

Fast model-based estimation of ancestry in unrelated individuals

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. <i>American Journal of Human Genetics</i> , 2010, 86, 661-673.	2.6	214
2	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	13.7	750
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4	New approaches to population stratification in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 459-463.	7.7	1,047
5	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001117.	1.5	123
6	Association of CR1, CLU and PICALM with Alzheimer's disease in a cohort of clinically characterized and neuropathologically verified individuals. <i>Human Molecular Genetics</i> , 2010, 19, 3295-3301.	1.4	223
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8	Genetic Ancestry in Lung-Function Predictions. <i>New England Journal of Medicine</i> , 2010, 363, 321-330.	13.9	230
9	Comparison of genome-wide variation between Malawians and African ancestry HapMap populations. <i>Journal of Human Genetics</i> , 2010, 55, 366-374.	1.1	13
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13	A world in a grain of sand: human history from genetic data. <i>Genome Biology</i> , 2011, 12, 234.	13.9	9
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16	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 245-274.	2.5	69
17	The Genetic Structure of the Swedish Population. <i>PLoS ONE</i> , 2011, 6, e22547.	1.1	67
18	Footprints of selection in the ancestral admixture of a New World Creole cattle breed. <i>Molecular Ecology</i> , 2011, 20, 3128-3143.	2.0	130

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21	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2011, 19, 995-1001.	1.4	59
22	Overview of techniques to account for confounding due to population stratification and cryptic relatedness in genomic data association analyses. <i>Heredity</i> , 2011, 106, 511-519.	1.2	70
23	Mathematical properties of $\langle \langle F \rangle \rangle$ admixed populations and their parental source populations. <i>Theoretical Population Biology</i> , 2011, 80, 208-216.	0.5	19
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38	Translational genomic medicine: common metabolic traits and ancestral components of Mexican Americans. <i>Journal of Medical Genetics</i> , 2012, 49, 545-546.	1.5	4
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88	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	1.2	142
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90	Genome-wide association study of shared components of reading disability and language impairment. <i>Genes, Brain and Behavior</i> , 2013, 12, 792-801.	1.1	95

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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1110	Polymorphisms in the TGFBI and IL2RA genes are associated with clinical forms of leprosy in Brazilian population. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e180274.	0.8	5
1111	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. Science, 2018, 362, 1309-1313.	6.0	172
1112	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. Genes, 2018, 9, 625.	1.0	16
1113	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. American Journal of Human Genetics, 2018, 103, 918-929.	2.6	38
1114	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. Plant Genome, 2018, 11, 170076.	1.6	26
1115	The evolutionary history of Southern Africa. Current Opinion in Genetics and Development, 2018, 53, 157-164.	1.5	10
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1118	Native ancestry is associated with optic neuritis and age of onset in hispanics with multiple sclerosis. Annals of Clinical and Translational Neurology, 2018, 5, 1362-1371.	1.7	20
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1124	Genomic analyses of human European diversity at the southwestern edge: isolation, African influence and disease associations in the Canary Islands. Molecular Biology and Evolution, 2018, 35, 3010-3026.	3.5	17
1125	A genomic Neolithic time transect of hunter-farmer admixture in central Poland. Scientific Reports, 2018, 8, 14879.	1.6	47
1126	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . Molecular Ecology, 2018, 27, 4397-4416.	2.0	160

#	ARTICLE	IF	CITATIONS
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1128	Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. <i>Genome Biology and Evolution</i> , 2018, 10, 2697-2708.	1.1	7
1129	Population structure, genetic diversity and selection signatures within seven indigenous Pakistani goat populations. <i>Animal Genetics</i> , 2018, 49, 592-604.	0.6	29
1130	Genomic African and Native American Ancestry and 15-Year Cognitive Trajectory: Bambui Study, Brazil. <i>Journal of the American Geriatrics Society</i> , 2018, 66, 1956-1962.	1.3	2
1131	Genome Wide Association Mapping of Grain and Straw Biomass Traits in the Rice Bengal and Assam Aus Panel (BAAP) Grown Under Alternate Wetting and Drying and Permanently Flooded Irrigation. <i>Frontiers in Plant Science</i> , 2018, 9, 1223.	1.7	41
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1134	Technical Advances and Challenges in Genome-Scale Analysis of Ancient DNA. <i>Population Genomics</i> , 2018, , 3-29.	0.2	2
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1137	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. <i>Science Advances</i> , 2018, 4, eaat4457.	4.7	76
1138	Inferring Population Structure and Admixture Proportions in Low-Depth NGS Data. <i>Genetics</i> , 2018, 210, 719-731.	1.2	426
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1144	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

#	ARTICLE	IF	CITATIONS
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1146	Genomic data recover previously undetectable fragmentation effects in an endangered amphibian. <i>Molecular Ecology</i> , 2018, 27, 4430-4443.	2.0	43
1147	Genetic Diversity Patterns and Heterosis Prediction Based on SSRs and SNPs in Hybrid Parents of Pearl Millet. <i>Crop Science</i> , 2018, 58, 2379-2390.	0.8	15
1148	Population genomic analyses of the chocolate tree, <i>Theobroma cacao</i> L., provide insights into its domestication process. <i>Communications Biology</i> , 2018, 1, 167.	2.0	73
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1151	Genetic diversities and population structures of four popular Myanmar local cattle breeds. <i>Animal Science Journal</i> , 2018, 89, 1648-1655.	0.6	7
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1153	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. <i>PLoS Genetics</i> , 2018, 14, e1007591.	1.5	23
1154	Human Population Genomics. <i>Computational Biology</i> , 2018, , 467-496.	0.1	0
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1161	Genomic characterization of Algerian Guelmoise cattle and their genetic relationship with other North African populations inferred from SNP genotyping arrays. <i>Livestock Science</i> , 2018, 217, 19-25.	0.6	12
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1165	Understanding 6th-century barbarian social organization and migration through paleogenomics. <i>Nature Communications</i> , 2018, 9, 3547.	5.8	111
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1222	Prediction of Cacao (<i>Theobroma cacao</i>) Resistance to <i>Moniliophthora</i> spp. Diseases via Genome-Wide Association Analysis and Genomic Selection. <i>Frontiers in Plant Science</i> , 2018, 9, 343.	1.7	43
1223	Association Study Reveals Novel Genes Related to Yield and Quality of Fruit in Cape Gooseberry (<i>Physalis peruviana</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 362.	1.7	12
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1267	Genome-wide scan reveals population stratification and footprints of recent selection in Nelore cattle. Genetics Selection Evolution, 2018, 50, 22.	1.2	23
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1275	Bioinformatics in Toxicology: Statistical Methods for Supervised Learning in High-Dimensional Omics Data. , 2018, , 447-472.		0
1276	Suitability of existing commercial single nucleotide polymorphism chips for genomic studies in <i>Bos indicus</i> cattle breeds and their <i>Bos taurus</i> crosses. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 432-441.	0.8	18
1277	An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2018, , 61-89.		0
1278	Genetic characterization of inbred lines from Shaan A and B groups for identifying loci associated with maize grain yield. <i>BMC Genetics</i> , 2018, 19, 63.	2.7	28
1279	Reduced-representation sequencing identifies small effective population sizes of <i>Anopheles gambiae</i> in the north-western Lake Victoria basin, Uganda. <i>Malaria Journal</i> , 2018, 17, 285.	0.8	7
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1283	Re-analysis of Whole Genome Sequence Data From 279 Ancient Eurasians Reveals Substantial Ancestral Heterogeneity. <i>Frontiers in Genetics</i> , 2018, 9, 268.	1.1	5
1284	Genome-wide SNP analysis unveils genetic structure and phylogeographic history of snow sheep (<i>Ovis nivicola</i>) populations inhabiting the Verkhoyansk Mountains and Minsky Ridge (northeastern Siberia). <i>Ecology and Evolution</i> , 2018, 8, 8000-8010.	0.8	9
1285	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , 2018, 7, .	3.3	55
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1287	Integrative Population and Physiological Genomics Reveals Mechanisms of Adaptation in Killifish. <i>Molecular Biology and Evolution</i> , 2018, 35, 2639-2653.	3.5	33
1288	Comparing SNP panels and statistical methods for estimating genomic breed composition of individual animals in ten cattle breeds. <i>BMC Genetics</i> , 2018, 19, 56.	2.7	27

#	ARTICLE	IF	CITATIONS
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1290	A tutorial on how not to over-interpret STRUCTURE and ADMIXTURE bar plots. <i>Nature Communications</i> , 2018, 9, 3258.	5.8	341
1291	Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation. <i>Nature Communications</i> , 2018, 9, 3336.	5.8	71
1292	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 433-456.	3.8	143
1293	Ancestry and genetic associations with bronchopulmonary dysplasia in preterm infants. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L858-L869.	1.3	24
1294	Genetic control of seed shattering during African rice domestication. <i>Nature Plants</i> , 2018, 4, 331-337.	4.7	55
1295	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018, 19, 505-517.	7.7	251
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1299	Demographic expansion and genetic load of the halophyte model plant <i>Eutrema salsugineum</i> . <i>Molecular Ecology</i> , 2018, 27, 2943-2955.	2.0	11
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1304	Genome-wide association studies suggest that APOL1-environment interactions more likely trigger kidney disease in African Americans with nondiabetic nephropathy than strong APOL1 "second gene" interactions. <i>Kidney International</i> , 2018, 94, 599-607.	2.6	58
1305	Analysis of 3800-year-old Yersinia pestis genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018, 9, 2234.	5.8	123
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1309	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. <i>PLoS Genetics</i> , 2018, 14, e1007329.	1.5	66
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1311	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018, 16, e2003703.	2.6	174
1312	Genetic diversity and relationships among six local cattle populations in semi-arid areas assessed by a bovine medium-density single nucleotide polymorphism data. <i>Animal</i> , 2019, 13, 8-14.	1.3	11
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1314	Variation within voltage-gated calcium channel genes and antipsychotic treatment response in a South African first episode schizophrenia cohort. <i>Pharmacogenomics Journal</i> , 2019, 19, 109-114.	0.9	7
1315	Target enrichment sequencing of 307 germplasm accessions identified ancestry of ancient and modern hybrids and signatures of adaptation and selection in sugarcane (<i>Saccharum</i> spp.), a "sweet" crop with "bitter" genomes. <i>Plant Biotechnology Journal</i> , 2019, 17, 488-498.	4.1	33
1316	<i>Genetics and Population Analysis.</i> , 2019, , 363-378.		0
1317	Domestication of cattle: Two or three events?. <i>Evolutionary Applications</i> , 2019, 12, 123-136.	1.5	80
1318	Phylogenomics of pike cichlids (Cichlidae: <i>Crenicichla</i>) of the <i>C. mandelburgeri</i> species complex: rapid ecological speciation in the Iguazú River and high endemism in the Middle Paraná basin. <i>Hydrobiologia</i> , 2019, 832, 355-375.	1.0	29
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1320	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. <i>PLoS ONE</i> , 2019, 14, e0220827.	1.1	14
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1323	Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India. <i>Nature Communications</i> , 2019, 10, 3670.	5.8	19
1324	Inferring the population structure of the Maghreb sheep breeds using a medium-density SNP chip. <i>Animal Genetics</i> , 2019, 50, 526-533.	0.6	12
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1328	Low genome-wide homozygosity in 11 Spanish ovine breeds. <i>Animal Genetics</i> , 2019, 50, 501-511.	0.6	8
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1330	Accurate ethnicity prediction from placental DNA methylation data. <i>Epigenetics and Chromatin</i> , 2019, 12, 51.	1.8	40
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1332	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17231-17238.	3.3	101
1333	The Genetic Architecture of Chronic Mountain Sickness in Peru. <i>Frontiers in Genetics</i> , 2019, 10, 690.	1.1	12
1336	Complex interplay of evolutionary forces shaping population genomic structure of invasive <i>Aedes albopictus</i> in southern Europe. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007554.	1.3	25
1337	Cranial deformation and genetic diversity in three adolescent male individuals from the Great Migration Period from Osijek, eastern Croatia. <i>PLoS ONE</i> , 2019, 14, e0216366.	1.1	13
1338	Ambient air pollution, asthma drug response, and telomere length in African American youth. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 839-845.e10.	1.5	24
1339	Mitochondrial SNP markers to monitor evolutionary lineage ancestry in <i>Apis mellifera</i> conservation programs. <i>Apidologie</i> , 2019, 50, 538-541.	0.9	3
1340	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019, 10, 3418.	5.8	26
1341	LEI: A Novel Allele Frequency-Based Feature Selection Method for Multi-ancestry Admixed Populations. <i>Scientific Reports</i> , 2019, 9, 11103.	1.6	2
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1344	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. <i>Hypertension</i> , 2019, 74, 614-622.	1.3	14
1345	The Role of Whole-Genome Studies in the Investigation of Honey Bee Biology. <i>Russian Journal of Genetics</i> , 2019, 55, 815-824.	0.2	6

