

# Rapid and Accurate Haplotype Phasing and Missing-Data Association Studies By Use of Localized Haplotype Clus

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Grouping preprocess to accurately extend application of EM algorithm to haplotype inference. <i>Journal of Human Genetics</i> , 2008, 53, 747-756.	1.1	3
2	Haplotypic analysis of Wellcome Trust Case Control Consortium data. <i>Human Genetics</i> , 2008, 123, 273-280.	1.8	65
3	Missing data imputation and haplotype phase inference for genome-wide association studies. <i>Human Genetics</i> , 2008, 124, 439-450.	1.8	142
5	Simple and Efficient Analysis of Disease Association with Missing Genotype Data. <i>American Journal of Human Genetics</i> , 2008, 82, 444-452.	2.6	87
6	Multipoint Approximations of Identity-by-Descent Probabilities for Accurate Linkage Analysis of Distantly Related Individuals. <i>American Journal of Human Genetics</i> , 2008, 82, 607-622.	2.6	9
7	The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research. <i>American Journal of Human Genetics</i> , 2008, 83, 347-358.	2.6	289
8	PRESTO: Rapid calculation of order statistic distributions and multiple-testing adjusted P-values via permutation for one and two-stage genetic association studies. <i>BMC Bioinformatics</i> , 2008, 9, 309.	1.2	43
9	Haplotype Association Analysis. <i>Advances in Genetics</i> , 2008, 60, 335-405.	0.8	116
10	Whole population, genome-wide mapping of hidden relatedness. <i>Genome Research</i> , 2009, 19, 318-326.	2.4	411
11	Practical Issues in Imputation-Based Association Mapping. <i>PLoS Genetics</i> , 2008, 4, e1000279.	1.5	155
12	Estimation of Pairwise Identity by Descent From Dense Genetic Marker Data in a Population Sample of Haplotypes. <i>Genetics</i> , 2008, 178, 2123-2132.	1.2	65
13	A better block partition and ligation strategy for individual haplotyping. <i>Bioinformatics</i> , 2008, 24, 2720-2725.	1.8	11
14	Efficient whole-genome association mapping using local phylogenies for unphased genotype data. <i>Bioinformatics</i> , 2008, 24, 2215-2221.	1.8	11
15	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. <i>PLoS ONE</i> , 2008, 3, e3551.	1.1	117
16	Structures and Assumptions: Strategies to Harness Gene $\times$ Gene and Gene $\times$ Environment Interactions in GWAS. <i>Statistical Science</i> , 2009, 24, 472-488.	1.6	24
17	Clustering of SNPs by a Structural EM Algorithm. , 2009, , .		7
18	Local Phylogeny Mapping of Quantitative Traits: Higher Accuracy and Better Ranking Than Single-Marker Association in Genomewide Scans. <i>Genetics</i> , 2009, 181, 747-753.	1.2	15
19	Global distribution of genomic diversity underscores rich complex history of continental human populations. <i>Genome Research</i> , 2009, 19, 795-803.	2.4	155

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20	Evaluation of Potential Power Gain with Imputed Genotypes in Genome-Wide Association Studies. <i>Human Heredity</i> , 2009, 68, 23-34.	0.4	3
21	Systematic haplotype analysis resolves a complex plasma plant sterol locus on the Micronesian Island of Kosrae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13886-13891.	3.3	23
22	Incorporating multiple-marker information to detect risk loci for rheumatoid arthritis. <i>BMC Proceedings</i> , 2009, 3, S28.	1.8	6
23	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. <i>PLoS Genetics</i> , 2009, 5, e1000456.	1.5	157
24	A Flexible and Accurate Genotype Imputation Method for the Next Generation of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2009, 5, e1000529.	1.5	3,526
25	High-Density SNP Screening of the Major Histocompatibility Complex in Systemic Lupus Erythematosus Demonstrates Strong Evidence for Independent Susceptibility Regions. <i>PLoS Genetics</i> , 2009, 5, e1000696.	1.5	109
26	Two-stage joint selection method to identify candidate markers from genome-wide association studies. <i>BMC Proceedings</i> , 2009, 3, S29.	1.8	8
27	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , 2009, 18, 3136-3144.	1.4	11
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29	Genotype determination for polymorphisms in linkage disequilibrium. <i>BMC Bioinformatics</i> , 2009, 10, 63.	1.2	7
30	A fast algorithm for genome-wide haplotype pattern mining. <i>BMC Bioinformatics</i> , 2009, 10, S74.	1.2	3
31	Association mapping by generalized linear regression with density-based haplotype clustering. <i>Genetic Epidemiology</i> , 2009, 33, 16-26.	0.6	6
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41	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009, 41, 35-46.	9.4	676
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57	The utility and predictive value of combinations of low penetrance genes for screening and risk prediction of colorectal cancer. <i>Human Genetics</i> , 2010, 128, 89-101.	1.8	40

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68	A haplotype inference algorithm for trios based on deterministic sampling. <i>BMC Genetics</i> , 2010, 11, 78.	2.7	5
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93	Case-Control Genome-Wide Association Study of Attention-Deficit/Hyperactivity Disorder. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2010, 49, 906-920.	0.3	150

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133	Population-Genetic Properties of Differentiated Human Copy-Number Polymorphisms. American Journal of Human Genetics, 2011, 88, 317-332.	2.6	89
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148	Identification of a functional rare variant in autism using genome-wide screen for monoallelic expression. Human Molecular Genetics, 2011, 20, 3632-3641.	1.4	69
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165	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	1.5	275
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995	Genetic structure, divergence and admixture of Han Chinese, Japanese and Korean populations. <i>Hereditas</i> , 2018, 155, 19.	0.5	90
996	Exploring the potential and limitations of genotyping-by-sequencing for SNP discovery and genotyping in tetraploid potato. <i>Genome</i> , 2018, 61, 449-456.	0.9	31
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998	Genomic investigation of porcine periweaning failure to thrive syndrome (PFTS). <i>Veterinary Record</i> , 2018, 183, 95-95.	0.2	4
999	Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982.	1.6	14
1000	Selection on Expected Maximum Haploid Breeding Values Can Increase Genetic Gain in Recurrent Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1173-1181.	0.8	42
1001	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. <i>Bioinformatics</i> , 2018, 34, 2781-2787.	1.8	217
1002	Genomic Prediction and Association Mapping of Curd-Related Traits in Gene Bank Accessions of Cauliflower. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 707-718.	0.8	29



