2.1	15
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2175	Applications of Support Vector Machine in Genomic Prediction in Pig and Maize Populations. <i>Frontiers in Genetics</i> , 2020, 11, 598318.	1.1	20
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2183	Personality in Nonhuman Animals. , 2020, , 235-246.		0
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2186	Cognitive Processes and Models. , 2020, , 295-315.		0
2187	Basic Needs, Goals and Motivation. , 2020, , 330-338.		1
2188	Personality and the Self. , 2020, , 339-351.		6
2189	Social Relations and Social Support. , 2020, , 386-399.		0
2190	Personality and Politics. , 2020, , 413-424.		1
2191	Personality at Work. , 2020, , 427-438.		2
2193	Personality in Clinical Psychology. , 2020, , 451-462.		0
2195	Conceptual and Historical Perspectives. , 2020, , 13-30.		3
2196	Personality and the Unconscious. , 2020, , 69-80.		0

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2205	Self-Regulation and Control in Personality Functioning. , 2020, , 316-329.		0
2206	Traits and Dynamic Processes. , 2020, , 352-363.		0
2207	Anxiety, Depression and Cognitive Dysfunction. , 2020, , 364-374.		0
2208	Personality in Cross-Cultural Perspective. , 2020, , 400-412.		1
2209	Personality, Preferences and Socioeconomic Behavior. , 2020, , 477-494.		2
2211	States and Situations, Traits and Environments. , 2020, , 56-68.		1
2212	Narrative Identity in the Social World. , 2020, , 377-385.		0
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2226	A genome-wide association study of interhemispheric theta EEG coherence: implications for neural connectivity and alcohol use behavior. <i>Molecular Psychiatry</i> , 2021, 26, 5040-5052.	4.1	22
2227	Efficient toolkit implementing best practices for principal component analysis of population genetic data. <i>Bioinformatics</i> , 2020, 36, 4449-4457.	1.8	76
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2229	The genetic basis of animal behavioural diversity in natural populations. <i>Molecular Ecology</i> , 2020, 29, 1957-1971.	2.0	18
2230	Deciphering Sex-Specific Genetic Architectures Using Local Bayesian Regressions. <i>Genetics</i> , 2020, 215, 231-241.	1.2	7
2231	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. <i>PLoS Genetics</i> , 2020, 16, e1008682.	1.5	31
2232	A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020, 582, 234-239.	13.7	39
2233	The quest for genetic sequence variants conferring risk of endometriosis. , 2020, , 91-109.		2
2234	On Negative Heritability and Negative Estimates of Heritability. <i>Genetics</i> , 2020, 215, 343-357.	1.2	27

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2236	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 424.	1.1	335
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2238	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. <i>American Journal of Human Genetics</i> , 2020, 107, 46-59.	2.6	30
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2240	Genomic prediction applied to multiple traits and environments in second season maize hybrids. <i>Heredity</i> , 2020, 125, 60-72.	1.2	12
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2242	Using single-step genomic best linear unbiased prediction to improve the efficiency of genetic evaluation on body weight in <i>Macrobrachium rosenbergii</i> . <i>Aquaculture</i> , 2020, 528, 735577.	1.7	9
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2244	Genomics of Pain and Co-Morbid Symptoms. , 2020, , .		0
2245	Phenotype-specific differences in polygenicity and effect size distribution across functional annotation categories revealed by Al-MiXeR. <i>Bioinformatics</i> , 2020, 36, 4749-4756.	1.8	6
2246	KAML: improving genomic prediction accuracy of complex traits using machine learning determined parameters. <i>Genome Biology</i> , 2020, 21, 146.	3.8	51
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2249	Natural Selection Shapes Codon Usage in the Human Genome. <i>American Journal of Human Genetics</i> , 2020, 107, 83-95.	2.6	44
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2251	Phenotypic Responses to and Genetic Architecture of Sterility Following Exposure to Sub-Lethal Temperature During Development. <i>Frontiers in Genetics</i> , 2020, 11, 573.	1.1	31