#	ARTICLE	IF	CITATIONS
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1349	Structure is more robust than other clustering methods in simulated mixed-ploidy populations. <i>Heredity</i> , 2019, 123, 429-441.	1.2	98
1350	Genomic analyses suggest adaptive differentiation of northern European native cattle breeds. <i>Evolutionary Applications</i> , 2019, 12, 1096-1113.	1.5	12
1351	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. <i>BMC Genetics</i> , 2019, 20, 52.	2.7	10
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1353	Genome Resequencing Reveals Congenital Causes of Embryo and Nestling Death in Crested Ibis (<i>Nipponia nippon</i>). <i>Genome Biology and Evolution</i> , 2019, 11, 2125-2135.	1.1	4
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1355	Whole-genome <scp>SNP</scp> data unravel population structure and signatures of selection for black plumage of indigenous chicken breeds from Jiangxi province, China. <i>Animal Genetics</i> , 2019, 50, 475-483.	0.6	10
1356	GRAF-pop: A Fast Distance-Based Method To Infer Subject Ancestry from Multiple Genotype Datasets Without Principal Components Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2447-2461.	0.8	41
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1358	Revealing the Genetic Impact of the Ottoman Occupation on Ethnic Groups of East-Central Europe and on the Roma Population of the Area. <i>Frontiers in Genetics</i> , 2019, 10, 558.	1.1	9
1359	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	15.2	177
1360	Long-distance dispersal, ice sheet dynamics and mountaintop isolation underlie the genetic structure of glacier ice worms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190983.	1.2	17
1361	Genomic analysis of the origins of extant casein variation in goats. <i>Journal of Dairy Science</i> , 2019, 102, 5230-5241.	1.4	7
1362	Genetic diversity and relationships among native Japanese horse breeds, the Japanese Thoroughbred and horses outside of Japan using genome-wide SNP data. <i>Animal Genetics</i> , 2019, 50, 449-459.	0.6	15
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#	ARTICLE	IF	CITATIONS
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1365	Genome-wide association study and candidate gene analysis of alkalinity tolerance in japonica rice germplasm at the seedling stage. <i>Rice</i> , 2019, 12, 24.	1.7	57
1366	Genetic Analyses of Tanzanian Local Chicken Ecotypes Challenged with Newcastle Disease Virus. <i>Genes</i> , 2019, 10, 546.	1.0	20
1367	Genome resequencing of the orange-spotted grouper (<i>Epinephelus coioides</i>) for a genome-wide association study on ammonia tolerance. <i>Aquaculture</i> , 2019, 512, 734332.	1.7	24
1368	Genetic architecture and adaptations of Nunavik Inuit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16012-16017.	3.3	14
1369	Genome Analysis Reveals Genetic Admixture and Signature of Selection for Productivity and Environmental Traits in Iraqi Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 609.	1.1	31
1370	Identification of genomewide single-nucleotide polymorphisms associated with presummer, summer and autumn bolls in upland cotton. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	1
1371	Genomic diversity and novel genome-wide association with fruit morphology in <i>Capsicum</i> , from 746k polymorphic sites. <i>Scientific Reports</i> , 2019, 9, 10067.	1.6	53
1372	Phased genome sequence of an interspecific hybrid flowering cherry, 'Somei-Yoshino' (<i>Cerasus</i> × <i>Tj</i>) ETQq0.0.0 rgBT /Overlock 1.5 59	1.5	59
1373	Lack of gene flow: Narrow and dispersed differentiation islands in a triplet of <i>Leptidea</i> butterfly species. <i>Molecular Ecology</i> , 2019, 28, 3756-3770.	2.0	31
1374	Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan. <i>Current Biology</i> , 2019, 29, 2526-2532.e4.	1.8	64
1375	Genetic diversity of the Sichuan snub-nosed monkey (<i>Rhinopithecus roxellana</i>) in Shennongjia National Park, China using RAD-seq analyses. <i>Genetica</i> , 2019, 147, 327-335.	0.5	6
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1377	Genomic differentiation tracks earth-historic isolation in an Indo-Australasian archipelagic pitta (<i>Pittidae</i> ; <i>Aves</i>) complex. <i>BMC Evolutionary Biology</i> , 2019, 19, 151.	3.2	14
1378	Genetic comparison of sickle cell anaemia cohorts from Brazil and the United States reveals high levels of divergence. <i>Scientific Reports</i> , 2019, 9, 10896.	1.6	9
1379	The Current Genomic Landscape of Western South America: Andes, Amazonia, and Pacific Coast. <i>Molecular Biology and Evolution</i> , 2019, 36, 2698-2713.	3.5	59
1380	The effect of a genetic variant at the schizophrenia associated AS3MT/BORCS7 locus on striatal dopamine function: A PET imaging study. <i>Psychiatry Research - Neuroimaging</i> , 2019, 291, 34-41.	0.9	13
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1383	Strengths and potential pitfalls of hay transfer for ecological restoration revealed by RAD-seq analysis in floodplain <i>Arabis</i> species. <i>Molecular Ecology</i> , 2019, 28, 3887-3901.	2.0	14
1384	Population-dependent reproducible deviation from natural bread wheat genome in synthetic hexaploid wheat. <i>Plant Journal</i> , 2019, 100, 801-812.	2.8	16
1385	The presence and impact of reference bias on population genomic studies of prehistoric human populations. <i>PLoS Genetics</i> , 2019, 15, e1008302.	1.5	137
1386	Rare DEGS1 variant significantly alters de novo ceramide synthesis pathway. <i>Journal of Lipid Research</i> , 2019, 60, 1630-1639.	2.0	16
1387	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081.	9.4	176
1388	Population Genomics and Demographic Sampling of the Ant-Plant <i>Vachellia drepanolobium</i> and Its Symbiotic Ants From Sites Across Its Range in East Africa. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	5
1389	Ancient Hybridization and Adaptive Introgression of an Invadolysin Gene in Schistosome Parasites. <i>Molecular Biology and Evolution</i> , 2019, 36, 2127-2142.	3.5	56
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1391	Conservation Genomics in the Sagebrush Sea: Population Divergence, Demographic History, and Local Adaptation in Sage-Grouse (<i>Centrocercus</i> spp.). <i>Genome Biology and Evolution</i> , 2019, 11, 2023-2034.	1.1	35
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1393	Ancient DNA sheds light on the genetic origins of early Iron Age Philistines. <i>Science Advances</i> , 2019, 5, eaax0061.	4.7	64
1394	Common BACE2 Polymorphisms are Associated with Altered Risk for Alzheimer's Disease and CSF Amyloid Biomarkers in APOE ϵ 4 Non-Carriers. <i>Scientific Reports</i> , 2019, 9, 9640.	1.6	14
1395	The Interplay between Incipient Species and Social Polymorphism in the Desert Ant <i>Cataglyphis</i> . <i>Scientific Reports</i> , 2019, 9, 9495.	1.6	11
1396	Inference of Population Structure from Time-Series Genotype Data. <i>American Journal of Human Genetics</i> , 2019, 105, 317-333.	2.6	23
1397	Genome-wide association studies for heat stress response in <i>Bos taurus</i> × <i>Bos indicus</i> crossbred cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8148-8158.	1.4	31
1398	Coevolution of Sites under Immune Selection Shapes Epstein-Barr Virus Population Structure. <i>Molecular Biology and Evolution</i> , 2019, 36, 2512-2521.	3.5	20
1399	EPAS1 Gain-of-Function Mutation Contributes to High-Altitude Adaptation in Tibetan Horses. <i>Molecular Biology and Evolution</i> , 2019, 36, 2591-2603.	3.5	80

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1401	Maternal genomic variability of the wild boar (<i>Sus scrofa</i>) reveals the uniqueness of East-Caucasian and Central Italian populations. <i>Ecology and Evolution</i> , 2019, 9, 9467-9478.	0.8	15
1402	Intraspecific genetic divergence within <i>Helianthus niveus</i> and the status of two new morphotypes from Mexico. <i>American Journal of Botany</i> , 2019, 106, 1229-1239.	0.8	7
1403	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. <i>Science</i> , 2019, 366, .	6.0	65
1404	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019, 179, 736-749.e15.	13.5	126
1405	Fast and Effective Clustering Method for Ancestry Estimation. <i>Procedia Computer Science</i> , 2019, 157, 306-312.	1.2	14
1406	The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191528.	1.2	35
1407	Genetic contributions to variation in human stature in prehistoric Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21484-21492.	3.3	64
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1409	Evolution and diversity of two cisco forms in an outlet of glacial Lake Algonquin. <i>Ecology and Evolution</i> , 2019, 9, 9654-9670.	0.8	13
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1411	Comparing and co-analysing microsatellite and morphological data for species delimitation in the New Zealand native <i>Myosotis pygmaea</i> species group (Boraginaceae). <i>Taxon</i> , 2019, 68, 731-750.	0.4	6
1412	Extensive phenotypic diversity in the cultivated Florist's Gloxinia, <i>Sinningia speciosa</i> (Lodd.) Hiern, is derived from the domestication of a single founder population. <i>Plants People Planet</i> , 2019, 1, 363-374.	1.6	4
1413	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. <i>Cell</i> , 2019, 179, 984-1002.e36.	13.5	152
1414	Ancient Rome: A genetic crossroads of Europe and the Mediterranean. <i>Science</i> , 2019, 366, 708-714.	6.0	164
1415	Physiological and genomic evidence that selection on the transcription factor <i>Epas1</i> has altered cardiovascular function in high-altitude deer mice. <i>PLoS Genetics</i> , 2019, 15, e1008420.	1.5	52
1416	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257.	2.4	19
1417	Genome assembly of the common pheasant <i>Phasianus colchicus</i> , a model for speciation and ecological genomics. <i>Genome Biology and Evolution</i> , 2019, 11, 3326-3331.	1.1	6

#	ARTICLE	IF	CITATIONS
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1419	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
1420	Network-based hierarchical population structure analysis for large genomic data sets. <i>Genome Research</i> , 2019, 29, 2020-2033.	2.4	10
1421	A global overview of cassava genetic diversity. <i>PLoS ONE</i> , 2019, 14, e0224763.	1.1	39
1422	<p>Diversity In Precision Medicine And Pharmacogenetics: Methodological And Conceptual Considerations For Broadening Participation</p>. <i>Pharmacogenomics and Personalized Medicine</i> , 2019, Volume 12, 257-271.	0.4	23
1423	Genome-Wide Methylation of Mild Cognitive Impairment in Mexican Americans Highlights Genes Involved in Synaptic Transport, Alzheimer's Disease-Precursor Phenotypes, and Metabolic Morbidities. <i>Journal of Alzheimer's Disease</i> , 2019, 72, 733-749.	1.2	21
1424	Multiple Selection Signatures in Farmed Atlantic Salmon Adapted to Different Environments Across Hemispheres. <i>Frontiers in Genetics</i> , 2019, 10, 901.	1.1	41
1425	GWAS Discovery Of Candidate Genes for Yield-Related Traits in Peanut and Support from Earlier QTL Mapping Studies. <i>Genes</i> , 2019, 10, 803.	1.0	25
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1427	Limited gene exchange between two sister species of leaf beetles within a hybrid zone in the Alps. <i>Journal of Evolutionary Biology</i> , 2019, 32, 1406-1417.	0.8	6
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1429	Urbanization impacts apex predator gene flow but not genetic diversity across an urban-rural divide. <i>Molecular Ecology</i> , 2019, 28, 4926-4940.	2.0	23
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#	ARTICLE	IF	CITATIONS
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1437	Landscape drivers of genomic diversity and divergence in woodland Eucalyptus. <i>Molecular Ecology</i> , 2019, 28, 5232-5247.	2.0	34
1438	Inference and analysis of population-specific fine-scale recombination maps across 26 diverse human populations. <i>Science Advances</i> , 2019, 5, eaaw9206.	4.7	111
1439	Reconstructed lost Native American populations from Eastern Brazil are shaped by differential J _A ³ /Tupi ancestry. <i>Genome Biology and Evolution</i> , 2019, 11, 2593-2604.	1.1	8
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1441	Chinese Fir Breeding in the High-Throughput Sequencing Era: Insights from SNPs. <i>Forests</i> , 2019, 10, 681.	0.9	10
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1445	Genomic GPS: using genetic distance from individuals to public data for genomic analysis without disclosing personal genomes. <i>Genome Biology</i> , 2019, 20, 175.	3.8	4
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#	ARTICLE	IF	CITATIONS
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1458	Core set construction and association analysis of <i>Pinus massoniana</i> from Guangdong province in southern China using SLAF-seq. <i>Scientific Reports</i> , 2019, 9, 13157.	1.6	12
1459	Population genomics reveals possible genetic evidence for parallel evolution of <i>Sebastiscus marmoratus</i> in the northwestern Pacific Ocean. <i>Open Biology</i> , 2019, 9, 190028.	1.5	8
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1464	Distribution of local ancestry and evidence of adaptation in admixed populations. <i>Scientific Reports</i> , 2019, 9, 13900.	1.6	24
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1469	Selection of Optimal Ancestry Informative Markers for Classification and Ancestry Proportion Estimation in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 183.	1.1	4
1470	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2019, 105, 763-772.	2.6	169
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#	ARTICLE	IF	CITATIONS
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1473	Exacerbation-prone asthma in the context of race and ancestry in Asthma Clinical Research Network trials. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1524-1533.	1.5	23
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1478	Genome Diversity and Signatures of Selection for Production and Performance Traits in Dromedary Camels. <i>Frontiers in Genetics</i> , 2019, 10, 893.	1.1	26
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1481	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. <i>Nature Communications</i> , 2019, 10, 358.	5.8	130
1482	Minor allele frequency thresholds strongly affect population structure inference with genomic data sets. <i>Molecular Ecology Resources</i> , 2019, 19, 639-647.	2.2	255
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1484	Medaka Population Genome Structure and Demographic History Described via Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 217-228.	0.8	14
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1489	Riverscape genetic variation, migration patterns, and morphological variation of the threatened Round Rocksnail, <i>Leptoxis ampla</i> . <i>Molecular Ecology</i> , 2019, 28, 1593-1610.	2.0	21

#	ARTICLE	IF	CITATIONS
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1491	Genome-wide association study identifies favorable SNP alleles and candidate genes for waterlogging tolerance in chrysanthemums. <i>Horticulture Research</i> , 2019, 6, 21.	2.9	40
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1493	Genome-wide association multi-locus and multi-variate linear mixed models reveal two linked loci with major effects on partial resistance of apricot to bacterial canker. <i>BMC Plant Biology</i> , 2019, 19, 31.	1.6	10
1494	The role of ecotype-environment interactions in intraspecific trophic niche partitioning subsequent to stocking. <i>Ecological Applications</i> , 2019, 29, e01857.	1.8	10
1495	Fractures in school age children in relation to sex and ethnic background: The Generation R Study. <i>Bone</i> , 2019, 121, 227-231.	1.4	7
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1498	Transethnic meta-analysis of rare coding variants in PLCG2, ABI3, and TREM2 supports their general contribution to Alzheimer's disease. <i>Translational Psychiatry</i> , 2019, 9, 55.	2.4	32
1499	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	1.6	77
1500	Risk Haplotypes Uniquely Associated with Radioiodine-Refractory Thyroid Cancer Patients of High African Ancestry. <i>Thyroid</i> , 2019, 29, 530-539.	2.4	8
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#	ARTICLE	IF	CITATIONS
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1510	Genetic homogenization of indigenous sheep breeds in Northwest Africa. <i>Scientific Reports</i> , 2019, 9, 7920.	1.6	20
1511	Genome-wide association study of important agronomic traits within a core collection of rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	1.6	25
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1513	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. <i>Circulation</i> , 2019, 140, 42-54.	1.6	97
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1522	Genome Sequence Analysis Reveals Selection Signatures in Endangered Trypanotolerant West African Muturu Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 442.	1.1	42
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1524	Palaeogenomic insights into the origins of French grapevine diversity. <i>Nature Plants</i> , 2019, 5, 595-603.	4.7	85
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#	ARTICLE	IF	CITATIONS
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1527	Genome-wide variation patterns between landraces and cultivars uncover divergent selection during modern wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2509-2523.	1.8	56
1528	Rapid identification and interpretation of gene-environment associations using the new R.Sambada landscape genomics pipeline. <i>Molecular Ecology Resources</i> , 2019, 19, 1355-1365.	2.2	16
1529	Phylogenetic and population structural inference from genomic ancestry maintained in present-day common wheat Chinese landraces. <i>Plant Journal</i> , 2019, 99, 201-215.	2.8	5
1530	A Social Determinant of Health May Modify Genetic Associations for Blood Pressure: Evidence From a SNP by Education Interaction in an African American Population. <i>Frontiers in Genetics</i> , 2019, 10, 428.	1.1	7
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1532	Damped Anderson Acceleration With Restarts and Monotonicity Control for Accelerating EM and EM-like Algorithms. <i>Journal of Computational and Graphical Statistics</i> , 2019, 28, 834-846.	0.9	40
1533	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. <i>Genome Biology</i> , 2019, 20, 106.	3.8	9
1534	Landscape genomics of an obligate mutualism: Concordant and discordant population structures between the leafcutter ant <i>Atta texana</i> and its two main fungal symbiont types. <i>Molecular Ecology</i> , 2019, 28, 2831-2845.	2.0	18
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1536	Genomic signatures of adaptation to Sahelian and Soudanian climates in sorghum landraces of Senegal. <i>Ecology and Evolution</i> , 2019, 9, 6038-6051.	0.8	30
1537	Purifying selection does not drive signatures of convergent local adaptation of lodgepole pine and interior spruce. <i>BMC Evolutionary Biology</i> , 2019, 19, 110.	3.2	1
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1541	Genome-wide association study identified novel candidate loci affecting wood formation in Norway spruce. <i>Plant Journal</i> , 2019, 100, 83-100.	2.8	49
1542	Genetic history of the population of Crete. <i>Annals of Human Genetics</i> , 2019, 83, 373-388.	0.3	2
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#	ARTICLE	IF	CITATIONS
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1547	PopNetD3â€”A Network-Based Web Resource for Exploring Population Structure. <i>Genome Biology and Evolution</i> , 2019, 11, 1730-1735.	1.1	1
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1549	Whole genome sequencing reveals the impact of recent artificial selection on red sea bream reared in fish farms. <i>Scientific Reports</i> , 2019, 9, 6487.	1.6	8
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1551	Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. <i>PLoS Genetics</i> , 2019, 15, e1008119.	1.5	70
1552	The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East. <i>Current Biology</i> , 2019, 29, 1701-1711.e16.	1.8	80
1553	Rare Variants Imputation in Admixed Populations: Comparison Across Reference Panels and Bioinformatics Tools. <i>Frontiers in Genetics</i> , 2019, 10, 239.	1.1	20
1554	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10705-10710.	3.3	119
1555	The Geography of Jewish Ethnogenesis. <i>Journal of Anthropological Research</i> , 2019, 75, 206-234.	0.1	3
1556	Ancient DNA from mastics solidifies connection between material culture and genetics of mesolithic hunter-gatherers in Scandinavia. <i>Communications Biology</i> , 2019, 2, 185.	2.0	32
1557	Genome scan for selection in South American chickens reveals a region under selection associated with aggressiveness. <i>Livestock Science</i> , 2019, 225, 135-139.	0.6	0
1558	The SYNBREED chicken diversity panel: a global resource to assess chicken diversity at high genomic resolution. <i>BMC Genomics</i> , 2019, 20, 345.	1.2	74
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1567	Random PCR-based genotyping by sequencing technology (GRAS-Seq) (genotyping by random amplicon) <i>Tj ETQq1 1 0.784314 rgBT</i> <i>19, 1153-1163.</i>	2.2	46
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1710	The coincidence of ecological opportunity with hybridization explains rapid adaptive radiation in Lake Mweru cichlid fishes. <i>Nature Communications</i> , 2019, 10, 5391.	5.8	79
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1712	Phenotypic and molecular assessment of genetic structure and diversity in a panel of winged yam (<i>Dioscorea alata</i>) clones and cultivars. <i>Scientific Reports</i> , 2019, 9, 18221.	1.6	42
1713	West Asian sources of the Eurasian component in Ethiopians: a reassessment. <i>Scientific Reports</i> , 2019, 9, 18811.	1.6	14
1714	Recurrent PTPRT/JAK2 mutations in lung adenocarcinoma among African Americans. <i>Nature Communications</i> , 2019, 10, 5735.	5.8	22
1715	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
1716	Genetic Diversity and Signatures of Selection in 15 Chinese Indigenous Dog Breeds Revealed by Genome-Wide SNPs. <i>Frontiers in Genetics</i> , 2019, 10, 1174.	1.1	12
1717	The combined use of raw and phylogenetically independent methods of outlier detection uncovers genome-wide dynamics of local adaptation in a lizard. <i>Ecology and Evolution</i> , 2019, 9, 14356-14367.	0.8	2
1718	Developing Growth-Associated Molecular Markers Via High-Throughput Phenotyping in Spinach. <i>Plant Genome</i> , 2019, 12, 190027.	1.6	15
1719	Profiling SNP and Nucleotide Diversity to Characterize Mekong Delta Rice Landraces in Southeast Asian Populations. <i>Plant Genome</i> , 2019, 12, 190042.	1.6	6
1720	Whole Genome Resequencing Reveals Selection Signatures Associated With Important Traits in Ethiopian Indigenous Goat Populations. <i>Frontiers in Genetics</i> , 2019, 10, 1190.	1.1	10
1721	Applications of Next-Generation Sequencing Technologies and Computational Tools in Molecular Evolution and Aquatic Animals Conservation Studies: A Short Review. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431989228.	0.6	17
1722	Comparing genomic signatures of domestication in two Atlantic salmon (<i>Salmo salar</i> L.) populations with different geographical origins. <i>Evolutionary Applications</i> , 2019, 12, 137-156.	1.5	58
1723	A new pelagic predatory pike cichlid (Teleostei: Cichlidae: Crenicichla) from the <i>C. mandelburgeri</i> species complex with parallel and reticulate evolution. <i>Hydrobiologia</i> , 2019, 832, 377-395.	1.0	10