#	ARTICLE	IF	CITATIONS
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1005	Genome-Wide Analysis of SNPs Is Consistent with No Domestic Dog Ancestry in the Endangered Mexican Wolf ( <i>Canis lupus baileyi</i> ). <i>Journal of Heredity</i> , 2018, 109, 372-383.	1.0	16
1006	Recent progress in alfalfa ( <i>Medicago sativa</i> L.) genomics and genomic selection. <i>Crop Journal</i> , 2018, 6, 565-575.	2.3	46
1007	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa. <i>Translational Psychiatry</i> , 2018, 8, 35.	2.4	95
1008	Signatures of Selection on Standing Genetic Variation Underlie Athletic and Navigational Performance in Racing Pigeons. <i>Molecular Biology and Evolution</i> , 2018, 35, 1176-1189.	3.5	25
1009	Preselection statistics and Random Forest classification identify population informative single nucleotide polymorphisms in cosmopolitan and autochthonous cattle breeds. <i>Animal</i> , 2018, 12, 12-19.	1.3	25
1010	Genome-wide meta-analysis of cognitive empathy: heritability, and correlates with sex, neuropsychiatric conditions and cognition. <i>Molecular Psychiatry</i> , 2018, 23, 1402-1409.	4.1	102
1011	Genome-wide regression models considering general and specific combining ability predict hybrid performance in oilseed rape with similar accuracy regardless of trait architecture. <i>Theoretical and Applied Genetics</i> , 2018, 131, 299-317.	1.8	41
1012	Comprehensive description of genomewide nucleotide and structural variation in short-season soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 749-759.	4.1	46
1013	Deconvolution of multiple infections in <i>Plasmodium falciparum</i> from high throughput sequencing data. <i>Bioinformatics</i> , 2018, 34, 9-15.	1.8	64
1014	Common variants in <i>DLC1</i> locus are associated with non-syndromic cleft lip with or without cleft palate. <i>Clinical Genetics</i> , 2018, 93, 784-793.	1.0	35
1015	Deciphering signature of selection affecting beef quality traits in Angus cattle. <i>Genes and Genomics</i> , 2018, 40, 63-75.	0.5	27
1016	Relevance of genetic relationship in GWAS and genomic prediction. <i>Journal of Applied Genetics</i> , 2018, 59, 1-8.	1.0	14
1017	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
1018	Association of Rare Predicted Loss-of-Function Variants in Cellular Pathways with Sub-Phenotypes in Age-Related Macular Degeneration. <i>Ophthalmology</i> , 2018, 125, 398-406.	2.5	12
1019	Heritable genotype contrast mining reveals novel gene associations specific to autism subgroups. <i>Journal of Biomedical Informatics</i> , 2018, 77, 50-61.	2.5	15
1020	A whole genome sequence association study for puberty in a large Duroc × Erhualian F2 population. <i>Animal Genetics</i> , 2018, 49, 29-35.	0.6	11

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1022	Which Individuals To Choose To Update the Reference Population? Minimizing the Loss of Genetic Diversity in Animal Genomic Selection Programs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 113-121.	0.8	18
1023	The cAMP responsive element-binding (CREB)-1 gene increases risk of major psychiatric disorders. <i>Molecular Psychiatry</i> , 2018, 23, 1957-1967.	4.1	38
1024	A germ-line deletion of APOBEC3B does not contribute to subtype-specific childhood acute lymphoblastic leukemia etiology. <i>Haematologica</i> , 2018, 103, e29-e31.	1.7	1
1025	Comprehensive Assessment of Genotype Imputation Performance. <i>Human Heredity</i> , 2018, 83, 107-116.	0.4	56
1026	Deflated preconditioned conjugate gradient method for solving single-step BLUP models efficiently. <i>Genetics Selection Evolution</i> , 2018, 50, 51.	1.2	18
1027	Parentage assignment with genotyping-by-sequencing data. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 102-112.	0.8	23
1028	Genome-wide detection of selective signatures in a Duroc pig population. <i>Journal of Integrative Agriculture</i> , 2018, 17, 2528-2535.	1.7	14
1029	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
1030	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3255-3267.	0.8	36
1031	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018, 9, 4674.	5.8	33
1032	Introgression of Chinese haplotypes contributed to the improvement of Danish Duroc pigs. <i>Evolutionary Applications</i> , 2019, 12, 292-300.	1.5	5
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1035	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , 2018, 50, 58.	1.2	87
1036	Genome-Wide Association Studies Reveal Genomic Regions Associated With the Response of Wheat ( <i>Triticum aestivum</i> L.) to Mycorrhizae Under Drought Stress Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1728.	1.7	48
1037	Accurate and adaptive imputation of summary statistics in mixed-ethnicity cohorts. <i>Bioinformatics</i> , 2018, 34, i687-i696.	1.8	6
1038	Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. <i>Genetics Selection Evolution</i> , 2018, 50, 53.	1.2	146

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1040	HisCoM-GGI: Hierarchical structural component analysis of gene-gene interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840026.	0.3	10
1041	Hybrid peeling for fast and accurate calling, phasing, and imputation with sequence data of any coverage in pedigrees. <i>Genetics Selection Evolution</i> , 2018, 50, 67.	1.2	46
1042	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0
1043	Genomic effects of population collapse in a critically endangered ironwood tree <i>Ostrya rehderiana</i> . <i>Nature Communications</i> , 2018, 9, 5449.	5.8	79
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1045	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. <i>American Journal of Human Genetics</i> , 2018, 103, 918-929.	2.6	38
1046	Genome wide association analysis in a mouse advanced intercross line. <i>Nature Communications</i> , 2018, 9, 5162.	5.8	47
1047	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. <i>Genetics</i> , 2018, 210, 1185-1196.	1.2	18
1048	Genetic Variation in Coat Colour Genes MC1R and ASIP Provides Insights Into Domestication and Management of South American Camelids. <i>Frontiers in Genetics</i> , 2018, 9, 487.	1.1	31
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1051	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. <i>Nature Communications</i> , 2018, 9, 3945.	5.8	31
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1054	Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. <i>Journal of Dairy Science</i> , 2018, 101, 11004-11019.	1.4	54
1055	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018, 175, 848-858.e6.	13.5	37
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1062	User considerations in assessing pharmacogenomic tests and their clinical support tools. Npj Genomic Medicine, 2018, 3, 26.	1.7	38
1063	Draft genome sequence of wild <i>Prunus yedoensis</i> reveals massive inter-specific hybridization between sympatric flowering cherries. Genome Biology, 2018, 19, 127.	3.8	89
1064	HSP90 as a global genetic modifier for male genital morphology in <i>Drosophila melanogaster</i> . Evolution; International Journal of Organic Evolution, 2018, 72, 2419-2434.	1.1	5
1065	Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. PLoS Genetics, 2018, 14, e1007661.	1.5	39
1066	Sequence-guided approach to genotyping plant clones and species using polymorphic NB-ARC-related genes. Plant Molecular Biology, 2018, 98, 219-231.	2.0	8
1067	A sorghum <i>&lt;sc&gt;NAC&lt;/sc&gt;</i> gene is associated with variation in biomass properties and yield potential. Plant Direct, 2018, 2, e00070.	0.8	39
1068	Genotype Imputation from Large Reference Panels. Annual Review of Genomics and Human Genetics, 2018, 19, 73-96.	2.5	158
1069	TriPoly: haplotype estimation for polyploids using sequencing data of related individuals. Bioinformatics, 2018, 34, 3864-3872.	1.8	28
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1072	Selection and environmental adaptation along a path to speciation in the Tibetan frog <i>&lt;i&gt;Nanorana parkeri&lt;/i&gt;</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5056-E5065.	3.3	49
1073	An intersection network based on combining SNP coassociation and RNA coexpression networks for feed utilization traits in Japanese Black cattle1. Journal of Animal Science, 2018, 96, 2553-2566.	0.2	11
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1078	Comparison of phasing strategies for whole human genomes. <i>PLoS Genetics</i> , 2018, 14, e1007308.	1.5	118
1079	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6526-E6535.	3.3	115
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1085	Exploring Cuba's population structure and demographic history using genome-wide data. <i>Scientific Reports</i> , 2018, 8, 11422.	1.6	31
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1088	Identification of recombination events in outbred species with next-generation sequencing data. <i>BMC Genomics</i> , 2018, 19, 398.	1.2	5
1089	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
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1097	Identification on novel locus of dairy traits of Kazakh horse in Xinjiang. <i>Gene</i> , 2018, 677, 105-110.	1.0	16
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1103	Genome-wide scan reveals population stratification and footprints of recent selection in Nelore cattle. <i>Genetics Selection Evolution</i> , 2018, 50, 22.	1.2	23
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1106	Adaptation of <i>S. cerevisiae</i> to Fermented Food Environments Reveals Remarkable Genome Plasticity and the Footprints of Domestication. <i>Molecular Biology and Evolution</i> , 2018, 35, 1712-1727.	3.5	214
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1108	The peopling of South America and the trans-Andean gene flow of the first settlers. <i>Genome Research</i> , 2018, 28, 767-779.	2.4	59
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1111	Weighted single-step GWAS and gene network analysis reveal new candidate genes for semen traits in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 40.	1.2	49
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1117	Advances in understanding the genetic basis of diabetic kidney disease. <i>Acta Diabetologica</i> , 2018, 55, 1093-1104.	1.2	16
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1123	Polymorphism analysis in genes associated with meat tenderness in Nelore cattle. <i>Meta Gene</i> , 2018, 18, 73-78.	0.3	3
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1127	A model selection approach for multiple sequence segmentation and dimensionality reduction. <i>Journal of Multivariate Analysis</i> , 2018, 167, 319-330.	0.5	3
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1130	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. <i>Science</i> , 2018, 360, 1355-1358.	6.0	234