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2255	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	5.8	85
2256	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	1.7	25
2257	Evaluating and improving heritability models using summary statistics. <i>Nature Genetics</i> , 2020, 52, 458-462.	9.4	128
2258	Self-reported hearing loss questions provide a good measure for genetic studies: a polygenic risk score analysis from UK Biobank. <i>European Journal of Human Genetics</i> , 2020, 28, 1056-1065.	1.4	21
2259	The genetic architecture of membranous nephropathy and its potential to improve non-invasive diagnosis. <i>Nature Communications</i> , 2020, 11, 1600.	5.8	120
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2262	Parentage and relatedness reconstruction in <i>Pinus sylvestris</i> using genotyping-by-sequencing. <i>Heredity</i> , 2020, 124, 633-646.	1.2	26
2263	Systematic Review of Polygenic Risk Scores for Type 1 and Type 2 Diabetes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1703.	1.8	46
2264	High-definition likelihood inference of genetic correlations across human complex traits. <i>Nature Genetics</i> , 2020, 52, 859-864.	9.4	114
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2266	Integrative bioinformatic analyses of genome-wide association studies for understanding the genetic bases of human height. <i>Biologia (Poland)</i> , 2020, 75, 2413-2420.	0.8	1
2267	Statistical methods for SNP heritability estimation and partition: A review. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1557-1568.	1.9	41
2268	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	5.8	75
2269	Coinherited genetics of multiple myeloma and its precursor, monoclonal gammopathy of undetermined significance. <i>Blood Advances</i> , 2020, 4, 2789-2797.	2.5	20
2270	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. <i>Heredity</i> , 2020, 124, 658-674.	1.2	10

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2272	Genomic Regions Associated With Skeletal Type Traits in Beef and Dairy Cattle Are Common to Regions Associated With Carcass Traits, Feed Intake and Calving Difficulty. <i>Frontiers in Genetics</i> , 2020, 11, 20.	1.1	21
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2275	Polygenic Architecture of Human Neuroanatomical Diversity. <i>Cerebral Cortex</i> , 2020, 30, 2307-2320.	1.6	16
2276	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
2277	Genomic dissection of maternal, additive and non-additive genetic effects for growth and carcass traits in Nile tilapia. <i>Genetics Selection Evolution</i> , 2020, 52, 1.	1.2	78
2278	A fast-linear mixed model for genome-wide haplotype association analysis: application to agronomic traits in maize. <i>BMC Genomics</i> , 2020, 21, 151.	1.2	6
2279	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. <i>PLoS Computational Biology</i> , 2020, 16, e1007565.	1.5	32
2280	Structured assessments for imminent aggression in mental health and correctional settings: Systematic review and meta-analysis. <i>International Journal of Nursing Studies</i> , 2020, 104, 103526.	2.5	16
2281	A Multiple-Trait Bayesian Lasso for Genome-Enabled Analysis and Prediction of Complex Traits. <i>Genetics</i> , 2020, 214, 305-331.	1.2	25
2282	Comments on: Hierarchical inference for genome-wide association studies by Jelle J. Goeman and Stefan Böhning. <i>Computational Statistics</i> , 2020, 35, 41-45.	0.8	1
2283	Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: I: feed efficiency and component traits. <i>BMC Genomics</i> , 2020, 21, 36.	1.2	49
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2285	A Multi-tissue Transcriptome Analysis of Human Metabolites Guides Interpretability of Associations Based on Multi-SNP Models for Gene Expression. <i>American Journal of Human Genetics</i> , 2020, 106, 188-201.	2.6	26
2286	Genomic Prediction of Columnaris Disease Resistance in Catfish. <i>Marine Biotechnology</i> , 2020, 22, 145-151.	1.1	6
2287	Multikernel linear mixed model with adaptive lasso for complex phenotype prediction. <i>Statistics in Medicine</i> , 2020, 39, 1311-1327.	0.8	9
2288	Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease. <i>Scientific Reports</i> , 2020, 10, 1433.	1.6	24