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1725	Pair Matcher (<i>PaM</i>): fast model-based optimization of treatment/case-control matches. <i>Bioinformatics</i> , 2019, 35, 2243-2250.	1.8	10
1726	The efficacy of whole human genome capture on ancient dental calculus and dentin. <i>American Journal of Physical Anthropology</i> , 2019, 168, 496-509.	2.1	24
1727	<i>Liriodendron</i> genome sheds light on angiosperm phylogeny and species pair differentiation. <i>Nature Plants</i> , 2019, 5, 18-25.	4.7	163
1728	Role of host genetics and heat-tolerant algal symbionts in sustaining populations of the endangered coral <i>Orbicella faveolata</i> in the Florida Keys with ocean warming. <i>Global Change Biology</i> , 2019, 25, 1016-1031.	4.2	111
1729	The natural selection that shapes our genomes. <i>Forensic Science International: Genetics</i> , 2019, 39, 57-60.	1.6	6
1730	Whole-Genome Resequencing of a Worldwide Collection of Rapeseed Accessions Reveals the Genetic Basis of Ecotype Divergence. <i>Molecular Plant</i> , 2019, 12, 30-43.	3.9	175
1731	A genomic map of climate adaptation in Mediterranean cattle breeds. <i>Molecular Ecology</i> , 2019, 28, 1009-1029.	2.0	46
1732	Genome-wide association study of callus induction variation to explore the callus formation mechanism of rice. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1134-1150.	4.1	20
1733	Genetic Architecture of Primary Open-Angle Glaucoma in Individuals of African Descent. <i>Ophthalmology</i> , 2019, 126, 38-48.	2.5	40
1734	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019, 122, 636-646.	1.2	42
1735	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey (<i>Rhinopithecus</i>) Tj ETQq1 1 0,784314 rgBT /Ove	3.5	20
1736	Patterns of transposable element variation and clinality in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2019, 28, 1523-1536.	2.0	13
1737	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
1738	Population genetic analyses of seven Chinese indigenous chicken breeds in a context of global breeds. <i>Animal Genetics</i> , 2019, 50, 82-86.	0.6	27
1739	Genomic Evidence of Local Adaptation to Climate and Diet in Indigenous Siberians. <i>Molecular Biology and Evolution</i> , 2019, 36, 315-327.	3.5	41
1740	Gene Flow and Subdivided Populations. , 2019, , 155-193.		0
1741	Impact of genomic leakage on the conservation of the endangered Milky Stork. <i>Biological Conservation</i> , 2019, 229, 59-66.	1.9	10

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1743	Disentangling structural genomic and behavioural barriers in a sea of connectivity. <i>Molecular Ecology</i> , 2019, 28, 1394-1411.	2.0	68
1744	On the postglacial spread of human commensal <i>Arabidopsis thaliana</i> : journey to the East. <i>New Phytologist</i> , 2019, 222, 1447-1457.	3.5	20
1745	Genetic variation in CRHR1 is associated with short-term respiratory response to corticosteroids in preterm infants at risk for bronchopulmonary dysplasia. <i>Pediatric Research</i> , 2019, 85, 625-633.	1.1	13
1746	Genetic diversity analysis of French goat populations reveals selective sweeps involved in their differentiation. <i>Animal Genetics</i> , 2019, 50, 54-63.	0.6	22
1747	Genetic diversity patterns and domestication origin of soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1179-1193.	1.8	44
1748	Identification of novel common breast cancer risk variants at the 6q25 locus among Latinas. <i>Breast Cancer Research</i> , 2019, 21, 3.	2.2	32
1749	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: <i>Nomia melanderi</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19
1750	Genome-Wide Variation, Candidate Regions and Genes Associated With Fat Deposition and Tail Morphology in Ethiopian Indigenous Sheep. <i>Frontiers in Genetics</i> , 2018, 9, 699.	1.1	56
1751	Investigating mitonuclear interactions in human admixed populations. <i>Nature Ecology and Evolution</i> , 2019, 3, 213-222.	3.4	60
1752	Facial masculinity does not appear to be a condition-dependent male ornament and does not reflect MHC heterozygosity in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1633-1638.	3.3	46
1753	A panel of 32 AIMs suitable for population stratification correction and global ancestry estimation in Mexican mestizos. <i>BMC Genetics</i> , 2019, 20, 5.	2.7	11
1754	Genome-Wide Association Studies Identified Resistance Loci to Orange Rust and Yellow Leaf Virus Diseases in Sugarcane (<i>Saccharum</i> spp.). <i>Phytopathology</i> , 2019, 109, 623-631.	1.1	34
1755	Phylotranscriptomic Insights into the Diversification of Endothermic <i>Thunnus</i> Tunas. <i>Molecular Biology and Evolution</i> , 2019, 36, 84-96.	3.5	15
1756	Enabling genome-wide association testing with multiple diseases and no healthy controls. <i>Gene</i> , 2019, 684, 118-123.	1.0	8
1757	Changes in Biological Pathways During 6,000 Years of Civilization in Europe. <i>Molecular Biology and Evolution</i> , 2019, 36, 127-140.	3.5	24
1758	Germline Mutations in ATM and BRCA1/2 Are Associated with Grade Reclassification in Men on Active Surveillance for Prostate Cancer. <i>European Urology</i> , 2019, 75, 743-749.	0.9	138
1759	Emergence and Spread of Basal Lineages of <i>Yersinia pestis</i> during the Neolithic Decline. <i>Cell</i> , 2019, 176, 295-305.e10.	13.5	168

#	ARTICLE	IF	CITATIONS
1760	Genomic comparisons reveal biogeographic and anthropogenic impacts in the koala (<i>Phascolarctos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 122, 525-544.	1.2	29
1761	Chromosomal fusion and life history-associated genomic variation contribute to within-river local adaptation of Atlantic salmon. <i>Molecular Ecology</i> , 2019, 28, 1439-1459.	2.0	56
1762	Adaptation to milking agropastoralism in Chilean goat herders and nutritional benefit of lactase persistence. <i>Annals of Human Genetics</i> , 2019, 83, 11-22.	0.3	12
1763	A dedicated target capture approach reveals variable genetic markers across micro- and macro-evolutionary time scales in palms. <i>Molecular Ecology Resources</i> , 2019, 19, 221-234.	2.2	42
1765	Genomic divergence in cotton germplasm related to maturity and heterosis. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 929-942.	4.1	21
1766	Novel insight into the genetic basis of high-altitude pulmonary hypertension in Kyrgyz highlanders. <i>European Journal of Human Genetics</i> , 2019, 27, 150-159.	1.4	14
1767	Inference and visualization of DNA damage patterns using a grade of membership model. <i>Bioinformatics</i> , 2019, 35, 1292-1298.	1.8	7
1768	The Origin of a New Sex Chromosome by Introgression between Two Stickleback Fishes. <i>Molecular Biology and Evolution</i> , 2019, 36, 28-38.	3.5	57
1769	Genomic selection efficiency and a priori estimation of accuracy in a structured dent maize panel. <i>Theoretical and Applied Genetics</i> , 2019, 132, 81-96.	1.8	42
1770	Genetic contributors to serum uric acid levels in Mexicans and their effect on premature coronary artery disease. <i>International Journal of Cardiology</i> , 2019, 279, 168-173.	0.8	15
1771	Phenotypic and life-history diversification in Amazonian frogs despite past introgressions. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 169-180.	1.2	9
1772	Genetic diversity and relationship between domesticated rye and its wild relatives as revealed through genotyping-by-sequencing. <i>Evolutionary Applications</i> , 2019, 12, 66-77.	1.5	50
1773	Population structure and admixture analysis in Frieswal crossbred cattle of India – a pilot study. <i>Animal Biotechnology</i> , 2020, 31, 86-92.	0.7	4
1774	Genome-wide sequence analyses of ethnic populations across Russia. <i>Genomics</i> , 2020, 112, 442-458.	1.3	19
1775	Mycorrhiza: genotype assignment using phylogenetic networks. <i>Bioinformatics</i> , 2020, 36, 212-220.	1.8	4
1776	Association of systemic lupus erythematosus (SLE) genetic susceptibility loci with lupus nephritis in childhood-onset and adult-onset SLE. <i>Rheumatology</i> , 2020, 59, 90-98.	0.9	40
1777	Whole-genome resequencing reveals selection signatures associated with milk production traits in African Kenana dairy zebu cattle. <i>Genomics</i> , 2020, 112, 880-885.	1.3	19
1778	Genomic and phenotypic consequences of two independent secondary contact zones between allopatric lineages of the anadromous ice goby <i>Leucopsarion petersii</i> . <i>Heredity</i> , 2020, 124, 223-235.	1.2	8

#	ARTICLE	IF	CITATIONS
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1780	Evaluation of two bovine SNP genotyping arrays for breed clustering and stratification analysis in well-known <i>taurine</i> and <i>indicine</i> breeds. <i>Animal Biotechnology</i> , 2020, 31, 268-275.	0.7	5
1781	OpenMendel: a cooperative programming project for statistical genetics. <i>Human Genetics</i> , 2020, 139, 61-71.	1.8	29
1782	The many faced symbiotic snakelocks anemone (<i>Anemonia viridis</i> , Anthozoa): host and symbiont genetic differentiation among colour morphs. <i>Heredity</i> , 2020, 124, 351-366.	1.2	7
1783	PGG.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D971-D976.	6.5	51
1784	A Polygenic Risk Score for Breast Cancer in US Latinas and Latin American Women. <i>Journal of the National Cancer Institute</i> , 2020, 112, 590-598.	3.0	53
1785	Genetic isolation by distance in the yellowfin goby populations revealed by RAD sequencing. <i>Ichthyological Research</i> , 2020, 67, 98-104.	0.5	13
1786	A genomics approach reveals the global genetic polymorphism, structure, and functional diversity of ten accessions of the marine model diatom <i>Phaeodactylum tricornutum</i> . <i>ISME Journal</i> , 2020, 14, 347-363.	4.4	50
1787	Along the Indian Ocean Coast: Genomic Variation in Mozambique Provides New Insights into the Bantu Expansion. <i>Molecular Biology and Evolution</i> , 2020, 37, 406-416.	3.5	32
1788	Invasion genomics supports an old hybrid swarm of pool frogs in Western Europe. <i>Biological Invasions</i> , 2020, 22, 205-210.	1.2	15
1789	The genetic diversity of multiple sclerosis risk among Hispanic and African American populations living in the United States. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1329-1339.	1.4	23
1790	Genomic Ancestry, <i>CYP2D6</i> , <i>CYP2C9</i> , and <i>CYP2C19</i> Among Latin Americans. <i>Clinical Pharmacology and Therapeutics</i> , 2020, 107, 257-268.	2.3	27
1791	Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass. <i>Plant Biotechnology Journal</i> , 2020, 18, 373-388.	4.1	51
1792	Population structure and genetic characterization of two native Danish sheep breeds. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2020, 69, 53-67.	0.2	2
1793	Genomic signatures of seed mass adaptation to global precipitation gradients in sorghum. <i>Heredity</i> , 2020, 124, 108-121.	1.2	28
1794	The population genetics of cypsis in vertebrates: recent insights from mice, hares, and lizards. <i>Heredity</i> , 2020, 124, 1-14.	1.2	24
1795	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. <i>Molecular Biology and Evolution</i> , 2020, 37, 134-148.	3.5	23
1796	Genomic analyses reveal three independent introductions of the invasive brown rat (<i>Rattus</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tj	1.2	12

#	ARTICLE	IF	CITATIONS
1797	Early diversification and permeable species boundaries in the Mediterranean firs. <i>Annals of Botany</i> , 2020, 125, 495-507.	1.4	24
1798	Ancient DNA Reconstructs the Genetic Legacies of Precontact Puerto Rico Communities. <i>Molecular Biology and Evolution</i> , 2020, 37, 611-626.	3.5	31
1799	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	3.5	22
1800	<i>Plasmodium vivax</i> Malaria Viewed through the Lens of an Eradicated European Strain. <i>Molecular Biology and Evolution</i> , 2020, 37, 773-785.	3.5	38
1801	Landscape genomics predicts climate change-related genetic offset for the widespread <i>Platycladus orientalis</i> (Cupressaceae). <i>Evolutionary Applications</i> , 2020, 13, 665-676.	1.5	47
1802	Predicting Benefit From Evolocumab Therapy in Patients With Atherosclerotic Disease Using a Genetic Risk Score. <i>Circulation</i> , 2020, 141, 616-623.	1.6	143
1803	Vacuolar invertase genes <i>SbVIN1</i> and <i>SbVIN2</i> are differently associated with stem and grain traits in sorghum (<i>Sorghum bicolor</i>). <i>Crop Journal</i> , 2020, 8, 299-312.	2.3	4
1804	The Effects of Rare <i>SERPINA1</i> Variants on Lung Function and Emphysema in SPIROMICS. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 540-554.	2.5	38
1805	Divergent Selection and Primary Gene Flow Shape Incipient Speciation of a Riparian Tree on Hawaii Island. <i>Molecular Biology and Evolution</i> , 2020, 37, 695-710.	3.5	21
1806	Restriction site-associated DNA sequencing reveals the molecular genetic diversity of grapevine and genes related to white rot disease. <i>Scientia Horticulturae</i> , 2020, 261, 108907.	1.7	8
1807	A 50K SNP array reveals genetic structure for bald eagles (<i>Haliaeetus leucocephalus</i>). <i>Conservation Genetics</i> , 2020, 21, 65-76.	0.8	8
1808	Genomic analyses reveal selection footprints in rice landraces grown under on-farm conservation conditions during a short-term period of domestication. <i>Evolutionary Applications</i> , 2020, 13, 290-302.	1.5	9
1809	Population structure and breed composition prediction in a multi-breed sheep population using genome-wide single nucleotide polymorphism genotypes. <i>Animal</i> , 2020, 14, 464-474.	1.3	5
1810	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
1811	Replicated anthropogenic hybridisations reveal parallel patterns of admixture in marine mussels. <i>Evolutionary Applications</i> , 2020, 13, 575-599.	1.5	45
1812	Increased genetic marker density reveals high levels of admixture between red deer and introduced Japanese sika in Kintyre, Scotland. <i>Evolutionary Applications</i> , 2020, 13, 432-441.	1.5	28
1813	Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292.	2.8	25
1814	A different view on fine-scale population structure in Western African populations. <i>Human Genetics</i> , 2020, 139, 45-59.	1.8	13