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1133	<i>Gene Mapping.</i> , 2019, , 242-250.		3
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1135	<i>Population Analysis of Pharmacogenetic Polymorphisms.</i> , 2019, , 379-387.		0
1136	Gene hunting with hidden Markov model knockoffs. <i>Biometrika</i> , 2019, 106, 1-18.	1.3	78
1137	Demography and rapid local adaptation shape Creole cattle genome diversity in the tropics. <i>Evolutionary Applications</i> , 2019, 12, 105-122.	1.5	41
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1148	Forensic genealogy—A comparison of methods to infer distant relationships based on dense SNP data. <i>Forensic Science International: Genetics</i> , 2019, 42, 113-124.	1.6	40
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1157	Genome-wide association studies for the number of animals born alive and dead in duroc pigs. Theriogenology, 2019, 139, 36-42.	0.9	25
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1173	Genome-Wide Association Analyses of Equine Metabolic Syndrome Phenotypes in Welsh Ponies and Morgan Horses. <i>Genes</i> , 2019, 10, 893.	1.0	10
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1177	Weighted Single-Step Genome-Wide Association Study of Semen Traits in Holstein Bulls of China. <i>Frontiers in Genetics</i> , 2019, 10, 1053.	1.1	20
1178	Identification of Climate and Genetic Factors That Control Fat Content and Fatty Acid Composition of <i>Theobroma cacao</i> L. Beans. <i>Frontiers in Plant Science</i> , 2019, 10, 1159.	1.7	19
1179	Landscape of Loci and Candidate Genes for Muscle Fatty Acid Composition in Pigs Revealed by Multiple Population Association Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1067.	1.1	7
1180	Oxamniquine resistance alleles are widespread in Old World <i>Schistosoma mansoni</i> and predate drug deployment. <i>PLoS Pathogens</i> , 2019, 15, e1007881.	2.1	28
1181	Network-Assisted Neural Adaptive Naked-Eye 3D Video Streaming Over Wireless Networks. <i>IEEE Access</i> , 2019, 7, 141363-141373.	2.6	3
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1185	Accuracies of genomic prediction for twenty economically important traits in Chinese Simmental beef cattle. <i>Animal Genetics</i> , 2019, 50, 634-643.	0.6	20
1186	Signatures of adaptive divergence among populations of an avian species of conservation concern. <i>Evolutionary Applications</i> , 2019, 12, 1661-1677.	1.5	9

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1206	Evaluation of Genomic Prediction for PasmO Resistance in Flax. <i>International Journal of Molecular Sciences</i> , 2019, 20, 359.	1.8	45
1207	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
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1214	Genome sequencing analysis identifies Epstein-Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. <i>Nature Genetics</i> , 2019, 51, 1131-1136.	9.4	133
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1218	Within-family genomic selection in rubber tree ( <i>Hevea brasiliensis</i> ) increases genetic gain for rubber production. <i>Industrial Crops and Products</i> , 2019, 138, 111464.	2.5	53
1219	Application of image-based phenotyping tools to identify QTL for in-field winter survival of winter wheat ( <i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2591-2604.	1.8	16
1220	Combined analysis of keratinocyte cancers identifies novel genome-wide loci. <i>Human Molecular Genetics</i> , 2019, 28, 3148-3160.	1.4	46
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1225	Exploring the performance of genomic prediction models for soybean yield using different validation approaches. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	12
1226	Sequence imputation from low density single nucleotide polymorphism panel in a black poplar breeding population. <i>BMC Genomics</i> , 2019, 20, 302.	1.2	6
1227	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. <i>Genome Biology</i> , 2019, 20, 79.	3.8	81
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1230	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , 2019, 212, 305-316.	1.2	19
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1233	Loss of function mutations in essential genes cause embryonic lethality in pigs. <i>PLoS Genetics</i> , 2019, 15, e1008055.	1.5	46
1234	Rapid Communication: Genome-wide association analyses identify loci associated with colostrum production in Jersey cattle. <i>Journal of Animal Science</i> , 2019, 97, 1117-1123.	0.2	3
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1236	A gene-based recessive diplotype exome scan discovers <i>FGF6</i> , a novel hepcidin-regulating iron-metabolism gene. <i>Blood</i> , 2019, 133, 1888-1898.	0.6	14
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1240	Fine-scale haplotype mapping of <i>MUT</i> , <i>AACS</i> , <i>SLC6A15</i> and <i>PRKCA</i> genes indicates association with insulin resistance of metabolic syndrome and relationship with branched chain amino acid metabolism or regulation. <i>PLoS ONE</i> , 2019, 14, e0214122.	1.1	12