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2291	Statistical Methods in Genome-Wide Association Studies. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 265-288.	2.8	6
2292	A decade of research on the genetics of entrepreneurship: a review and view ahead. <i>Small Business Economics</i> , 2021, 57, 1303-1317.	4.4	17
2293	Maternal and paternal effects on offspring internalizing problems: Results from genetic and family-based analyses. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 258-267.	1.1	17
2294	What is creating the height premium? New evidence from a Mendelian randomization analysis in China. <i>PLoS ONE</i> , 2020, 15, e0230555.	1.1	4
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2296	The contribution of rare genetic variants to the pathogenesis of polycystic ovary syndrome. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2020, 12, 26-32.	0.6	21
2297	Lost in translation: Population genomics and long-read sequencing reveals relaxation of concerted evolution of the ribosomal DNA cistron. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106804.	1.2	16
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2299	Common variation at 16p11.2 is associated with glycosuria in pregnancy: findings from a genome-wide association study in European women. <i>Human Molecular Genetics</i> , 2020, 29, 2098-2106.	1.4	3
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2302	Genome-wide association analysis of insomnia using data from Partners Biobank. <i>Scientific Reports</i> , 2020, 10, 6928.	1.6	11
2303	Accurate and Scalable Construction of Polygenic Scores in Large Biobank Data Sets. <i>American Journal of Human Genetics</i> , 2020, 106, 679-693.	2.6	80
2304	Genetic Contributions to Multivariate Data-Driven Brain Networks Constructed via Source-Based Morphometry. <i>Cerebral Cortex</i> , 2020, 30, 4899-4913.	1.6	7
2305	Liability threshold modeling of case-control status and family history of disease increases association power. <i>Nature Genetics</i> , 2020, 52, 541-547.	9.4	60
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2309	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
2310	Dissecting the heritable risk of breast cancer: From statistical methods to susceptibility genes. <i>Seminars in Cancer Biology</i> , 2021, 72, 175-184.	4.3	10
2311	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. <i>Biological Psychiatry</i> , 2021, 89, 11-19.	0.7	59
2312	Genetic influence on cognitive development between childhood and adulthood. <i>Molecular Psychiatry</i> , 2021, 26, 656-665.	4.1	28
2313	The influence of X chromosome variants on trait neuroticism. <i>Molecular Psychiatry</i> , 2021, 26, 483-491.	4.1	17
2314	Individual Differences in Cognitive Performance Are Better Predicted by Global Rather Than Localized BOLD Activity Patterns Across the Cortex. <i>Cerebral Cortex</i> , 2021, 31, 1478-1488.	1.6	24
2315	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. <i>Journal of the American Statistical Association</i> , 2021, 116, 531-545.	1.8	3
2316	Dynamic shifts in social network structure and composition within a breeding hybrid population. <i>Journal of Animal Ecology</i> , 2021, 90, 197-211.	1.3	3
2317	The neurobiology of human aggressive behavior: Neuroimaging, genetic, and neurochemical aspects. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 106, 110059.	2.5	39
2318	Where Are the Disease-Associated eQTLs?. <i>Trends in Genetics</i> , 2021, 37, 109-124.	2.9	163
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2321	Genetic Data: Potential Uses and Misuses in Marketing. <i>Journal of Marketing</i> , 2022, 86, 7-26.	7.0	15
2322	Periodontal health and disease: The contribution of genetics. <i>Periodontology 2000</i> , 2021, 85, 161-181.	6.3	33
2323	Urinary metabolite quantitative trait loci in children and their interaction with dietary factors. <i>Human Molecular Genetics</i> , 2021, 29, 3830-3844.	1.4	7
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2329	A genome-wide association study reveals a substantial genetic basis underlying the Ebbinghaus illusion. <i>Journal of Human Genetics</i> , 2021, 66, 261-271.	1.1	4
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2331	“Reports of My Death Were Greatly Exaggerated” Behavior Genetics in the Postgenomic Era. <i>Annual Review of Psychology</i> , 2021, 72, 37-60.	9.9	49