#	ARTICLE	IF	CITATIONS
1815	Genetic assignment of individuals to source populations using network estimation tools. <i>Methods in Ecology and Evolution</i> , 2020, 11, 333-344.	2.2	5
1816	Population structure of indigenous southern African goats based on the Illumina Goat50K SNP panel. <i>Tropical Animal Health and Production</i> , 2020, 52, 1795-1802.	0.5	11
1817	Global evaluation of taxonomic relationships and admixture within the <i>Culex pipiens</i> complex of mosquitoes. <i>Parasites and Vectors</i> , 2020, 13, 8.	1.0	25
1818	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	3.6	61
1819	Ancestry informative DIP loci for dissecting genetic structure and ancestry proportions of Qinghai Tibetan and Tibet Tibetan groups. <i>Molecular Biology Reports</i> , 2020, 47, 1079-1087.	1.0	5
1820	Relationship of Icelandic cattle with Northern and Western European cattle breeds, admixture and population structure. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2020, 69, 25-38.	0.2	6
1821	Genome-Wide Association Study (GWAS) for Mesocotyl Elongation in Rice (<i>Oryza sativa</i> L.) under Multiple Culture Conditions. <i>Genes</i> , 2020, 11, 49.	1.0	36
1822	Exome sequencing reveals a high prevalence of BRCA1 and BRCA2 founder variants in a diverse population-based biobank. <i>Genome Medicine</i> , 2020, 12, 2.	3.6	68
1823	Do different rates of gene flow underlie variation in phenotypic and phenological clines in a montane grasshopper community?. <i>Ecology and Evolution</i> , 2020, 10, 980-997.	0.8	4
1824	Genome-wide profiles indicate wolf population connectivity within the eastern Carpathian Mountains. <i>Genetica</i> , 2020, 148, 33-39.	0.5	3
1825	Parallel Seed Color Adaptation during Multiple Domestication Attempts of an Ancient New World Grain. <i>Molecular Biology and Evolution</i> , 2020, 37, 1407-1419.	3.5	47
1826	Demographic history has shaped the strongly differentiated corkwing wrasse populations in Northern Europe. <i>Molecular Ecology</i> , 2020, 29, 160-171.	2.0	20
1827	Single marker and haplotype based association analysis of anthracnose (<i>Colletotrichum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.0	11
1828	Genetic architecture of subspecies divergence in trace mineral accumulation and elemental correlations in the rice grain. <i>Theoretical and Applied Genetics</i> , 2020, 133, 529-545.	1.8	38
1829	Pharmacogenomics implications of population diversity in Latin America: TPMT and NUDT15 polymorphisms and thiopurine dosing. <i>Pharmacogenetics and Genomics</i> , 2020, 30, 1-4.	0.7	9
1830	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). <i>Molecular Ecology</i> , 2020, 29, 344-362.	2.0	12
1831	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 994-1006.	3.5	43
1832	scRAD Seq Refines Previous Estimates of Genetic Structure in Lake Erie Walleye. <i>Transactions of the American Fisheries Society</i> , 2020, 149, 159-173.	0.6	17

#	ARTICLE	IF	CITATIONS
1833	Genetic diversity, population structure and runs of homozygosity in Ethiopian short fat-tailed and Awassi sheep breeds using genome-wide 50k SNP markers. <i>Livestock Science</i> , 2020, 232, 103899.	0.6	9
1834	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 336-350.	3.9	73
1835	Human Genomic Diversity Where the Mediterranean Joins the Atlantic. <i>Molecular Biology and Evolution</i> , 2020, 37, 1041-1055.	3.5	11
1836	A bird's-eye view of Italian genomic variation through whole-genome sequencing. <i>European Journal of Human Genetics</i> , 2020, 28, 435-444.	1.4	29
1837	Skeletal maturation in relation to ethnic background in children of school age: The Generation R Study. <i>Bone</i> , 2020, 132, 115180.	1.4	18
1838	Ancestry-informative marker (AIM) SNP panel for the Malay population. <i>International Journal of Legal Medicine</i> , 2020, 134, 123-134.	1.2	2
1839	Spatiotemporal landscape genetics: Investigating ecology and evolution through space and time. <i>Molecular Ecology</i> , 2020, 29, 218-246.	2.0	51
1840	Unraveling the genetic diversity of Belgian Milk Sheep using medium-density SNP genotypes. <i>Animal Genetics</i> , 2020, 51, 258-265.	0.6	14
1841	Genome-wide scan of selection signatures in Dehong humped cattle for heat tolerance and disease resistance. <i>Animal Genetics</i> , 2020, 51, 292-299.	0.6	34
1842	Weak genetic structure despite strong genomic signal in lesser sandeel in the North Sea. <i>Evolutionary Applications</i> , 2020, 13, 376-387.	1.5	17
1843	Assessing changes in genomic divergence following a century of human-mediated secondary contact among wild and captive-bred ducks. <i>Molecular Ecology</i> , 2020, 29, 578-595.	2.0	35
1844	Genomic and Fitness Consequences of Genetic Rescue in Wild Populations. <i>Current Biology</i> , 2020, 30, 517-522.e5.	1.8	81
1845	While neither universally applicable nor practical operationally, the biological species concept continues to offer a compelling framework for studying species and speciation. <i>National Science Review</i> , 2020, 7, 1398-1400.	4.6	9
1846	Parasite turnover zone at secondary contact: A new pattern in host-parasite population genetics. <i>Molecular Ecology</i> , 2020, 29, 4653-4664.	2.0	7
1847	A chromosome-scale reference genome of trifoliate orange (<i>Poncirus trifoliata</i>) provides insights into disease resistance, cold tolerance and genome evolution in <i>Citrus</i> . <i>Plant Journal</i> , 2020, 104, 1215-1232.	2.8	56
1848	Genomic Phylogeography of <i>Gymnocarpus przewalskii</i> (Caryophyllaceae): Insights into Habitat Fragmentation in Arid Northwestern China. <i>Diversity</i> , 2020, 12, 335.	0.7	12
1849	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. <i>Nature Metabolism</i> , 2020, 2, 1126-1134.	5.1	43
1850	Interspecific introgression and natural selection in the evolution of Japanese apricot (<i>Prunus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 16	2.8	16

#	ARTICLE	IF	CITATIONS
1851	Omega-3 fatty acids and risk of cardiovascular disease in Inuit: First prospective cohort study. <i>Atherosclerosis</i> , 2020, 312, 28-34.	0.4	6
1852	SNP genotyping and population analysis of five indigenous Kazakh sheep breeds. <i>Livestock Science</i> , 2020, 241, 104252.	0.6	4
1853	Genome-wide association study reveals novel genetic loci contributing to cold tolerance at the germination stage in indica rice. <i>Plant Science</i> , 2020, 301, 110669.	1.7	11
1854	Postzygotic isolation drives genomic speciation between highly cryptic <i>Hypocnemis</i> antbirds from Amazonia. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2512-2525.	1.1	22
1855	An integrated personal and population-based Egyptian genome reference. <i>Nature Communications</i> , 2020, 11, 4719.	5.8	20
1856	The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism. <i>Nature Genetics</i> , 2020, 52, 1099-1110.	9.4	61
1857	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	1.6	2
1858	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. <i>Circulation</i> , 2020, 142, 1633-1646.	1.6	78
1859	A low-density SNP genotyping panel for the accurate prediction of cattle breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	10
1860	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. <i>Breast Cancer Research</i> , 2020, 22, 108.	2.2	9
1861	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
1862	An integrated peach genome structural variation map uncovers genes associated with fruit traits. <i>Genome Biology</i> , 2020, 21, 258.	3.8	77
1863	Genotyping-by-Sequencing to Unlock Genetic Diversity and Population Structure in White Yam (<i>Dioscorea rotundata</i> Poir.). <i>Agronomy</i> , 2020, 10, 1437.	1.3	16
1864	High site fidelity does not equate to population genetic structure for common goldeneye and Barrow's goldeneye in North America. <i>Journal of Avian Biology</i> , 2020, 51, .	0.6	4
1865	Whole genome sequencing of <i>Plasmodium vivax</i> isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008234.	1.3	25
1866	High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation. <i>American Journal of Human Genetics</i> , 2020, 107, 473-486.	2.6	12
1867	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. <i>Annals of Human Biology</i> , 2020, 47, 620-628.	0.4	14
1868	Limited genetic parallelism underlies recent, repeated incipient speciation in geographically proximate populations of an Arctic fish (<i>Salvelinus alpinus</i>). <i>Molecular Ecology</i> , 2020, 29, 4280-4294.	2.0	17

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1871	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
1872	Genomic diversity revealed by whole-genome sequencing in three Danish commercial pig breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	9
1873	Secondary contact and genomic admixture between rhesus and long-tailed macaques in the Indochina Peninsula. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1164-1179.	0.8	13
1874	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. <i>BMC Genomics</i> , 2020, 21, 496.	1.2	14
1875	Identifying the fitness costs of a pyrethroid-resistant genotype in the major arboviral vector <i>Aedes aegypti</i> . <i>Parasites and Vectors</i> , 2020, 13, 358.	1.0	20
1876	Investigating the genetic characteristics of the Csangos, a traditionally Hungarian speaking ethnic group residing in Romania. <i>Journal of Human Genetics</i> , 2020, 65, 1093-1103.	1.1	2
1877	Integration of ancient DNA with transdisciplinary dataset finds strong support for Inca resettlement in the south Peruvian coast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18359-18368.	3.3	21
1878	European genetic ancestry associated with risk of childhood ependymoma. <i>Neuro-Oncology</i> , 2020, 22, 1637-1646.	0.6	16
1879	Genomic insights on the contribution of balancing selection and local adaptation to the long-term survival of a widespread living fossil tree, <i>Cercidiphyllum japonicum</i> . <i>New Phytologist</i> , 2020, 228, 1674-1689.	3.5	22
1880	The Genomic Landscape of Divergence Across the Speciation Continuum in Island-Colonising Silvereyes (<i>Zosterops lateralis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3147-3163.	0.8	21
1881	Fast genomic analysis of aquatic bird populations from short single-end reads considering sex-related pitfalls. <i>Ecological Informatics</i> , 2020, 56, 101058.	2.3	3
1882	The Chromosome-Level Genome Sequence of the Autotetraploid Alfalfa and Resequencing of Core Germplasm Provide Genomic Resources for Alfalfa Research. <i>Molecular Plant</i> , 2020, 13, 1250-1261.	3.9	120
1883	Fine-scale genomic analyses of admixed individuals reveal unrecognized genetic ancestry components in Argentina. <i>PLoS ONE</i> , 2020, 15, e0233808.	1.1	23
1884	Genomic, Transcriptomic and Epigenomic Tools to Study the Domestication of Plants and Animals: A Field Guide for Beginners. <i>Frontiers in Genetics</i> , 2020, 11, 742.	1.1	21
1885	QTL mapping and candidate gene analysis of cadmium accumulation in polished rice by genome-wide association study. <i>Scientific Reports</i> , 2020, 10, 11791.	1.6	25
1886	Evolutionary Genomics of Structural Variation in Asian Rice (<i>Oryza sativa</i>) Domestication. <i>Molecular Biology and Evolution</i> , 2020, 37, 3507-3524.	3.5	58

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1888	The Genetic Population Structure of Robinson Crusoe Island, Chile. <i>Frontiers in Genetics</i> , 2020, 11, 669.	1.1	0
1889	Admixture and natural selection shaped genomes of an Austronesian-speaking population in the Solomon Islands. <i>Scientific Reports</i> , 2020, 10, 6872.	1.6	7
1890	Genomic differentiation and intercontinental population structure of mosquito vectors <i>Culex pipiens pipiens</i> and <i>Culex pipiens molestus</i> . <i>Scientific Reports</i> , 2020, 10, 7504.	1.6	24
1891	MC1R variants and associations with pigmentation characteristics and genetic ancestry in a Hispanic, predominately Puerto Rican, population. <i>Scientific Reports</i> , 2020, 10, 7303.	1.6	9
1892	The direction of genital asymmetry is expressed stochastically in internally fertilizing anablepid fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200969.	1.2	2
1893	Cooperation between <i>Broussonetia papyrifera</i> and Its Symbiotic Fungal Community To Improve Local Adaptation of the Host. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	7
1894	Genomic Profiling of Prostate Cancers from Men with African and European Ancestry. <i>Clinical Cancer Research</i> , 2020, 26, 4651-4660.	3.2	68
1895	Exploiting interspecific heterosis between African rice and Asian rice. <i>Crop Science</i> , 2020, 60, 2343-2353.	0.8	2
1896	Long-lived marine species may be resilient to environmental variability through a temporal portfolio effect. <i>Ecology and Evolution</i> , 2020, 10, 6435-6448.	0.8	1
1897	Unravelling selection signatures in a single dog breed suggests recent selection for morphological and behavioral traits. <i>Genetics & Genomics Next</i> , 2020, 1, e10024.	0.8	10
1898	Multiple waves of freshwater colonization of the three-spined stickleback in the Japanese Archipelago. <i>BMC Evolutionary Biology</i> , 2020, 20, 143.	3.2	6
1899	Genomic Characterization of the Istrian Shorthaired Hound. <i>Animals</i> , 2020, 10, 2013.	1.0	2
1900	WGVD: an integrated web-database for wheat genome variation and selective signatures. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	7
1901	Exome Sequencing of Native Populations From the Amazon Reveals Patterns on the Peopling of South America. <i>Frontiers in Genetics</i> , 2020, 11, 548507.	1.1	10
1902	Population structure, diversifying selection, and local adaptation in <i>Pinus patula</i> . <i>American Journal of Botany</i> , 2020, 107, 1555-1566.	0.8	14
1903	Genotype imputation and variability in polygenic risk score estimation. <i>Genome Medicine</i> , 2020, 12, 100.	3.6	28
1904	Variation under domestication in animal models: the case of the Mexican axolotl. <i>BMC Genomics</i> , 2020, 21, 827.	1.2	1