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1245	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1897-1908.	1.8	28
1246	Genomic Prediction using Existing Historical Data Contributing to Selection in Biparental Populations: A Study of Kernel Oil in Maize. <i>Plant Genome</i> , 2019, 12, 180025.	1.6	16
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1249	Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. <i>Genome Research</i> , 2019, 29, 848-856.	2.4	27
1250	Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. <i>Nature Communications</i> , 2019, 10, 1489.	5.8	220
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1253	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
1254	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.1	2
1255	Evaluation on the genomic selection in <i>Litopenaeus vannamei</i> for the resistance against <i>Vibrio parahaemolyticus</i> . <i>Aquaculture</i> , 2019, 505, 212-216.	1.7	34
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1258	Quantitative trait loci mapping in hybrids between Dent and Flint maize multiparental populations reveals group-specific QTL for silage quality traits with variable pleiotropic effects on yield. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1523-1542.	1.8	12

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1266	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4166-4175.	3.3	40
1267	Genome-Wide Association Study of Resistance to <i>Xanthomonas gardneri</i> in the USDA Pepper ( <i>Capsicum</i> ) Collection. <i>Phytopathology</i> , 2019, 109, 1217-1225.	1.1	10
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1270	Genome-wide Significance Thresholds for Admixture Mapping Studies. <i>American Journal of Human Genetics</i> , 2019, 104, 454-465.	2.6	25
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1282	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 62.	1.2	23
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1284	Accurate, scalable and integrative haplotype estimation. <i>Nature Communications</i> , 2019, 10, 5436.	5.8	336
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1286	Genome-Wide Association Study of Meat Quality Traits in Hanwoo Beef Cattle Using Imputed Whole-Genome Sequence Data. <i>Frontiers in Genetics</i> , 2019, 10, 1235.	1.1	30
1287	Characterization and quantitative trait locus mapping of late-flowering from a Thai soybean cultivar introduced into a photoperiod-insensitive genetic background. <i>PLoS ONE</i> , 2019, 14, e0226116.	1.1	20
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1290	Identification of Candidate Signature Genes and Key Regulators Associated With Trypanotolerance in the Sheko Breed. <i>Frontiers in Genetics</i> , 2019, 10, 1095.	1.1	18
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1292	Very low-depth whole-genome sequencing in complex trait association studies. <i>Bioinformatics</i> , 2019, 35, 2555-2561.	1.8	68
1293	Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. <i>Aquaculture</i> , 2019, 503, 225-230.	1.7	21
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1298	Chromosomal inversions associated with environmental adaptation in honeybees. <i>Molecular Ecology</i> , 2019, 28, 1358-1374.	2.0	50
1299	Genetic association and differential expression of PITX2 with acute appendicitis. <i>Human Genetics</i> , 2019, 138, 37-47.	1.8	14
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1301	Genomic dissection of pod shattering in common bean: mutations at non-orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. <i>Plant Journal</i> , 2019, 97, 693-714.	2.8	54
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1303	Genotyping-by-Sequencing on the Ion Torrent Platform in Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 233-252.	0.4	27
1304	Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. <i>Genome Research</i> , 2019, 29, 125-134.	2.4	16
1305	Patterns of genetic differentiation in Colorado potato beetle correlate with contemporary, not historic, potato land cover. <i>Evolutionary Applications</i> , 2019, 12, 804-814.	1.5	14
1306	Combining population genomics and forward simulations to investigate stocking impacts: A case study of Muskellunge ( <i>Esox masquinongy</i> ) from the St. Lawrence River basin. <i>Evolutionary Applications</i> , 2019, 12, 902-922.	1.5	13
1307	Impact of polymorphic transposable elements on linkage disequilibrium along chromosomes. <i>Molecular Ecology</i> , 2019, 28, 1550-1562.	2.0	12
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1309	QTL Mapping Identifies Novel Source of Resistance to Fusarium Wilt Race 1 in <i>Citrullus amarus</i> . <i>Plant Disease</i> , 2019, 103, 984-989.	0.7	16
1310	Genetic diversity patterns and domestication origin of soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1179-1193.	1.8	44
1311	Prediction of genetic value for sweet cherry fruit maturity among environments using a 6K SNP array. <i>Horticulture Research</i> , 2019, 6, 6.	2.9	25
1312	Off the street phasing (OTSP): no hassle haplotype phasing for molecular PGD applications. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 727-739.	1.2	2
1313	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

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1315	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid <i>Pseudocrenilabrus philander</i> . Genome Biology and Evolution, 2019, 11, 439-458.	1.1	26
1316	Complex Structural Variant Associated with Non-syndromic Canine Retinal Degeneration. G3: Genes, Genomes, Genetics, 2019, 9, 425-437.	0.8	13
1317	Context-specific Genomic Selection Strategies Outperform Phenotypic Selection for Soybean Quantitative Traits in the Progeny Row Stage. Crop Science, 2019, 59, 54-67.	0.8	15
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1324	Statistical methods for genome-wide association studies. Seminars in Cancer Biology, 2019, 55, 53-60.	4.3	59
1325	Pathway-based polygene risk for severe depression implicates drug metabolism in CONVERGE. Psychological Medicine, 2020, 50, 793-798.	2.7	3
1326	A Novel Model to Explain Extreme Feather Pecking Behavior in Laying Hens. Behavior Genetics, 2020, 50, 41-50.	1.4	19
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1328	Inference of differential gene regulatory networks based on gene expression and genetic perturbation data. Bioinformatics, 2020, 36, 197-204.	1.8	15
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1330	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. Molecular Biology and Evolution, 2020, 37, 134-148.	3.5	23
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1333	Exploratory Data Mining for Subgroup Cohort Discoveries and Prioritization. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 1456-1468.	3.9	12
1334	Leveraging whole genome sequencing data for demographic inference with approximate Bayesian computation. <i>Molecular Ecology Resources</i> , 2020, 20, 125-139.	2.2	14
1335	Twin introductions by independent invader mussel lineages are both associated with recent admixture with a native congener in Australia. <i>Evolutionary Applications</i> , 2020, 13, 515-532.	1.5	43
1336	Optical dispersion and bandgap of pure and Mn-doped $0.92\text{Na}_{0.5}\text{Bi}_{0.5}\text{TiO}_3 \cdot 0.08\text{K}_{0.5}\text{Bi}_{0.5}\text{TiO}_3$ lead-free single crystals. <i>Journal of the American Ceramic Society</i> , 2020, 103, 1241-1247.	1.2	10
1337	Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 27.	1.2	47
1338	A shared genetic basis of mimicry across swallowtail butterflies points to ancestral co-option of doublesex. <i>Nature Communications</i> , 2020, 11, 6.	5.8	55
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1342	Convergent genomic signatures of high-altitude adaptation among domestic mammals. <i>National Science Review</i> , 2020, 7, 952-963.	4.6	52
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1346	Genome-wide association study identifies genomic loci associated with flight reaction in cattle. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 477-485.	0.8	6
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1348	Construction of a high-density genetic map with whole genome sequencing in <i>Nicotiana tabacum</i> L. <i>Genomics</i> , 2020, 112, 2028-2033.	1.3	14
1349	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