2332	Extended application of genomic selection to screen multiomics data for prognostic signatures of prostate cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
2333	Heritability jointly explained by host genotype and microbiome: will improve traits prediction?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
2334	Genetic potential and height velocity during childhood and adolescence do not fully account for shorter stature in cystic fibrosis. <i>Pediatric Research</i> , 2021, 89, 653-659.	1.1	7
2335	Genetic and environmental contributions to diagnostic fluctuation in anorexia nervosa and bulimia nervosa. <i>Psychological Medicine</i> , 2021, 51, 62-69.	2.7	17
2336	Heritability, causal influence and locality. <i>Synthese</i> , 2021, 198, 6689-6715.	0.6	13
2337	Linear Mixed Models: Part I. Springer Series in Statistics, 2021, , 1-61.	0.9	6
2338	Heritability and family-based GWAS analyses of the <i>N</i> -acyl ethanolamine and ceramide plasma lipidome. <i>Human Molecular Genetics</i> , 2021, 30, 500-513.	1.4	13
2340	Genetic mapping of developmental trajectories for complex traits and diseases. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3458-3469.	1.9	1
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2345	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. <i>Genome Biology</i> , 2021, 22, 1.	3.8	239
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2352	Combining twin-family designs with measured genetic variants to study the causes of epigenetic variation. , 2021, , 239-259.		0
2353	The genetic architecture of human complex phenotypes is modulated by linkage disequilibrium and heterozygosity. <i>Genetics</i> , 2021, 217, .	1.2	10
2354	OUP accepted manuscript. <i>Human Molecular Genetics</i> , 2021, 30, 1521-1534.	1.4	32
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2357	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	1.4	32
2358	The indigenous populations as the model by nature to understand human genomicâ€“phenomics interactions. <i>Quantitative Biology</i> , 2022, 10, 35-43.	0.3	0
2359	Problem of Genetic Inheritance, The. , 2021, , 6280-6287.		0
2360	Whole genome sequencing in the Middle Eastern Qatari population identifies genetic associations with 45 clinically relevant traits. <i>Nature Communications</i> , 2021, 12, 1250.	5.8	37
2361	Analysis of the primary sources of quantitative adult plant resistance to stripe rust in U.S. soft red winter wheat germplasm. <i>Plant Genome</i> , 2021, 14, e20082.	1.6	1
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2364	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	5.8	50

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2367	A new algorithm for fitting semi-parametric variance regression models. <i>Computational Statistics</i> , 2021, 36, 2313-2335.	0.8	3
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2370	Heuristic hyperparameter optimization of deep learning models for genomic prediction. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	16
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2372	Marker-trait association analysis for drought tolerance in smooth bromegrass. <i>BMC Plant Biology</i> , 2021, 21, 116.	1.6	1
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2375	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	5.8	19
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2385	The Epigenetics of Gametes and Early Embryos and Potential Long-Range Consequences in Livestock Speciesâ€”Filling in the Picture With Epigenomic Analyses. <i>Frontiers in Genetics</i> , 2021, 12, 557934.	1.1	22

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2388	VTRNA2-1: Genetic Variation, Heritable Methylation and Disease Association. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2535.	1.8	15
2389	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612045.	1.1	0
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3467	The role of spatial structure in multi-deme models of evolutionary rescue. <i>Journal of Evolutionary Biology</i> , 2022, 35, 986-1001.	0.8	0
3468	Moment estimators of relatedness from low-depth whole-genome sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
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