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1906	Population genomic data in spider mites point to a role for local adaptation in shaping range shifts. <i>Evolutionary Applications</i> , 2020, 13, 2821-2835.	1.5	13
1907	Genome-wide scan for selection signatures reveals novel insights into the adaptive capacity in local North African cattle. <i>Scientific Reports</i> , 2020, 10, 19466.	1.6	24
1908	Genome-Wide Population Genetic Analysis of Commercial, Indigenous, Game, and Wild Chickens Using 600K SNP Microarray Data. <i>Frontiers in Genetics</i> , 2020, 11, 543294.	1.1	31
1909	Genomic and Phenotypic Divergence in Wild Barley Driven by Microgeographic Adaptation. <i>Advanced Science</i> , 2020, 7, 2000709.	5.6	8
1910	Detecting Genetic Ancestry and Adaptation in the Taiwanese Han People. <i>Molecular Biology and Evolution</i> , 2021, 38, 4149-4165.	3.5	12
1911	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. <i>Genome Biology</i> , 2020, 21, 291.	3.8	23
1912	New Transcriptome-Based SNP Markers for Noug (<i>Guizotia abyssinica</i>) and Their Conversion to KASP Markers for Population Genetics Analyses. <i>Genes</i> , 2020, 11, 1373.	1.0	16
1913	AdmixSim: A Forward-Time Simulator for Various Complex Scenarios of Population Admixture. <i>Frontiers in Genetics</i> , 2020, 11, 601439.	1.1	4
1914	Genetic Diversity of Cameroon Cattle and a Putative Genomic Map for Resistance to Bovine Tuberculosis. <i>Frontiers in Genetics</i> , 2020, 11, 550215.	1.1	2
1915	Novel Variants in LRRK2 and GBA Identified in Latino Parkinson Disease Cohort Enriched for Caribbean Origin. <i>Frontiers in Neurology</i> , 2020, 11, 573733.	1.1	6
1916	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020, 11, 6014.	5.8	63
1917	The apple REFPOPâ€”a reference population for genomics-assisted breeding in apple. <i>Horticulture Research</i> , 2020, 7, 189.	2.9	37
1918	Estimating the contribution of Greenland Halibut (<i>Reinhardtius hippoglossoides</i>) stocks to nurseries by means of genotyping-by-sequencing: Sex and time matter. <i>Evolutionary Applications</i> , 2020, 13, 2155-2167.	1.5	19
1919	Identification of New Leaf Rust Resistance Loci in Wheat and Wild Relatives by Array-Based SNP Genotyping and Association Genetics. <i>Frontiers in Plant Science</i> , 2020, 11, 583738.	1.7	29
1920	Insights from Population Genomics to Enhance and Sustain Biological Control of Insect Pests. <i>Insects</i> , 2020, 11, 462.	1.0	19
1921	Host plants and <i>Wolbachia</i> shape the population genetics of sympatric herbivore populations. <i>Evolutionary Applications</i> , 2020, 13, 2740-2753.	1.5	13
1922	Genetic diversity and population structure of <i>Quercus fabri</i> Hance in China revealed by genotyping-by-sequencing. <i>Ecology and Evolution</i> , 2020, 10, 8949-8958.	0.8	6

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1924	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
1925	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. <i>Nature Communications</i> , 2020, 11, 3719.	5.8	108
1926	Convolutional Embedded Networks for Population Scale Clustering and Bio-Ancestry Inferencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 369-382.	1.9	6
1927	Genetic Dissection of Growth Traits in a Unique Chicken Advanced Intercross Line. <i>Frontiers in Genetics</i> , 2020, 11, 894.	1.1	14
1928	Genetic Consequences of the Transatlantic Slave Trade in the Americas. <i>American Journal of Human Genetics</i> , 2020, 107, 265-277.	2.6	99
1929	Mining whole genome sequence data to efficiently attribute individuals to source populations. <i>Scientific Reports</i> , 2020, 10, 12124.	1.6	10
1930	Breeding history and candidate genes responsible for black skin of Xichuan black-bone chicken. <i>BMC Genomics</i> , 2020, 21, 511.	1.2	32
1931	Whole Genome Sequencing of Four Representatives From the Admixed Population of the United Arab Emirates. <i>Frontiers in Genetics</i> , 2020, 11, 681.	1.1	5
1932	Genetic Basis of Response of Ghanaian Local Chickens to Infection With a Lentogenic Newcastle Disease Virus. <i>Frontiers in Genetics</i> , 2020, 11, 739.	1.1	8
1933	Genomic diversity and population structure of the indigenous Greek and Cypriot cattle populations. <i>Genetics Selection Evolution</i> , 2020, 52, 43.	1.2	15
1934	Genetic Diversity and Selection Signatures Within Diannan Small-Ear Pigs Revealed by Next-Generation Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 733.	1.1	25
1935	Statistical approaches to ancestry estimation: New and established methods for the quantification of cranial variation for forensic casework. , 2020, , 227-247.		2
1936	Population structure, genetic diversity, and selective signature of Chaka sheep revealed by whole genome sequencing. <i>BMC Genomics</i> , 2020, 21, 520.	1.2	13
1937	Genome-wide association study of turnip mosaic virus resistance in non-heading Chinese cabbage. <i>3 Biotech</i> , 2020, 10, 363.	1.1	5
1938	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
1939	Morphological divergence and the Quaternary speciation of <i>Actaea purpurea</i> (Ranunculaceae) and its relatives. <i>Journal of Systematics and Evolution</i> , 2022, 60, 43-54.	1.6	2
1940	Adaptive and maladaptive genetic diversity in small populations: Insights from the Brook Charr (<i>Salvelinus fontinalis</i>) case study. <i>Molecular Ecology</i> , 2020, 29, 3429-3445.	2.0	8

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1941	Population genomics identifies a distinct <i>Plasmodium vivax</i> population on the China-Myanmar border of Southeast Asia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008506.	1.3	18
1942	Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. <i>Nature Communications</i> , 2020, 11, 3868.	5.8	28
1943	Insight into the Current Genetic Diversity and Population Structure of Domestic Reindeer (<i>Rangifer</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	9
1944	Genetic diversity in Iranian indigenous sheep visâ€™vis selected exogenous sheep breeds and wild mouflon. <i>Animal Genetics</i> , 2020, 51, 772-787.	0.6	11
1945	Lousy grouse: Comparing evolutionary patterns in Alaska galliform lice to understand host evolution and hostâ€™parasite interactions. <i>Ecology and Evolution</i> , 2020, 10, 8379-8393.	0.8	11
1946	Climate and Urbanization Drive Mosquito Preference for Humans. <i>Current Biology</i> , 2020, 30, 3570-3579.e6.	1.8	153
1947	Demographic history and genomics of local adaptation in blue tit populations. <i>Evolutionary Applications</i> , 2020, 13, 1145-1165.	1.5	11
1948	A Genomewide Scan for Genetic Structure and Demographic History of Two Closely Related Species, <i>Rhododendron dauricum</i> and <i>R. mucronulatum</i> (<i>Rhododendron</i> , <i>Ericaceae</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 1093.	1.7	7
1949	Robust genome-wide ancestry inference for heterogeneous datasets: illustrated using the 1,000 genome project with 3D facial images. <i>Scientific Reports</i> , 2020, 10, 11850.	1.6	7
1950	Genomic diversity in pearl millet inbred lines derived from landraces and improved varieties. <i>BMC Genomics</i> , 2020, 21, 469.	1.2	12
1951	ContamLD: estimation of ancient nuclear DNA contamination using breakdown of linkage disequilibrium. <i>Genome Biology</i> , 2020, 21, 199.	3.8	29
1952	The influence of a priori grouping on inference of genetic clusters: simulation study and literature review of the DAPC method. <i>Heredity</i> , 2020, 125, 269-280.	1.2	77
1953	A genome-wide signatures of selection study of Welsh ponies and draft horses revealed five genes associated with horse type variation. <i>Gene Reports</i> , 2020, 21, 100833.	0.4	4
1954	Native American ancestry significantly contributes to neuromyelitis optica susceptibility in the admixed Mexican population. <i>Scientific Reports</i> , 2020, 10, 13706.	1.6	18
1955	Population analysis of the Korean native duck using whole-genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 554.	1.2	5
1956	Unsupervised detection of ancestry tracks with the GHap <sc>r</sc> package. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1448-1454.	2.2	6
1957	Opioid and Dopamine Genes Interact to Predict Naltrexone Response in a Randomized Alcohol Use Disorder Clinical Trial. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 2084-2096.	1.4	4
1958	Impact of Genetic Ancestry on Prognostic Biomarkers in Uveal Melanoma. <i>Cancers</i> , 2020, 12, 3208.	1.7	2

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1959	Landscape Genomics of a Widely Distributed Snake, <i>Dolichophis caspius</i> (Gmelin, 1789) across Eastern Europe and Western Asia. <i>Genes</i> , 2020, 11, 1218.	1.0	6
1960	The Phenotypic Consequences of Genetic Divergence between Admixed Latin American Populations: Antioquia and Chocó ³ , Colombia. <i>Genome Biology and Evolution</i> , 2020, 12, 1516-1527.	1.1	3
1961	Genome-wide detection of signatures of selection in indicine and Brazilian locally adapted taurine cattle breeds using whole-genome re-sequencing data. <i>BMC Genomics</i> , 2020, 21, 624.	1.2	10
1962	Population genetic structure of the great star coral, <i>Montastraea cavernosa</i> , across the Cuban archipelago with comparisons between microsatellite and SNP markers. <i>Scientific Reports</i> , 2020, 10, 15432.	1.6	17
1963	Genomic and transcriptomic analysis unveils population evolution and development of pesticide resistance in fall armyworm <i>Spodoptera frugiperda</i> . <i>Protein and Cell</i> , 2022, 13, 513-531.	4.8	72
1964	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	13.7	197
1965	Major QTL with pleiotropic effects controlling time of leaf budburst and flowering-related traits in walnut (<i>Juglans regia</i> L.). <i>Scientific Reports</i> , 2020, 10, 15207.	1.6	14
1966	Genetic Variability in Local and Imported Germplasm Chicken Populations as Revealed by Analyzing Runs of Homozygosity. <i>Animals</i> , 2020, 10, 1887.	1.0	11
1967	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	5.8	67
1968	Contrasting signatures of genomic divergence during sympatric speciation. <i>Nature</i> , 2020, 588, 106-111.	13.7	115
1969	Landscape genomics reveals genetic evidence of local adaptation in a widespread tree, the Chinese wingnut (<i>Pterocarya stenoptera</i>). <i>Journal of Systematics and Evolution</i> , 2022, 60, 386-397.	1.6	10
1970	Origins and genetic legacy of prehistoric dogs. <i>Science</i> , 2020, 370, 557-564.	6.0	152
1971	Genomic Selection for Prediction of Fruit-Related Traits in Pepper (<i>Capsicum</i> spp.). <i>Frontiers in Plant Science</i> , 2020, 11, 570871.	1.7	19
1972	Genetic affinity between Ningxia Hui and eastern Asian populations revealed by a set of InDel loci. <i>Royal Society Open Science</i> , 2020, 7, 190358.	1.1	13
1973	Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. <i>BMC Plant Biology</i> , 2020, 20, 404.	1.6	28
1974	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
1975	Population genetic structure and gene flow of rare and endangered <i>Tetraena mongolica</i> Maxim. revealed by reduced representation sequencing. <i>BMC Plant Biology</i> , 2020, 20, 391.	1.6	27
1976	Haplotype Block Analysis Reveals Candidate Genes and QTLs for Meat Quality and Disease Resistance in Chinese Jiangquhai Pig Breed. <i>Frontiers in Genetics</i> , 2020, 11, 752.	1.1	6

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1978	Genome diversity of Chinese indigenous chicken and the selective signatures in Chinese gamecock chicken. <i>Scientific Reports</i> , 2020, 10, 14532.	1.6	39
1979	Genome-wide patterns of divergence and introgression after secondary contact between <i>Pungitius</i> sticklebacks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190548.	1.8	32
1980	Species complex diversification by host plant use in an herbivorous insect: The source of Puerto Rican cactus mealybug pest and implications for biological control. <i>Ecology and Evolution</i> , 2020, 10, 10463-10480.	0.8	9
1981	The evolution of strong reproductive isolation between sympatric intertidal snails. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190545.	1.8	23
1982	Ecological divergence and hybridization of Neotropical <i>Leishmania</i> parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25159-25168.	3.3	60
1983	Resequencing of 1,143 indica rice accessions reveals important genetic variations and different heterosis patterns. <i>Nature Communications</i> , 2020, 11, 4778.	5.8	47
1984	Genome-wide association studies of ionomic and agronomic traits in USDA mini core collection of rice and comparative analyses of different mapping methods. <i>BMC Plant Biology</i> , 2020, 20, 441.	1.6	25
1985	Whole-Exome Profiling of NSCLC Among African Americans. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1880-1892.	0.5	19
1986	Sunshine versus gold: The effect of population age on genetic structure of an invasive mosquito. <i>Ecology and Evolution</i> , 2020, 10, 9588-9599.	0.8	4
1987	Defining relictual biodiversity: Conservation units in speckled dace (Leuciscidae: <i>Rhinichthys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	0.8	15
1988	ddRAD sequencing-based genotyping for population structure analysis in cultivated tomato provides new insights into the genomic diversity of Mediterranean "da serbo" type long shelf-life germplasm. <i>Horticulture Research</i> , 2020, 7, 134.	2.9	30
1989	The role of agro-ecological factors and transboundary transhumance in shaping the genetic diversity in four indigenous cattle populations of Benin. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 622-640.	0.8	9
1990	Characterization of Celiac Disease-Related Epitopes and Gluten Fractions, and Identification of Associated Loci in Durum Wheat. <i>Agronomy</i> , 2020, 10, 1231.	1.3	6
1991	Genetic Diversity and Population Structure of Maize Inbred Lines with Varying Levels of Resistance to <i>Striga Hermonthica</i> Using Agronomic Trait-Based and SNP Markers. <i>Plants</i> , 2020, 9, 1223.	1.6	8
1992	Genetic Characterization of Russian Rapeseed Collection and Association Mapping of Novel Loci Affecting Glucosinolate Content. <i>Genes</i> , 2020, 11, 926.	1.0	4
1993	Size reductions and genomic changes within two generations in wild walleye populations: associated with harvest?. <i>Evolutionary Applications</i> , 2020, 13, 1128-1144.	1.5	25
1994	Hybrid Versus Autochthonous Turkey Populations: Homozygous Genomic Regions Occurrences Due to Artificial and Natural Selection. <i>Animals</i> , 2020, 10, 1318.	1.0	8

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1995	Increased Genetic Diversity via Gene Flow Provides Hope for <i>Acacia whibleyana</i> , an Endangered Wattle Facing Extinction. <i>Diversity</i> , 2020, 12, 299.	0.7	12
1996	Amerindian Ancestry Influences Genetic Susceptibility to Chronic Obstructive Pulmonary Disease. <i>Journal of Personalized Medicine</i> , 2020, 10, 93.	1.1	7
1997	Demographic history shaped geographical patterns of deleterious mutation load in a broadly distributed Pacific Salmon. <i>PLoS Genetics</i> , 2020, 16, e1008348.	1.5	38
1998	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
1999	Comparative analysis of racial differences in breast tumor microbiome. <i>Scientific Reports</i> , 2020, 10, 14116.	1.6	37
2000	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020, 3, 437.	2.0	44
2001	Optimization of the genotyping-by-sequencing SNP calling for diversity analysis in cape gooseberry (<i>Physalis peruviana</i> L.) and related taxa. <i>PLoS ONE</i> , 2020, 15, e0238383.	1.1	5
2002	STAGdb: a 30K SNP genotyping array and Science Gateway for <i>Acropora</i> corals and their dinoflagellate symbionts. <i>Scientific Reports</i> , 2020, 10, 12488.	1.6	25
2003	Multiple ancestral haplotypes harboring regulatory mutations cumulatively contribute to a QTL affecting chicken growth traits. <i>Communications Biology</i> , 2020, 3, 472.	2.0	19
2004	Spatial gradients of introgressed ancestry reveal cryptic connectivity patterns in a high gene flow marine fish. <i>Molecular Ecology</i> , 2020, 29, 3857-3871.	2.0	9
2005	Genetic diversity of <i>Faidherbia albida</i> populations in the Sudano Sahelian region of Cameroon, using simple sequence repeat (SSR) markers. <i>African Journal of Biotechnology</i> , 2020, 19, 415-425.	0.3	1
2006	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	5.8	60
2007	Selection Signatures Analysis Reveals Genes Associated with High-Altitude Adaptation in Tibetan Goats from Nagqu, Tibet. <i>Animals</i> , 2020, 10, 1599.	1.0	21
2008	An evolutionary population structure model reveals pleiotropic effects of <i>GmPDAT</i> for traits related to seed size and oil content in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 6988-7002.	2.4	35
2009	Interactions between genetics and environment shape <i>Camelina</i> seed oil composition. <i>BMC Plant Biology</i> , 2020, 20, 423.	1.6	22
2010	Berbers and Arabs: Tracing the genetic diversity and history of Southern Tunisia through genome wide analysis. <i>American Journal of Physical Anthropology</i> , 2020, 173, 697-708.	2.1	5
2011	Genome Wide Association Studies in Multiple Spinach Breeding Populations Refine Downy Mildew Race 13 Resistance Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 563187.	1.7	23
2012	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143