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1351	Selection signatures of Fuzhong Buffalo based on whole-genome sequences. <i>BMC Genomics</i> , 2020, 21, 674.	1.2	12
1352	A Survey of Rare Epigenetic Variation in 23,116 Human Genomes Identifies Disease-Relevant Epivariations and CGG Expansions. <i>American Journal of Human Genetics</i> , 2020, 107, 654-669.	2.6	40
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1354	Genetic variation associated with PPO-inhibiting herbicide tolerance in sorghum. <i>PLoS ONE</i> , 2020, 15, e0233254.	1.1	4
1355	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
1356	Genome-wide association study (GWAS) reveals genetic basis of ear-related traits in maize. <i>Euphytica</i> , 2020, 216, 1.	0.6	9
1357	Whole genome sequencing of Plasmodium vivax isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008234.	1.3	25
1358	Assessment of Genetic Diversity in Azerbaijani Buffalo Population in Iran Based on Runs of Homozygosity Stretches. <i>Russian Journal of Genetics</i> , 2020, 56, 1224-1231.	0.2	0
1359	Resequencing of 145 Landmark Cultivars Reveals Asymmetric Sub-genome Selection and Strong Founder Genotype Effects on Wheat Breeding in China. <i>Molecular Plant</i> , 2020, 13, 1733-1751.	3.9	129
1360	Genomic diversity revealed by whole-genome sequencing in three Danish commercial pig breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	9
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1363	The accuracy of different strategies for building training sets for genomic predictions in segregating soybean populations. <i>Crop Science</i> , 2020, 60, 3115-3126.	0.8	7
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1366	Genetic architecture of individual variation in recombination rate on the X chromosome in cattle. <i>Heredity</i> , 2020, 125, 304-316.	1.2	10
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1369	Genomic Characterization of the Istrian Shorthaired Hound. <i>Animals</i> , 2020, 10, 2013.	1.0	2
1370	Attacks on genetic privacy via uploads to genealogical databases. <i>ELife</i> , 2020, 9, .	2.8	27
1371	Novel haplotypes responsible for prenatal death in Nordic Red and Danish Jersey cattle. <i>Journal of Dairy Science</i> , 2020, 103, 4570-4578.	1.4	12
1372	Periostin Circulating Levels and Genetic Variants in Patients with Non-Alcoholic Fatty Liver Disease. <i>Diagnostics</i> , 2020, 10, 1003.	1.3	0
1373	A CNTNAP1 Missense Variant Is Associated with Canine Laryngeal Paralysis and Polyneuropathy. <i>Genes</i> , 2020, 11, 1426.	1.0	9
1374	The apple REFPOPâ€”a reference population for genomics-assisted breeding in apple. <i>Horticulture Research</i> , 2020, 7, 189.	2.9	37
1375	Performances of Adaptive MultiBLUP, Bayesian regressions, and weighted-GBLUP approaches for genomic predictions in Belgian Blue beef cattle. <i>BMC Genomics</i> , 2020, 21, 545.	1.2	9
1376	An integrative analysis of genome-wide association study and regulatory SNP annotation datasets identified candidate genes for bipolar disorder. <i>International Journal of Bipolar Disorders</i> , 2020, 8, 6.	0.8	5
1377	Whole genome re-sequencing reveals recent signatures of selection in three strains of farmed Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>Scientific Reports</i> , 2020, 10, 11514.	1.6	34
1378	A general framework for integrative analysis of incomplete multiomics data. <i>Genetic Epidemiology</i> , 2020, 44, 646-664.	0.6	9
1379	The Origin and Spread of Locally Adaptive Seasonal Camouflage in Snowshoe Hares. <i>American Naturalist</i> , 2020, 196, 316-332.	1.0	29
1380	Genome Resequencing, Improvement of Variant Calling, and Population Genomic Analyses Provide Insights into the Seedlessness in the Genus <i>Vitis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3365-3377.	0.8	6
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1383	Genomic Breed Composition of Selection Signatures in Brangus Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 710.	1.1	21
1384	Identification of Ear Morphology Genes in Maize ( <i>Zea mays</i> L.) Using Selective Sweeps and Association Mapping. <i>Frontiers in Genetics</i> , 2020, 11, 747.	1.1	10
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1387	Long term effects of outbreeding: experimental founding of island population eliminates malformations and improves hatching success in sand lizards. <i>Biological Conservation</i> , 2020, 249, 108710.	1.9	4
1388	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. <i>Nature Communications</i> , 2020, 11, 3519.	5.8	213
1389	Genomic insights into speciation history and local adaptation of an alpine aspen in the Qinghai-Tibet Plateau and adjacent highlands. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1220-1231.	1.6	20
1390	ddRAD-seq derived genome-wide SNPs, high density linkage map and QTLs for fruit quality traits in strawberry ( <i>Fragaria x ananassa</i> ). <i>3 Biotech</i> , 2020, 10, 353.	1.1	4
1391	Genomic diversity in pearl millet inbred lines derived from landraces and improved varieties. <i>BMC Genomics</i> , 2020, 21, 469.	1.2	12
1392	Selective sweep analysis reveals extensive parallel selection traits between large white and Duroc pigs. <i>Evolutionary Applications</i> , 2020, 13, 2807-2820.	1.5	14
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1395	A Genomic Study of Myxomatous Mitral Valve Disease in Cavalier King Charles Spaniels. <i>Animals</i> , 2020, 10, 1895.	1.0	4
1396	A complex phenotype in salmon controlled by a simple change in migratory timing. <i>Science</i> , 2020, 370, 609-613.	6.0	65
1397	Local ancestry inference provides insight into Tilapia breeding programmes. <i>Scientific Reports</i> , 2020, 10, 18613.	1.6	3
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1399	Draft Genomes of <i>Amaranthus tuberculatus</i> , <i>Amaranthus hybridus</i> , and <i>Amaranthus palmeri</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1988-1993.	1.1	51
1400	Assessment of the potential role of natural selection in type 2 diabetes and related traits across human continental ancestry groups: comparison of phenotypic with genotypic divergence. <i>Diabetologia</i> , 2020, 63, 2616-2627.	2.9	2
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1402	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. <i>Nature Communications</i> , 2020, 11, 4739.	5.8	50
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1405	Identity by descent analysis identifies founder events and links SOD1 familial and sporadic ALS cases. <i>Npj Genomic Medicine</i> , 2020, 5, 32.	1.7	20
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1409	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
1410	Evolution of strong reproductive isolation in plants: broad-scale patterns and lessons from a perennial model group. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190544.	1.8	16
1411	Identification of loci controlling mineral element concentration in soybean seeds. <i>BMC Plant Biology</i> , 2020, 20, 419.	1.6	12
1412	Genome-Wide Detection of Selection Signatures in Duroc Revealed Candidate Genes Relating to Growth and Meat Quality. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3765-3773.	0.8	15
1413	Inferring the ancestry of parents and grandparents from genetic data. <i>PLoS Computational Biology</i> , 2020, 16, e1008065.	1.5	9
1414	A systematic comparison of pharmacogene star allele calling bioinformatics algorithms: a focus on CYP2D6 genotyping. <i>Npj Genomic Medicine</i> , 2020, 5, 30.	1.7	35
1415	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3741-3749.	0.8	16
1416	Gene reuse facilitates rapid radiation and independent adaptation to diverse habitats in the Asian honeybee. <i>Science Advances</i> , 2020, 6, .	4.7	42
1418	Genome-wide association identifies several QTLs controlling cysteine and methionine content in soybean seed including some promising candidate genes. <i>Scientific Reports</i> , 2020, 10, 21812.	1.6	12
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1420	Candidate Genetic Modifiers for RPGR Retinal Degeneration. , 2020, 61, 20.		7
1421	Improving the accuracy of genomic evaluation for linear body measurement traits using single-step genomic best linear unbiased prediction in Hanwoo beef cattle. <i>BMC Genetics</i> , 2020, 21, 144.	2.7	9
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1424	Probabilistic Estimation of Identity by Descent Segment Endpoints and Detection of Recent Selection. <i>American Journal of Human Genetics</i> , 2020, 107, 895-910.	2.6	22
1425	Whole genome variants across 57 pig breeds enable comprehensive identification of genetic signatures that underlie breed features. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 115.	2.1	14
1426	Technologies for Pharmacogenomics: A Review. <i>Genes</i> , 2020, 11, 1456.	1.0	37
1427	Steelhead ( <i>Oncorhynchus mykiss</i> ) lineages and sexes show variable patterns of association of adult migration timing and age-at-maturity traits with two genomic regions. <i>Evolutionary Applications</i> , 2020, 13, 2836-2856.	1.5	19
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1429	A Review of Integrative Imputation for Multi-Omics Datasets. <i>Frontiers in Genetics</i> , 2020, 11, 570255.	1.1	57
1430	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. <i>Cancers</i> , 2020, 12, 3254.	1.7	16
1431	Assessment of Imputation from Low-Pass Sequencing to Predict Merit of Beef Steers. <i>Genes</i> , 2020, 11, 1312.	1.0	55
1432	Identification of Genetic Susceptibility Factors Associated with Canine Gastric Dilatation-Volvulus. <i>Genes</i> , 2020, 11, 1313.	1.0	6
1433	An Out-of-Patagonia migration explains the worldwide diversity and distribution of <i>Saccharomyces eubayanus</i> lineages. <i>PLoS Genetics</i> , 2020, 16, e1008777.	1.5	34
1434	Genome-wide association study of semen volume, sperm concentration, testis size, and plasma inhibin B levels. <i>Journal of Human Genetics</i> , 2020, 65, 683-691.	1.1	9
1435	Genome-Wide Association Study of Muscle Glycogen in Jingxing Yellow Chicken. <i>Genes</i> , 2020, 11, 497.	1.0	16
1436	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. <i>Scientific Reports</i> , 2020, 10, 8165.	1.6	12
1437	Complement genes contribute sex-biased vulnerability in diverse disorders. <i>Nature</i> , 2020, 582, 577-581.	13.7	158
1438	Structural equation modeling for investigating multi-trait genetic architecture of udder health in dairy cattle. <i>Scientific Reports</i> , 2020, 10, 7751.	1.6	18
1439	Genome-wide association mapping of <i>Sclerotinia sclerotiorum</i> resistance in soybean using whole-genome resequencing data. <i>BMC Plant Biology</i> , 2020, 20, 195.	1.6	25
1440	Genomic history and ecology of the geographic spread of rice. <i>Nature Plants</i> , 2020, 6, 492-502.	4.7	143