#	ARTICLE	IF	CITATIONS
2013	Polygenic Scores for Height in Admixed Populations. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4027-4036.	0.8	78
2014	Evolution of putative barrier loci at an intermediate stage of speciation with gene flow in campions (<i>Silene</i>). <i>Molecular Ecology</i> , 2020, 29, 3511-3525.	2.0	10
2015	Genomic variation among populations provides insight into the causes of metacommunity survival. <i>Ecology</i> , 2020, 101, e03182.	1.5	5
2016	Population sequencing enhances understanding of tea plant evolution. <i>Nature Communications</i> , 2020, 11, 4447.	5.8	123
2017	<i>Yersinia pestis</i> strains from Latvia show depletion of the <i>pla</i> virulence gene at the end of the second plague pandemic. <i>Scientific Reports</i> , 2020, 10, 14628.	1.6	25
2018	The genomic architecture of South African mutton, pelt, dual-purpose and nondescript sheep breeds relative to global sheep populations. <i>Animal Genetics</i> , 2020, 51, 910-923.	0.6	9
2019	Digging into the Genomic Past of Swiss Honey Bees by Whole-Genome Sequencing Museum Specimens. <i>Genome Biology and Evolution</i> , 2020, 12, 2535-2551.	1.1	26
2020	Genome-wide detection of tandem DNA repeats that are expanded in autism. <i>Nature</i> , 2020, 586, 80-86.	13.7	155
2021	Genomic Regions 10q22.2, 17q21.31, and 2p23.1 Can Contribute to a Lower Lung Function in African Descent Populations. <i>Genes</i> , 2020, 11, 1047.	1.0	3
2022	Dutch population structure across space, time and GWAS design. <i>Nature Communications</i> , 2020, 11, 4556.	5.8	21
2023	A transcriptomic variation map provides insights into the genetic basis of <i>Pinus massoniana</i> Lamb. evolution and the association with oleoresin yield. <i>BMC Plant Biology</i> , 2020, 20, 375.	1.6	9
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2025	The Multisite <i>PeachRefPop</i> Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. <i>Plant Physiology</i> , 2020, 184, 632-646.	2.3	12
2026	Mining of candidate genes for nitrogen use efficiency in maize based on genome-wide association study. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	8
2027	Genome sequencing and population genomics modeling provide insights into the local adaptation of weeping forsythia. <i>Horticulture Research</i> , 2020, 7, 130.	2.9	33
2028	Genetics and geography of leukocyte telomere length in sub-Saharan Africans. <i>Human Molecular Genetics</i> , 2020, 29, 3014-3020.	1.4	5
2029	The Influence of Environmental Variation on the Genetic Structure of a Poison Frog Distributed Across Continuous Amazonian Rainforest. <i>Journal of Heredity</i> , 2020, 111, 457-470.	1.0	9
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#	ARTICLE	IF	CITATIONS
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2032	Adaptation by copy number variation increases insecticide resistance in the fall armyworm. <i>Communications Biology</i> , 2020, 3, 664.	2.0	41
2033	Identification and population genetic analyses of copy number variations in six domestic goat breeds and Bezoar ibexes using next-generation sequencing. <i>BMC Genomics</i> , 2020, 21, 840.	1.2	7
2034	A Deep Learning Approach to Population Structure Inference in Inbred Lines of Maize. <i>Frontiers in Genetics</i> , 2020, 11, 543459.	1.1	13
2035	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. <i>Frontiers in Plant Science</i> , 2020, 11, 569905.	1.7	44
2036	The Genomic Variation in the Aosta Cattle Breeds Raised in an Extensive Alpine Farming System. <i>Animals</i> , 2020, 10, 2385.	1.0	8
2037	Diversity Patterns of Bermuda Grass along Latitudinal Gradients at Different Temperatures in Southeastern China. <i>Plants</i> , 2020, 9, 1778.	1.6	5
2038	Genomic Analyses Reveal Adaptation to Hot Arid and Harsh Environments in Native Chickens of China. <i>Frontiers in Genetics</i> , 2020, 11, 582355.	1.1	19
2039	Signatures of Selection in Composite Vrindavani Cattle of India. <i>Frontiers in Genetics</i> , 2020, 11, 589496.	1.1	27
2040	Improving Genomic Prediction of Crossbred and Purebred Dairy Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 598580.	1.1	21
2041	No Population Genetic Structure of Skipjack Tuna (<i>Katsuwonus pelamis</i>) in the Tropical Western and Central Pacific Assessed Using Single Nucleotide Polymorphisms. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	3
2042	Genetic Diversity of South African Indigenous Goat Population from Four Provinces Using Genome-Wide SNP Data. <i>Sustainability</i> , 2020, 12, 10361.	1.6	5
2043	Population Genetic Structure and Gene Expression Plasticity of the Deep-Sea Vent and Seep Squat Lobster <i>Shinkaia crosnieri</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	16
2044	Identification of New <i>Helicobacter pylori</i> Subpopulations in Native Americans and Mestizos From Peru. <i>Frontiers in Microbiology</i> , 2020, 11, 601839.	1.5	7
2045	A Causality Perspective of Genomic Breed Composition for Composite Animals. <i>Frontiers in Genetics</i> , 2020, 11, 546052.	1.1	4
2046	Composite modeling of leaf shape along shoots discriminates <i>Vitis</i> species better than individual leaves. <i>Applications in Plant Sciences</i> , 2020, 8, e11404.	0.8	29
2047	Genetic adaptation of Tibetan poplar (<i>Populus szechuanica</i> var. <i>tibetica</i>) to high altitudes on the Qinghai-Tibetan Plateau. <i>Ecology and Evolution</i> , 2020, 10, 10974-10985.	0.8	4
2048	Evaluating wildlife translocations using genomics: A bighorn sheep case study. <i>Ecology and Evolution</i> , 2020, 10, 13687-13704.	0.8	16

#	ARTICLE	IF	CITATIONS
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2050	Insights into genomic structure and evolutionary processes of coastal <i>Suaeda</i> species in East Asia using cpDNA, nDNA, and genome-wide SNPs. <i>Scientific Reports</i> , 2020, 10, 20950.	1.6	2
2051	The patterns of admixture, divergence, and ancestry of African cattle populations determined from genome-wide SNP data. <i>BMC Genomics</i> , 2020, 21, 869.	1.2	16
2052	Application of genome-wide insertion/deletion markers on genetic structure analysis and identity signature of <i>Malus</i> accessions. <i>BMC Plant Biology</i> , 2020, 20, 540.	1.6	7
2053	Genome-Wide Association Study of Root System Development at Seedling Stage in Rice. <i>Genes</i> , 2020, 11, 1395.	1.0	13
2054	Population Connectivity Predicts Vulnerability to White-Nose Syndrome in the Chilean <i>Myotis</i> (<i>Myotis chiloensis</i>) - A Genomics Approach. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2117-2126.	0.8	9
2055	Genomic Heritability and Genome-Wide Association Studies of Plasma Metabolites in Crossbred Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 538600.	1.1	9
2056	Genetic Signatures of Selection for Cashmere Traits in Chinese Goats. <i>Animals</i> , 2020, 10, 1905.	1.0	21
2057	Genome-wide investigation of a Korean synthetic breed, Woori-Heukdon using the Illumina PorcineSNP60K BeadChip. <i>Genes and Genomics</i> , 2020, 42, 1443-1453.	0.5	2
2058	Early medieval genetic data from Ural region evaluated in the light of archaeological evidence of ancient Hungarians. <i>Scientific Reports</i> , 2020, 10, 19137.	1.6	16
2059	Whole Transcriptome Analysis Identifies the Taxonomic Status of a New Chinese Native Cattle Breed and Reveals Genes Related to Body Size. <i>Frontiers in Genetics</i> , 2020, 11, 562855.	1.1	2
2060	How Ancestry Influences the Chances of Finding Unrelated Donors: An Investigation in Admixed Brazilians. <i>Frontiers in Immunology</i> , 2020, 11, 584950.	2.2	12
2061	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
2062	The story of the lost twins: decoding the genetic identities of the Kumhar and Kurcha populations from the Indian subcontinent. <i>BMC Genetics</i> , 2020, 21, 117.	2.7	5
2063	The Simons Genome Diversity Project: A Global Analysis of Mobile Element Diversity. <i>Genome Biology and Evolution</i> , 2020, 12, 779-794.	1.1	20
2064	RAD-seq-Based High-Density Linkage Map Construction and QTL Mapping of Biomass-Related Traits in Sorghum using the Japanese Landrace Takakibi NOG. <i>Plant and Cell Physiology</i> , 2020, 61, 1262-1272.	1.5	25
2065	Targeted conservation genetics of the endangered chimpanzee. <i>Heredity</i> , 2020, 125, 15-27.	1.2	11
2066	Comparing the diversity of the casein genes in the Asian mouflon and domestic sheep. <i>Animal Genetics</i> , 2020, 51, 470-475.	0.6	9

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2068	Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008766.	1.5	5
2069	Identification of Distinct Heterogenic Subtypes and Molecular Signatures Associated with African Ancestry in Triple Negative Breast Cancer Using Quantified Genetic Ancestry Models in Admixed Race Populations. <i>Cancers</i> , 2020, 12, 1220.	1.7	19
2070	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	13.5	69
2071	Developing ancestry informative marker panel for Nigeria-Cameroonian chimpanzees. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	2
2072	Ancestral Haplotype Mapping for GWAS and Detection of Signatures of Selection in Admixed Dairy Cattle of Kenya. <i>Frontiers in Genetics</i> , 2020, 11, 544.	1.1	12
2073	Genetic Connectedness Between Norwegian White Sheep and New Zealand Composite Sheep Populations With Similar Development History. <i>Frontiers in Genetics</i> , 2020, 11, 371.	1.1	11
2074	The Genetic Basis of Morphological Diversity in Domesticated Goldfish. <i>Current Biology</i> , 2020, 30, 2260-2274.e6.	1.8	52
2075	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
2076	Spatial variation in gene flow across a hybrid zone reveals causes of reproductive isolation and asymmetric introgression in wall lizards*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1289-1300.	1.1	23
2077	Discordant evolution of mitochondrial and nuclear yeast genomes at population level. <i>BMC Biology</i> , 2020, 18, 49.	1.7	42
2078	Polyploidy breaks speciation barriers in Australian burrowing frogs <i>Neobatrachus</i> . <i>PLoS Genetics</i> , 2020, 16, e1008769.	1.5	40
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2081	A positively selected <i>FBN1</i> missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020, 582, 234-239.	13.7	39
2082	A Custom Genotyping Array Reveals Population-Level Heterogeneity for the Genetic Risks of Prostate Cancer and Other Cancers in Africa. <i>Cancer Research</i> , 2020, 80, 2956-2966.	0.4	25
2083	Ancestry-specific predisposing germline variants in cancer. <i>Genome Medicine</i> , 2020, 12, 51.	3.6	35
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#	ARTICLE	IF	CITATIONS
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2086	Recent introgression between Taiga Bean Goose and Tundra Bean Goose results in a largely homogeneous landscape of genetic differentiation. <i>Heredity</i> , 2020, 125, 73-84.	1.2	13
2087	Conservation of the dark bee (<i>Apis mellifera mellifera</i>): Estimating C-lineage introgression in Nordic breeding stocks. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2020, 69, 157-168.	0.2	1
2088	Patterns of hybridization and cryptic introgression among one- and four-needled pinyon pines. <i>Annals of Botany</i> , 2020, 126, 401-411.	1.4	10
2089	Population-specific reference panels are crucial for genetic analyses: an example of the CREBRF locus in Native Hawaiians. <i>Human Molecular Genetics</i> , 2020, 29, 2275-2284.	1.4	27
2090	Optimizing Sample Size for Population Genomic Study in a Global Invasive Lady Beetle, <i>Harmonia Axyridis</i> . <i>Insects</i> , 2020, 11, 290.	1.0	22
2091	Ancient DNA reveals two paternal lineages C2a1a1b1a/F3830 and C2b1b/F845 in past nomadic peoples distributed on the Mongolian Plateau. <i>American Journal of Physical Anthropology</i> , 2020, 172, 402-411.	2.1	5
2092	Ancient DNA indicates human population shifts and admixture in northern and southern China. <i>Science</i> , 2020, 369, 282-288.	6.0	214
2093	Genomic Diversity, Population Structure, and Signature of Selection in Five Chinese Native Sheep Breeds Adapted to Extreme Environments. <i>Genes</i> , 2020, 11, 494.	1.0	20
2094	Coalescent Models of Demographic History: Application to Plant Domestication. <i>Population Genomics</i> , 2020, , 1.	0.2	0
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2097	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. <i>Genetics Selection Evolution</i> , 2020, 52, 25.	1.2	58
2098	Genome-defined African ancestry is associated with distinct mutations and worse survival in patients with diffuse large B-cell lymphoma. <i>Cancer</i> , 2020, 126, 3493-3503.	2.0	15
2099	Study of the genetic diversity of cocoa populations (<i>Theobroma cacao</i> L.) of Martinique (FWI) and potential for processing and the cocoa industry. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 1969-1979.	0.8	4
2100	Genome-wide DNA methylation and gene expression patterns reflect genetic ancestry and environmental differences across the Indonesian archipelago. <i>PLoS Genetics</i> , 2020, 16, e1008749.	1.5	30
2101	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
2102	Big data challenges in genomics. <i>Handbook of Statistics</i> , 2020, 43, 337-348.	0.4	2