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1442	Prospective avenues for human population genomics and disease mapping in southern Africa. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1079-1089.	1.0	7
1443	A Fast and Simple Method for Detecting Identity-by-Descent Segments in Large-Scale Data. <i>American Journal of Human Genetics</i> , 2020, 106, 426-437.	2.6	89
1444	Rapid, Phase-free Detection of Long Identity-by-Descent Segments Enables Effective Relationship Classification. <i>American Journal of Human Genetics</i> , 2020, 106, 453-466.	2.6	42
1445	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
1446	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 962-972.	2.5	11
1447	Linkage Disequilibrium-Based Inference of Genome Homology and Chromosomal Rearrangements Between Species. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2327-2343.	0.8	4
1448	Population-Specific Recombination Maps from Segments of Identity by Descent. <i>American Journal of Human Genetics</i> , 2020, 107, 137-148.	2.6	24
1449	Identification of Genomic Characteristics and Selective Signals in a Duâ€™an Goat Flock. <i>Animals</i> , 2020, 10, 994.	1.0	6
1450	Genomic predictions improve clonal selection in oil palm ( <i>Elaeis guineensis</i> Jacq.) hybrids. <i>Plant Science</i> , 2020, 299, 110547.	1.7	10
1451	Genome-wide association study of bone mineral density trait among three pig breeds. <i>Animal</i> , 2020, 14, 2443-2451.	1.3	5
1452	A dynastic elite in monumental Neolithic society. <i>Nature</i> , 2020, 582, 384-388.	13.7	94
1453	IBDkin: fast estimation of kinship coefficients from identity by descent segments. <i>Bioinformatics</i> , 2020, 36, 4519-4520.	1.8	15
1454	Mining for Candidate Genes Controlling Secondary Growth of the Carrot Storage Root. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4263.	1.8	7
1455	BGVD: An Integrated Database for Bovine Sequencing Variations and Selective Signatures. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 186-193.	3.0	47
1456	Genealogical search using whole-genome genotype profiles. , 2020, , 51-94.		1
1457	Tracking human population structure through time from whole genome sequences. <i>PLoS Genetics</i> , 2020, 16, e1008552.	1.5	71
1458	Genome-Wide Association Study of Salinity Tolerance During Germination in Barley ( <i>Hordeum vulgare</i> ) TJ ETQq1 1 0.784314 rgBT /Over	1.7	79

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1460	Revisiting hybrid breeding designs using genomic predictions: simulations highlight the superiority of incomplete factorials between segregating families over topcross designs. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1995-2010.	1.8	20
1461	8q24 genetic variation and comprehensive haplotypes altering familial risk of prostate cancer. <i>Nature Communications</i> , 2020, 11, 1523.	5.8	10
1462	Diverse genetic mechanisms underlie worldwide convergent rice feralization. <i>Genome Biology</i> , 2020, 21, 70.	3.8	55
1463	Genome-Wide Association Study and Fine Mapping Reveals Candidate Genes for Birth Weight of Yorkshire and Landrace Pigs. <i>Frontiers in Genetics</i> , 2020, 11, 183.	1.1	11
1464	Equine recombination map updated to EquCab3.0. <i>Animal Genetics</i> , 2020, 51, 341-342.	0.6	5
1465	Genomic Prediction Accuracy of Seven Breeding Selection Traits Improved by QTL Identification in Flax. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1577.	1.8	21
1466	Insight into unique somitogenesis of yak ( <i>Bos grunniens</i> ) with one additional thoracic vertebra. <i>BMC Genomics</i> , 2020, 21, 201.	1.2	7
1467	Concordance rate between copy number variants detected using either high- or medium-density single nucleotide polymorphism genotype panels and the potential of imputing copy number variants from flanking high density single nucleotide polymorphism haplotypes in cattle. <i>BMC Genomics</i> , 2020, 21, 205.	1.2	8
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1472	Postadmixture Selection on Chileans Targets Haplotype Involved in Pigmentation, Thermogenesis and Immune Defense against Pathogens. <i>Genome Biology and Evolution</i> , 2020, 12, 1459-1470.	1.1	11
1473	Allele-specific expression is widespread in <i>Bos indicus</i> muscle and affects meat quality candidate genes. <i>Scientific Reports</i> , 2020, 10, 10204.	1.6	13
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1476	Toehold probe-based interrogation for haplotype phasing of long nucleic acid strands. <i>Analytical Methods</i> , 2020, 12, 4185-4190.	1.3	3