#	ARTICLE	IF	CITATIONS
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2104	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020, 30, 2078-2091.e11.	1.8	34
2105	Long-read bitter gourd (<i>Momordica charantia</i>) genome and the genomic architecture of nonclassic domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14543-14551.	3.3	43
2106	Korean Genome Project: 1094 Korean personal genomes with clinical information. <i>Science Advances</i> , 2020, 6, eaaz7835.	4.7	75
2107	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
2108	Gene flow in the anemone <i>Anthopleura elegantissima</i> limits signatures of local adaptation across an extensive geographic range. <i>Molecular Ecology</i> , 2020, 29, 2550-2566.	2.0	11
2109	Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa. <i>Science Advances</i> , 2020, 6, eaaz0183.	4.7	56
2110	Estimation of Genomic Breed Composition for Purebred and Crossbred Animals Using Sparsely Regularized Admixture Models. <i>Frontiers in Genetics</i> , 2020, 11, 576.	1.1	8
2111	Genome-wide analysis of unrecognised ethnic group Chuanqing people revealing a close affinity with Southern Han Chinese. <i>Annals of Human Biology</i> , 2020, 47, 465-471.	0.4	9
2112	Fine mapping of the Ca3GT gene controlling anthocyanin biosynthesis in mature unripe fruit of <i>Capsicum annuum</i> L.. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2729-2742.	1.8	18
2113	Evaluating individual genome similarity with a topic model. <i>Bioinformatics</i> , 2020, 36, 4757-4764.	1.8	1
2114	Secondary contact zones of closely related <i>Erebia</i> butterflies overlap with narrow phenotypic and parasitic clines. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1152-1163.	0.8	17
2115	Conservation Assessment of the State Goat Farms by Using SNP Genotyping Data. <i>Genes</i> , 2020, 11, 652.	1.0	7
2116	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. <i>Nature Communications</i> , 2020, 11, 2815.	5.8	142
2117	The Origin and Composition of Korean Ethnicity Analyzed by Ancient and Present-Day Genome Sequences. <i>Genome Biology and Evolution</i> , 2020, 12, 553-565.	1.1	17
2118	Genomic insights into the early peopling of the Caribbean. <i>Science</i> , 2020, 369, 456-460.	6.0	44
2119	The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. <i>American Journal of Physical Anthropology</i> , 2020, 172, 638-649.	2.1	20
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#	ARTICLE	IF	CITATIONS
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2122	Genome-wide association reveals a complex architecture for rust resistance in 2300 worldwide bread wheat accessions screened under various Australian conditions. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2695-2712.	1.8	22
2123	Phylogenomics and molecular species delimitation reveals great cryptic diversity of leaf-toed geckos (Phyllodactylidae: <i>Phyllodactylus</i>), ancient origins, and diversification in Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106880.	1.2	11
2124	Genomic evidence for gene flow between monarchs with divergent migratory phenotypes and flight performance. <i>Molecular Ecology</i> , 2020, 29, 2567-2582.	2.0	35
2125	Genotyping-by-Sequencing Derived Single Nucleotide Polymorphisms Provide the First Well-Resolved Phylogeny for the Genus <i>Triticum</i> (Poaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 688.	1.7	16
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2127	A dynastic elite in monumental Neolithic society. <i>Nature</i> , 2020, 582, 384-388.	13.7	94
2128	Genomics of Clinal Local Adaptation in <i>Pinus sylvestris</i> Under Continuous Environmental and Spatial Genetic Setting. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2683-2696.	0.8	24
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2131	Identification of Selective Sweeps in the Domesticated Table and Wine Grape (<i>Vitis vinifera</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 572.	1.7	14
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2134	Population Genomics Reveals Shallow Genetic Structure in a Connected and Ecologically Important Fish From the Northwestern Pacific Ocean. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	11
2135	Genetic Diversity and Ancestral Study for Korean Native Pigs Using 60K SNP Chip. <i>Animals</i> , 2020, 10, 760.	1.0	5
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2137	A regulatory variant in the C1Q gene cluster is associated with tuberculosis susceptibility and C1qA plasma levels in a South African population. <i>Immunogenetics</i> , 2020, 72, 305-314.	1.2	7
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#	ARTICLE	IF	CITATIONS
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2141	Enabling population assignment from cancer genomes with SNP2pop. <i>Scientific Reports</i> , 2020, 10, 4846.	1.6	7
2142	Within-island diversification in a passerine bird. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192999.	1.2	16
2143	Rapid and strong population genetic differentiation and genomic signatures of climatic adaptation in an invasive mealybug. <i>Diversity and Distributions</i> , 2020, 26, 610-622.	1.9	15
2144	Population structure of <i>Apodemus flavicollis</i> and comparison to <i>Apodemus sylvaticus</i> in northern Poland based on RAD-seq. <i>BMC Genomics</i> , 2020, 21, 241.	1.2	10
2145	Can introgression in M-lineage honey bees be detected by abdominal colour patterns?. <i>Apidologie</i> , 2020, 51, 583-593.	0.9	2
2146	Genome-Wide Analysis Reveals Human-Mediated Introgression from Western Pigs to Indigenous Chinese Breeds. <i>Genes</i> , 2020, 11, 275.	1.0	11
2147	Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing. <i>Genes</i> , 2020, 11, 276.	1.0	14
2148	Dispersal patterns of <i>Trypanosoma cruzi</i> in Arequipa, Peru. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007910.	1.3	4
2149	What is ancestry?. <i>PLoS Genetics</i> , 2020, 16, e1008624.	1.5	91
2150	Evolution and diversity of the wild rice <i>Oryza officinalis</i> complex, across continents genome types, and ploidy levels. <i>Genome Biology and Evolution</i> , 2020, 12, 413-428.	1.1	17
2151	Deciphering lifelong thermal niche using otolith $\delta^{18}O$ thermometry within supplemented lake trout (<i>Salvelinus namaycush</i>) populations. <i>Freshwater Biology</i> , 2020, 65, 1114-1127.	1.2	5
2152	Parallel selection on thermal physiology facilitates repeated adaptation of city lizards to urban heat islands. <i>Nature Ecology and Evolution</i> , 2020, 4, 652-658.	3.4	102
2153	Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. <i>GigaScience</i> , 2020, 9, .	3.3	31
2154	Stable species boundaries despite ten million years of hybridization in tropical eels. <i>Nature Communications</i> , 2020, 11, 1433.	5.8	53
2155	Gene-flow from steppe individuals into Cucuteni-Trypillia associated populations indicates long-standing contacts and gradual admixture. <i>Scientific Reports</i> , 2020, 10, 4253.	1.6	15
2156	The German Shorthair Pointer Dog Breed (<i>Canis lupus familiaris</i>): Genomic Inbreeding and Variability. <i>Animals</i> , 2020, 10, 498.	1.0	6

#	ARTICLE	IF	CITATIONS
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2248	The genetic history of France. <i>European Journal of Human Genetics</i> , 2020, 28, 853-865.	1.4	15
2249	Whole-Genome Signatures of Selection in Sport Horses Revealed Selection Footprints Related to Musculoskeletal System Development Processes. <i>Animals</i> , 2020, 10, 53.	1.0	15
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2253	Association of <i>HSD17B13</i> rs72613567:TA with non-alcoholic fatty liver disease in Hispanics/Latinos. <i>Liver International</i> , 2020, 40, 889-893.	1.9	20
2254	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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2259	Genomic insight into the origins and dispersal of the Brazilian coastal natives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2372-2377.	3.3	27
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#	ARTICLE	IF	CITATIONS
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2270	Comparative selection signature analyses identify genomic footprints in Reggiana cattle, the traditional breed of the Parmigiano-Reggiano cheese production system. <i>Animal</i> , 2020, 14, 921-932.	1.3	12
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2274	Genome-Wide Discovery of Single-Nucleotide Polymorphisms and Their Application in Population Genetic Studies in the Endangered Japanese Eel (<i>Anguilla japonica</i>). <i>Frontiers in Marine Science</i> , 2020, 6, .	1.2	1
2275	Genomic regions under selection in the feralization of the dingoes. <i>Nature Communications</i> , 2020, 11, 671.	5.8	49
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2277	Genetic structure and admixture in sheep from terminal breeds in the United States. <i>Animal Genetics</i> , 2020, 51, 284-291.	0.6	21
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#	ARTICLE	IF	CITATIONS
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2285	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	9.4	146
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2287	Genome-wide association study of multiple yield traits in a diversity panel of polyploid sugarcane (<i>Saccharum</i> spp.). <i>Plant Genome</i> , 2020, 13, e20006.	1.6	27
2288	Genetic position of Hungarian Grey among European cattle and identification of breed-specific markers. <i>Animal</i> , 2020, 14, 1786-1792.	1.3	9
2289	Estimating narrow-sense heritability using family data from admixed populations. <i>Heredity</i> , 2020, 124, 751-762.	1.2	6
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2298	Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program. <i>Animals</i> , 2020, 10, 542.	1.0	4
2299	A Two-Stage Mutual Information Based Bayesian Lasso Algorithm for Multi-Locus Genome-Wide Association Studies. <i>Entropy</i> , 2020, 22, 329.	1.1	5
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2436	Genetic ancestry changes in Stone to Bronze Age transition in the East European plain. <i>Science Advances</i> , 2021, 7, .	4.7	32
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#	ARTICLE	IF	CITATIONS
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2462	Population structure, inbreeding and admixture in local cattle populations managed by community-based breeding programs in Burkina Faso. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 379-388.	0.8	9
2463	Genome-Wide Association Study Dissects Resistance Loci against Bacterial Blight in a Diverse Rice Panel from the 3000 Rice Genomes Project. <i>Rice</i> , 2021, 14, 22.	1.7	14
2464	Admixture mapping identifies African and Amerindigenous local ancestry loci associated with fetal growth. <i>Human Genetics</i> , 2021, 140, 985-997.	1.8	5
2466	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	133
2467	A chromosome-level genome assembly for the tertiary relict plant <i>Tetracentron sinense</i> Oliv. (Trochodendraceae). <i>Molecular Ecology Resources</i> , 2021, 21, 1186-1199.	2.2	12
2468	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of <i>Plasmodium falciparum</i> within and between continents. <i>PLoS Genetics</i> , 2021, 17, e1009269.	1.5	20
2469	Complex genetic admixture histories reconstructed with Approximate Bayesian Computation. <i>Molecular Ecology Resources</i> , 2021, 21, 1098-1117.	2.2	13
2470	A meta-analysis uncovers the first sequence variant conferring risk of Bell's palsy. <i>Scientific Reports</i> , 2021, 11, 4188.	1.6	8

#	ARTICLE	IF	CITATIONS
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2473	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	13.7	216
2474	A Matter of Scale: Population Genomic Structure and Connectivity of Fisheries At-Risk Common Dolphins (<i>Delphinus delphis</i>) From Australasia. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
2475	SambaR: An R package for fast, easy and reproducible population genetic analyses of biallelic SNP data sets. <i>Molecular Ecology Resources</i> , 2021, 21, 1369-1379.	2.2	37
2476	Later Stone Age human hair from Vaalkrans Shelter, Cape Floristic Region of South Africa, reveals genetic affinity to Khoe groups. <i>American Journal of Physical Anthropology</i> , 2021, 174, 701-713.	2.1	3
2477	Genetic diversity and population structure of Tibetan sheep breeds determined by whole genome resequencing. <i>Tropical Animal Health and Production</i> , 2021, 53, 174.	0.5	3
2478	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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2480	Genetic Architecture Underlying the Metabolites of Chlorogenic Acid Biosynthesis in <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2386.	1.8	7
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2492	Genetic status of lowland-type Racka sheep colour variants. <i>Animal</i> , 2021, 15, 100080.	1.3	3
2495	A new <i>Cannabis</i> genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. <i>New Phytologist</i> , 2021, 230, 1665-1679.	3.5	87
2496	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
2497	Genetic dissection of rice appearance quality and cooked rice elongation by genome-wide association study. <i>Crop Journal</i> , 2021, 9, 1470-1480.	2.3	10
2498	Genomic population structure of sympatric sexual and asexual populations in a parasitic wasp, <i>Meteorus pulchricornis</i> (Hymenoptera: Braconidae), inferred from six hundred single nucleotide polymorphism loci. <i>Molecular Ecology</i> , 2021, 30, 1612-1623.	2.0	5
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2502	Incomplete lineage sorting and ancient admixture, and speciation without morphological change in ghost-worm cryptic species. <i>PeerJ</i> , 2021, 9, e10896.	0.9	15
2503	Genetic diversity and population structure of popcorn germplasm resources using genome-wide SNPs through genotyping-by-sequencing. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2379-2389.	0.8	8
2505	Comprehensive genotyping of a Brazilian cassava (<i>Manihot esculenta</i> Crantz) germplasm bank: insights into diversification and domestication. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1343-1362.	1.8	15
2506	Model-based genotype and ancestry estimation for potential hybrids with mixed ploidy. <i>Molecular Ecology Resources</i> , 2021, 21, 1434-1451.	2.2	35
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2508	High-depth resequencing of 312 accessions reveals the local adaptation of foxtail millet. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1303-1317.	1.8	16
2509	Genomic scans for selective sweeps through haplotype homozygosity and allelic fixation in 14 indigenous sheep breeds from Middle East and South Asia. <i>Scientific Reports</i> , 2021, 11, 2834.	1.6	16
2510	Kaiso (ZBTB33) subcellular partitioning functionally links LC3A/B, the tumor microenvironment, and breast cancer survival. <i>Communications Biology</i> , 2021, 4, 150.	2.0	10
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2516	Genotyping by Sequencing Reveals Genetic Relatedness of Southwestern U.S. Blue Maize Landraces. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3436.	1.8	4
2517	Sex-linked genetic diversity and differentiation in a globally distributed avian species complex. <i>Molecular Ecology</i> , 2021, 30, 2313-2332.	2.0	12
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2522	A genome-wide case-control association study of dark cutting in beef cattle. <i>Canadian Journal of Animal Science</i> , 2021, 101, 158-167.	0.7	1
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2524	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	2.4	30
2525	The population genomics of repeated freshwater colonizations by Gulf pipefish. <i>Molecular Ecology</i> , 2021, 30, 1672-1687.	2.0	4
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2527	Manipulating <i>ZmEXPA4</i> expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. <i>Plant Cell</i> , 2021, 33, 2058-2071.	3.1	33
2528	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.	1.6	8
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2531	SNP panels for the estimation of dairy breed proportion and parentage assignment in African crossbred dairy cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 21.	1.2	12
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#	ARTICLE	IF	CITATIONS
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2535	Molecular mechanisms of local adaptation for salt tolerance in a treefrog. <i>Molecular Ecology</i> , 2021, 30, 2065-2086.	2.0	18
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2537	Assessing the genetic background and genomic relatedness of red cattle populations originating from Northern Europe. <i>Genetics Selection Evolution</i> , 2021, 53, 23.	1.2	15
2538	Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. <i>Communications Biology</i> , 2021, 4, 375.	2.0	11
2539	Elucidation of Japanese pepper (<i>Zanthoxylum piperitum</i> De Candolle) domestication using RAD-Seq. <i>Scientific Reports</i> , 2021, 11, 6464.	1.6	7
2540	Suitability of Pedigree Information and Genomic Methods for Analyzing Inbreeding of Polish Cold-Blooded Horses Covered by Conservation Programs. <i>Genes</i> , 2021, 12, 429.	1.0	12
2542	The evolutionary dynamics of biological invasions: A multi-approach perspective. <i>Evolutionary Applications</i> , 2021, 14, 1463-1484.	1.5	48
2543	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	3.5	14
2544	Short communication: Genome wide association study for gastrointestinal nematodes resistance in <i>Bos taurus</i> x <i>Bos indicus</i> crossbred cattle. <i>Livestock Science</i> , 2021, 245, 104403.	0.6	0
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2547	Unraveling a fine-scale high genetic heterogeneity and recent continental connections of an Arabian Peninsula population. <i>European Journal of Human Genetics</i> , 2022, 30, 307-319.	1.4	3
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2549	The genic view of hybridization in the Anthropocene. <i>Evolutionary Applications</i> , 2021, 14, 2342-2360.	1.5	59
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2551	Genomic Signature for Stem Swollen of Kohlrabi Morphotype in <i>Brassica oleracea</i> . <i>Plant Breeding and Biotechnology</i> , 2021, 9, 45-54.	0.3	0
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#	ARTICLE	IF	CITATIONS
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2556	Risk Factors Associated with Vitamin D Status among Older Puerto Rican Adults. <i>Journal of Nutrition</i> , 2021, 151, 999-1007.	1.3	4
2557	Genetic basis for variation in the number of cephalic pores in a hybrid zone between closely related species of goby, <i>Gymnogobius breunigii</i> and <i>Gymnogobius castaneus</i> . <i>Biological Journal of the Linnean Society</i> , 2021, 133, 143-154.	0.7	0
2558	Genomic Variation and Recent Population Histories of Spotted (<i>Strix occidentalis</i>) and Barred (<i>Strix varia</i>) Owls. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
2559	Genome-Wide Association Study Reveals Marker-Trait Associations for Early Vegetative Stage Salinity Tolerance in Rice. <i>Plants</i> , 2021, 10, 559.	1.6	16
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2561	New insights into the fine-scale history of western-eastern admixture of the northwestern Chinese population in the Hexi Corridor via genome-wide genetic legacy. <i>Molecular Genetics and Genomics</i> , 2021, 296, 631-651.	1.0	38
2563	Genotyping-by-Sequencing in <i>Vigna unguiculata</i> Landraces and Its Utility for Assessing Taxonomic Relationships. <i>Plants</i> , 2021, 10, 509.	1.6	10
2564	Loquat (<i>Eriobotrya japonica</i> (Thunb.) Lindl) population genomics suggests a two-staged domestication and identifies genes showing convergence/parallel selective sweeps with apple or peach. <i>Plant Journal</i> , 2021, 106, 942-952.	2.8	2
2565	Insights into adaption and growth evolution: a comparative genomics study on two distinct cattle breeds from Northern and Southern China. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 23, 959-967.	2.3	9
2566	The structure and diversity of strain-level variation in vaginal bacteria. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
2568	Ethnic Identity and Genome Wide Runs of Homozygosity. <i>Behavior Genetics</i> , 2021, 51, 405-413.	1.4	1
2569	Changes in the fine-scale genetic structure of Finland through the 20th century. <i>PLoS Genetics</i> , 2021, 17, e1009347.	1.5	8
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2573	Genome-wide ancestry and introgression in a Zambian baboon hybrid zone. <i>Molecular Ecology</i> , 2021, 30, 1907-1920.	2.0	9
2574	Evidence for ephemeral ring species formation during the diversification history of western fence lizards (<i>Sceloporus occidentalis</i>). <i>Molecular Ecology</i> , 2022, 31, 620-631.	2.0	17
2575	Genome-wide association studies reveal the coordinated regulatory networks underlying photosynthesis and wood formation in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 5372-5389.	2.4	12
2577	An introgressed gene causes meiotic drive in <i>Neurospora sitophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26