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1504	Genetic differentiation and intrinsic genomic features explain variation in recombination hotspots among cocoa tree populations. <i>BMC Genomics</i> , 2020, 21, 332.	1.2	14
1505	Genomic prediction enables early but low-intensity selection in soybean segregating progenies. <i>Crop Science</i> , 2020, 60, 1346-1361.	0.8	4
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1529	Genome-wide analyses reveal footprints of divergent selection and popping-related traits in CIMMYT's maize inbred lines. <i>Journal of Experimental Botany</i> , 2021, 72, 1307-1320.	2.4	11
1530	Association mapping and genomic selection for sorghum adaptation to tropical soils of Brazil in a sorghum multiparental random mating population. <i>Theoretical and Applied Genetics</i> , 2021, 134, 295-312.	1.8	9
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1539	Whole-genome resequencing reveals diversity and selective signals in Longlin goat. <i>Gene</i> , 2021, 771, 145371.	1.0	8
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1546	Detecting selected haplotype blocks in evolve and resequence experiments. <i>Molecular Ecology Resources</i> , 2021, 21, 93-109.	2.2	20
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1574	Genome-wide association studies for sperm traits in Assaf sheep breed. <i>Animal</i> , 2021, 15, 100065.	1.3	17
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1618	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. <i>Genes</i> , 2021, 12, 534.	1.0	3
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2558	Utility of Ugandan genomic selection cassava breeding populations for prediction of cassava viral disease resistance and yield in West African clones. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2559	Accurate genome-wide phasing from IBD data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	0
2560	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
2562	The genomic analysis of current-day North African populations reveals the existence of trans-Saharan migrations with different origins and dates. <i>Human Genetics</i> , 2023, 142, 305-320.	1.8	5
2563	Identification of crucial genes and metabolites regulating the eggshell brownness in chicken. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
2564	Dissection of the Pearl of Csaba pedigree identifies key genomic segments related to early ripening in grape. <i>Plant Physiology</i> , 2023, 191, 1153-1166.	2.3	1
2565	Exome sequencing of affected duos and trios uncovers PRUNE2 as a novel prostate cancer predisposition gene. <i>British Journal of Cancer</i> , 0, , .	2.9	2
2566	Genomic adaptation of Ethiopian indigenous cattle to high altitude. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
2567	On the origin and structure of haplotype blocks. <i>Molecular Ecology</i> , 2023, 32, 1441-1457.	2.0	9
2568	The role of genomic signatures of directional selection and demographic history in the population structure of a marine teleost with high gene flow. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
2569	The mutational dynamics of short tandem repeats in large, multigenerational families. <i>Genome Biology</i> , 2022, 23, .	3.8	10
2570	Chromosome-level genome sequence of the Genetically Improved Farmed Tilapia (GIFT, <i>Oreochromis</i> ) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 5	1.2	0
2571	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
2573	Genome-Wide Association Study Revealed the Effect of rs312715211 in ZNF652 Gene on Abdominal Fat Percentage of Chickens. <i>Biology</i> , 2022, 11, 1849.	1.3	1
2575	Plant Genomic Selection: a Concept That Uses Genomics Data in Plant Breeding. , 2022, , 190-204.		0
2576	Genetic architecture and evolution of color variation in American black bears. <i>Current Biology</i> , 2023, 33, 86-97.e10.	1.8	9
2577	A Pipeline for Phasing and Genotype Imputation on Mixed Human Data (Parents-Offspring Trios and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	0
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2579	Genome-wide screen of otosclerosis in population biobanks: 27 loci and shared associations with skeletal structure. <i>Nature Communications</i> , 2023, 14, .	5.8	2
2580	<i>MaLAdapt</i> Reveals Novel Targets of Adaptive Introgression From Neanderthals and Denisovans in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	7
2581	Genetic and ecological drivers of molt in a migratory bird. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
2582	Selection signature analysis and genome-wide divergence of South African Merino breeds from their founders. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
2583	Large-Scale Chromosomal Changes Lead to Genome-Level Expression Alterations, Environmental Adaptation, and Speciation in the Gayal ( <i>Bos frontalis</i> ). <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	5
2584	Genetic predictors of lifelong medication-use patterns in cardiometabolic diseases. <i>Nature Medicine</i> , 2023, 29, 209-218.	15.2	7
2585	Fast integration and accumulation of beneficial breeding alleles through an AB <sup>2</sup> NAMIC strategy in wheat. <i>Plant Communications</i> , 2023, 4, 100549.	3.6	5
2586	Genome-wide association study in a rat model of temperament identifies multiple loci for exploratory locomotion and anxiety-like traits. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
2587	653. Investigation on inheritance transmission modes using breeding values estimated from genomic or pedigree information. , 2022, , .		0
2588	192. Genetic diversity and population structure of Slovenian local breed DreÅ¾nica goat. , 2022, , .		0
2590	Genomic insight into the influence of selection, crossbreeding, and geography on population structure in poultry. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	2
2591	Analysis of dog breed diversity using a composite selection index. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
2592	An efficient exact algorithm for identifying hybrids using population genomic sequences. <i>Genetics</i> , 2023, 223, .	1.2	4
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2594	A 21-bp InDel in the promoter of <i>STP1</i> selected during tomato improvement accounts for soluble solid content in fruits. <i>Horticulture Research</i> , 2023, 10, .	2.9	3
2595	Comparing Methods to Select Candidates for Re-Genotyping to Impute Higher-Density Genotype Data in a Japanese Black Cattle Population: A Case Study. <i>Animals</i> , 2023, 13, 638.	1.0	1
2596	Genomic heritability and correlation between carcass traits in Japanese Black cattle evaluated under different ceilings of relatedness among individuals. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
2597	Structure and origin of Tuvan gene pool according to autosome SNP and Y-chromosome haplogroups. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2023, 27, 36-45.	0.4	1

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2599	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. <i>Nature Communications</i> , 2023, 14, .	5.8	8
2601	Genome-wide association study for growth-related traits in golden pompano ( <i>Trachinotus ovatus</i> ). <i>Aquaculture</i> , 2023, 572, 739549.	1.7	4
2602	Genomic evidence for adaptation to tuberculosis in the Andes before European contact. <i>IScience</i> , 2023, 26, 106034.	1.9	3
2603	Quantitative trait locus for calving traits on <i>Bos taurus</i> autosome 18 in Holstein cattle is embedded in a complex genomic region. <i>Journal of Dairy Science</i> , 2023, 106, 1925-1941.	1.4	1
2604	Identification of leaf rust resistance loci in a geographically diverse panel of wheat using genome-wide association analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
2606	Robust SNP-based prediction of rheumatoid arthritis through machine-learning-optimized polygenic risk score. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	5
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2608	A complex genomic architecture underlies reproductive isolation in a North American oriole hybrid zone. <i>Communications Biology</i> , 2023, 6, .	2.0	0
2609	105. Heritability of scurs in Wagyu and tropically adapted composite beef cattle. , 2022, , .		0
2610	189. Exploring genetic diversity and selection signatures in indigenous African cattle breeds. , 2022, , .		0
2611	273. Genomic evaluation for two-way crossbred performance in cattle. , 2022, , .		0
2612	536. Genetic regulation of ear size in Slovenian and Greek sheep breeds. , 2022, , .		0
2613	Development and characterization of a sorghum multi-parent advanced generation intercross (MAGIC) population for capturing diversity among seed parent gene pool. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
2614	651. Genomic prediction with non-additive genetic effects for carcass weight and beef marbling in Japanese Black cattle. , 2022, , .		0
2615	Intercross population study reveals that co-mutation of <i>mitfa</i> genes in two subgenomes induces red skin color in common carp ( <i>Cyprinus carpio wuyuanensis</i> ). <i>Zoological Research</i> , 2023, 44, 276-286.	0.9	0
2616	Improving Genomic Prediction Accuracy in the Chinese Holstein Population by Combining with the Nordic Holstein Reference Population. <i>Animals</i> , 2023, 13, 636.	1.0	1
2618	The idiosyncratic genome of Korean long-tailed chicken as a valuable genetic resource. <i>IScience</i> , 2023, 26, 106236.	1.9	0

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2620	An atlas of expression quantitative trait loci of microRNAs in longissimus muscle of eight-way crossbred pigs. <i>Journal of Genetics and Genomics</i> , 2023, 50, 398-409.	1.7	0
2621	New insights into trait introgression with the look-ahead intercrossing strategy. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	1
2622	The genetic and evolutionary basis of gene expression variation in East Africans. <i>Genome Biology</i> , 2023, 24, .	3.8	3
2623	Traces of Introgression from cAus into Tropical Japonica Observed in African Upland Rice Varieties. <i>Rice</i> , 2023, 16, .	1.7	1
2625	A Genetic Risk Score Distinguishes Different Types of Autoantibody-Mediated Membranous Nephropathy. <i>Glomerular Diseases</i> , 0, , 116-125.	0.2	0
2626	Three amphioxus reference genomes reveal gene and chromosome evolution of chordates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	11
2627	Limited Song Mixing Without Genomic Gene Flow in a Contact Zone Between Two Songbird Species. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
2628	Blocks identical by descent in the genomes of the indigenous population of Siberia demonstrate genetic links between populations. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2023, 27, 55-62.	0.4	0
2629	Relationship of the gene pool of the Khants with the peoples of Western Siberia, Cis-Urals and the Altai-Sayan Region according to the data on the polymorphism of autosomic locus and the Y-chromosome. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2023, 27, 46-54.	0.4	0
2631	Genome-wide association study reveals new <i>QTL</i> and functional candidate genes for the number of ribs and carcass length in pigs. <i>Animal Genetics</i> , 2023, 54, 435-445.	0.6	4
2632	The genomic characteristics affect phenotypic diversity from the perspective of genetic improvement of economic traits. <i>IScience</i> , 2023, 26, 106426.	1.9	3
2633	Natural disease history of a canine model of oligogenic <i>RPGRI1</i> -cone-rod dystrophy establishes variable effects of previously and newly mapped modifier loci. <i>Human Molecular Genetics</i> , 2023, 32, 2139-2151.	1.4	4
2634	Detection of Genetic Differences between Holstein and Iranian North-West Indigenous Hybrid Cattles using Genomic Data. <i>Research on Animal Production</i> , 2022, 13, 175-186.	0.2	0
2635	Identification of Genomic Signatures in Bullmastiff Dogs Using Composite Selection Signals Analysis of 23 Purebred Clades. <i>Animals</i> , 2023, 13, 1149.	1.0	1
2637	Genomic evaluation for two-way crossbred performance in cattle. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	0
2638	Integrative genomics analysis highlights functionally relevant genes for equine behaviour. <i>Animal Genetics</i> , 2023, 54, 457-469.	0.6	2
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2642	Genome-wide association study in two-row spring barley landraces identifies QTL associated with plantlets root system architecture traits in well-watered and osmotic stress conditions. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
2643	Genome-wide association study reveals that the IBSP locus affects ear size in cattle. <i>Heredity</i> , 0, , .	1.2	0
2644	Mating allocations in Holstein combining genomic information and linear programming optimization at the herd level. <i>Journal of Dairy Science</i> , 2023, 106, 3359-3375.	1.4	1
2645	Deep learning-based polygenic risk analysis for Alzheimerâ€™s disease prediction. <i>Communications Medicine</i> , 2023, 3, .	1.9	8
2646	Whole Genome Resequencing Reveals Genetic Diversity and Selection Signatures of Ethiopian Indigenous Cattle Adapted to Local Environments. <i>Diversity</i> , 2023, 15, 540.	0.7	5
2647	GWAS using low-pass whole genome sequence reveals a novel locus in canine congenital idiopathic megaesophagus. <i>Mammalian Genome</i> , 0, , .	1.0	0
2648	Genotyping, characterization, and imputation of known and novel CYP2A6 structural variants using SNP array data. <i>Journal of Human Genetics</i> , 2023, 68, 533-541.	1.1	1
2649	Potential of publicly available <i>Beta vulgaris</i> germplasm for sustainable sugarbeet improvement indicated by combining analysis of genetic diversity and historic resistance evaluation. <i>Crop Science</i> , 0, , .	0.8	0
2650	Ancient DNA from a lost Negev Highlands desert grape reveals a Late Antiquity wine lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
2652	Population Genomics Analysis with RAD, Reprised: Stacks 2. <i>Methods in Molecular Biology</i> , 2022, , 99-149.	0.4	14
2669	Embryonenbiopsien f¼r die genomische Selektion. , 2023, , 93-107.		0
2694	Tutorial: a statistical genetics guide to identifying HLA alleles driving complex disease. <i>Nature Protocols</i> , 2023, 18, 2625-2641.	5.5	5
2737	Computational Genomics Approaches for Livestock Improvement and Management. <i>Livestock Diseases and Management</i> , 2023, , 351-376.	0.5	0
2797	Associating CYP2A6 structural variants with ovarian and lung cancer risk in the UK Biobank: replication and extension. <i>European Journal of Human Genetics</i> , 0, , .	1.4	1
2810	Challenges in using genetic genealogy in forensics. , 2024, , 511-530.		0