#	ARTICLE	IF	CITATIONS
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2581	Genomic Basis of Striking Fin Shapes and Colors in the Fighting Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 3383-3396.	3.5	33
2582	Population genomic evidence of <i>Plasmodium vivax</i> Southeast Asian origin. <i>Science Advances</i> , 2021, 7, .	4.7	21
2583	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	13.7	100
2585	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. <i>Genome Biology</i> , 2021, 22, 113.	3.8	32
2586	Analysis of whole-genome re-sequencing data of ducks reveals a diverse demographic history and extensive gene flow between Southeast/South Asian and Chinese populations. <i>Genetics Selection Evolution</i> , 2021, 53, 35.	1.2	5
2587	Characterization of a haplotype-reference panel for genotyping by low-pass sequencing in Swiss Large White pigs. <i>BMC Genomics</i> , 2021, 22, 290.	1.2	16
2588	Population genomics and conservation of Gila Trout (<i>Oncorhynchus gilae</i>). <i>Conservation Genetics</i> , 2021, 22, 729-743.	0.8	9
2589	The distinct morphological phenotypes of Southeast Asian aborigines are shaped by novel mechanisms for adaptation to tropical rainforests. <i>National Science Review</i> , 2022, 9, nwab072.	4.6	3
2590	Genetic diversity, population structure, and selection signature in Ethiopian sorghum [<i>Sorghum bicolor</i> L. (Moench)] germplasm. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
2592	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. <i>PLoS ONE</i> , 2021, 16, e0249305.	1.1	5
2593	The genomic basis of geographic differentiation and fiber improvement in cultivated cotton. <i>Nature Genetics</i> , 2021, 53, 916-924.	9.4	75
2594	The Chilean socio-ethno-genomic cline. <i>Biodemography and Social Biology</i> , 2021, 66, 156-171.	0.4	8
2595	Population structure and relatedness estimates in a Mexican sample. <i>Annals of Human Genetics</i> , 2021, 85, 245-248.	0.3	1
2596	Whole-genome resequencing of 445 <i>Lactuca</i> accessions reveals the domestication history of cultivated lettuce. <i>Nature Genetics</i> , 2021, 53, 752-760.	9.4	64
2597	Genome-Wide Association Study Reveals the QTLs for Seed Storability in World Rice Core Collections. <i>Plants</i> , 2021, 10, 812.	1.6	9
2598	Germline variants at SOHLH2 influence multiple myeloma risk. <i>Blood Cancer Journal</i> , 2021, 11, 76.	2.8	6

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2601	Whole-genome re-sequencing data to infer historical demography and speciation processes in land snails: the study of two <i>Candidula</i> sister species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200156.	1.8	8
2602	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	6.0	358
2603	Migration through a Major Andean Ecogeographic Disruption as a Driver of Genetic and Phenotypic Diversity in a Wild Tomato Species. <i>Molecular Biology and Evolution</i> , 2021, 38, 3202-3219.	3.5	14
2604	SNP detection and population structure evaluation of <i>Salix gordejewii</i> Y. L. Chang et Skv. in Hunshandake Sandland, Inner Mongolia, China. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 997-1005.	1.4	1
2605	Tracing evolutionary history and admixture in mixed ploidy systems. <i>Molecular Ecology Resources</i> , 2021, 21, 1413-1415.	2.2	4
2606	Archaeogenomic distinctiveness of the Isthmo-Colombian area. <i>Cell</i> , 2021, 184, 1706-1723.e24.	13.5	30
2608	On the Unfounded Enthusiasm for Soft Selective Sweeps III: The Supervised Machine Learning Algorithm That Isn't. <i>Genes</i> , 2021, 12, 527.	1.0	2
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2611	Genetic substructure and complex demographic history of South African Bantu speakers. <i>Nature Communications</i> , 2021, 12, 2080.	5.8	47
2612	Chromosome-scale assembly and analysis of biomass crop <i>Miscanthus lutarioriparius</i> genome. <i>Nature Communications</i> , 2021, 12, 2458.	5.8	25
2613	Reconstructing the Human Genetic History of Mainland Southeast Asia: Insights from Genome-Wide Data from Thailand and Laos. <i>Molecular Biology and Evolution</i> , 2021, 38, 3459-3477.	3.5	49
2615	Comprehensive omic characterization of breast cancer in Mexican-Hispanic women. <i>Nature Communications</i> , 2021, 12, 2245.	5.8	14
2616	Genome-wide insights on gastrointestinal nematode resistance in autochthonous Tunisian sheep. <i>Scientific Reports</i> , 2021, 11, 9250.	1.6	19
2619	On species delimitation, hybridization and population structure of cassava whitefly in Africa. <i>Scientific Reports</i> , 2021, 11, 7923.	1.6	9
2620	Low effective population size in the genetically bottlenecked Australian sea lion is insufficient to maintain genetic variation. <i>Animal Conservation</i> , 2021, 24, 847.	1.5	2
2624	Nitrogen Use Efficiency in Sorghum: Exploring Native Variability for Traits Under Variable N-Regimes. <i>Frontiers in Plant Science</i> , 2021, 12, 643192.	1.7	13
2625	Genomic inbreeding and population structure of northern pike (<i>Esox lucius</i>) in Xinjiang, China. <i>Ecology and Evolution</i> , 2021, 11, 5657-5668.	0.8	3

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2628	Phylogeographic history of Japanese macaques. <i>Journal of Biogeography</i> , 2021, 48, 1420-1431.	1.4	12
2629	Evaluating population affinity estimates in forensic anthropology: Insights from the forensic anthropology database for assessing methods accuracy (FADAMA). <i>Journal of Forensic Sciences</i> , 2021, 66, 1210-1219.	0.9	15
2630	Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights. <i>PLoS ONE</i> , 2021, 16, e0249773.	1.1	8
2631	Chloroplast genomes in <i>Populus</i> (Salicaceae): comparisons from an intensively sampled genus reveal dynamic patterns of evolution. <i>Scientific Reports</i> , 2021, 11, 9471.	1.6	15
2632	The genetic history of Greenlandic-European contact. <i>Current Biology</i> , 2021, 31, 2214-2219.e4.	1.8	9
2633	Development and application of rose (<i>Rosa chinensis</i> Jacq.) SNP markers based on SLAF-seq technology. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 173-182.	0.8	5
2634	Introgression between <i>Sphyrapicus nuchalis</i> and <i>S. varius</i> sapsuckers in a hybrid zone in west-central Alberta. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	4
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#	ARTICLE	IF	CITATIONS
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2645	Analysis of Genomic DNA from Medieval Plague Victims Suggests Long-Term Effect of <i>Yersinia pestis</i> on Human Immunity Genes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4059-4076.	3.5	29
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2809	Admixture mapping analysis reveals differential genetic ancestry associated with Chagas disease susceptibility in the Colombian population. <i>Human Molecular Genetics</i> , 2021, 30, 2503-2512.	1.4	5
2810	LINADMIX: evaluating the effect of ancient admixture events on modern populations. <i>Bioinformatics</i> , 2021, 37, 4744-4755.	1.8	1
2811	Multi-omics analyses on <i>Kandelia obovata</i> reveal its response to transplanting and genetic differentiation among populations. <i>BMC Plant Biology</i> , 2021, 21, 341.	1.6	4
2813	Combining population genomics and ecological niche modeling to assess taxon limits between <i>Carex jemtlandica</i> and <i>C. lepidocarpa</i> . <i>Journal of Systematics and Evolution</i> , 2021, 59, 627-641.	1.6	5
2814	A SNP assay for assessing diversity in immune genes in the honey bee (<i>Apis mellifera</i> L.). <i>Scientific Reports</i> , 2021, 11, 15317.	1.6	4
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2819	Human population history at the crossroads of East and Southeast Asia since 11,000 years ago. <i>Cell</i> , 2021, 184, 3829-3841.e21.	13.5	78
2821	Local climate adaptation and gene flow in the native range of two co-occurring fruit moths with contrasting invasiveness. <i>Molecular Ecology</i> , 2021, 30, 4204-4219.	2.0	12
2822	Increased burden of rare variants in genes of the endosomal Toll-like receptor pathway in patients with systemic lupus erythematosus. <i>Lupus</i> , 2021, 30, 1756-1763.	0.8	2
2823	SNP-Based Genotyping Provides Insight Into the West Asian Origin of Russian Local Goats. <i>Frontiers in Genetics</i> , 2021, 12, 708740.	1.1	12
2824	Genetic basis of maize kernel oil-related traits revealed by high-density SNP markers in a recombinant inbred line population. <i>BMC Plant Biology</i> , 2021, 21, 344.	1.6	10
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2826	Genetic ancestry differences in pediatric asthma readmission are mediated by socioenvironmental factors. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1210-1218.e4.	1.5	16
2827	The different fates of two Asian horseshoe crab species with different dispersal abilities. <i>Evolutionary Applications</i> , 2021, 14, 2124-2133.	1.5	3
2828	Accurate prediction and genome-wide association analysis of digital intramuscular fat content in longissimus muscle of pigs. <i>Animal Genetics</i> , 2021, 52, 633-644.	0.6	12
2830	Genetic diversity and population structure of the amyolytic yeast <i>Saccharomycopsis fibuligera</i> associated with Baijiu fermentation in China. <i>Journal of Microbiology</i> , 2021, 59, 753-762.	1.3	14
2831	Diversification of mandarin citrus by hybrid speciation and apomixis. <i>Nature Communications</i> , 2021, 12, 4377.	5.8	31
2832	Genome Divergence and Dynamics in the Thin-Tailed Desert Sheep From Sudan. <i>Frontiers in Genetics</i> , 2021, 12, 659507.	1.1	5
2833	Genome-Wide SNPs Clarify a Complex Radiation and Support Recognition of an Additional Cat Species. <i>Molecular Biology and Evolution</i> , 2021, 38, 4987-4991.	3.5	6
2834	Whole-genome resequencing of 240 <i>Gossypium barbadense</i> accessions reveals genetic variation and genes associated with fiber strength and lint percentage. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3249-3261.	1.8	19
2835	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003300.	1.6	7
2836	Evidence that geographic variation in genetic ancestry associates with uterine fibroids. <i>Human Genetics</i> , 2021, 140, 1433-1440.	1.8	9

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2839	Genome-Wide Association Study of Root and Shoot Related Traits in Spring Soybean (<i>Glycine max</i> L.) at Seedling Stages Using SLAF-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 568995.	1.7	17
2840	Genotyping and lipid profiling of 601 cultivated sunflower lines reveals novel genetic determinants of oil fatty acid content. <i>BMC Genomics</i> , 2021, 22, 505.	1.2	16
2841	Polygenic risk score and risk of monoclonal B-cell lymphocytosis in caucasians and risk of chronic lymphocytic leukemia (CLL) in African Americans. <i>Leukemia</i> , 2022, 36, 119-125.	3.3	10
2842	A multi-phenotype genome-wide association study of clades causing tuberculosis in a Ghanaian- and South African cohort. <i>Genomics</i> , 2021, 113, 1802-1815.	1.3	8
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2845	Large-scale whole-genome resequencing unravels the domestication history of <i>Cannabis sativa</i> . <i>Science Advances</i> , 2021, 7, .	4.7	79
2846	Summix: A method for detecting and adjusting for population structure in genetic summary data. <i>American Journal of Human Genetics</i> , 2021, 108, 1270-1282.	2.6	5
2847	Genome-Wide Association Study Identifies Candidate Genes Associated with Feet and Leg Conformation Traits in Chinese Holstein Cattle. <i>Animals</i> , 2021, 11, 2259.	1.0	8
2848	Genome-wide analysis of genetic diversity and artificial selection in Large White pigs in Russia. <i>PeerJ</i> , 2021, 9, e11595.	0.9	5
2849	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. <i>Plant Biotechnology Journal</i> , 2021, 19, 2206-2220.	4.1	23
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2851	Whole-genome sequencing of <i>Schistosoma mansoni</i> reveals extensive diversity with limited selection despite mass drug administration. <i>Nature Communications</i> , 2021, 12, 4776.	5.8	28
2852	Genomic divergence during feralization reveals both conserved and distinct mechanisms of parallel weediness evolution. <i>Communications Biology</i> , 2021, 4, 952.	2.0	12
2853	Gudgeon fish with and without genetically determined countershading coexist in heterogeneous littoral environments of an ancient lake. <i>Ecology and Evolution</i> , 2021, 11, 13283-13294.	0.8	3
2854	Strong isolation by distance among local populations of an endangered butterfly species (<i>Euphydryas aurinia</i>). <i>Ecology and Evolution</i> , 2021, 11, 12790-12800.	0.8	6
2855	500 years of breeding in the <i>Carthusian Strain</i> of Pura Raza Española horse: An evolutionary analysis using genealogical and genomic data. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 84-99.	0.8	10

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2857	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. <i>Molecular Biology and Evolution</i> , 2021, 38, 5107-5121.	3.5	11
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2859	The genetic structure of the Turkish population reveals high levels of variation and admixture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	42
2860	Genome-Wide Evidence for Complex Hybridization and Demographic History in a Group of <i>Cycas</i> From China. <i>Frontiers in Genetics</i> , 2021, 12, 717200.	1.1	10
2862	Phylogenomics of <i>Porites</i> from the Arabian Peninsula. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107173.	1.2	9
2864	GWAS provides biological insights into mechanisms of the parasitic plant (<i>Striga</i>) resistance in sorghum. <i>BMC Plant Biology</i> , 2021, 21, 392.	1.6	18
2865	Whole-genome sequencing of endangered Zhoushan cattle suggests its origin and the association of MC1R with black coat colour. <i>Scientific Reports</i> , 2021, 11, 17359.	1.6	11
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2867	Development of a genomic tool for breed assignment by comparison of different classification models: Application to three local cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 40-61.	0.8	15
2868	Search for Selection Signatures Related to Trypanosomosis Tolerance in African Goats. <i>Frontiers in Genetics</i> , 2021, 12, 715732.	1.1	8
2869	Fine-Scale Genetic Structure and Natural Selection Signatures of Southwestern Hans Inferred From Patterns of Genome-Wide Allele, Haplotype, and Haplogroup Lineages. <i>Frontiers in Genetics</i> , 2021, 12, 727821.	1.1	15
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2871	Taxonomic Uncertainty and the Anomaly Zone: Phylogenomics Disentangle a Rapid Radiation to Resolve Contentious Species (<i>Gila robusta</i> Complex) in the Colorado River. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
2872	Genetic diversity and population structure of <i>Leptosphaeria maculans</i> isolates in Western Canada. <i>Journal of Genetics and Genomics</i> , 2021, 48, 994-1006.	1.7	0
2873	Dissecting the genetic history of the Roman Catholic populations of West Coast India. <i>Human Genetics</i> , 2021, 140, 1487-1498.	1.8	4
2874	Population structure, gene flow, and sex-biased dispersal in the reticulated flatwoods salamander (<i>Pseudacris</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	2
2875	Population structure, genomic diversity and demographic history of Komodo dragons inferred from whole-genome sequencing. <i>Molecular Ecology</i> , 2021, 30, 6309-6324.	2.0	11

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2878	Unraveling the Genetic Diversity and Population Structure of Bangladeshi Indigenous Cattle Populations Using 50K SNP Markers. <i>Animals</i> , 2021, 11, 2381.	1.0	7
2880	Phylogenomics reveals ancient and contemporary gene flow contributing to the evolutionary history of sea ducks (Tribe Mergini). <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107164.	1.2	9
2885	Responses of an endemic species (<i>Roscoea humeana</i>) in the Hengduan Mountains to climate change. <i>Diversity and Distributions</i> , 2021, 27, 2231.	1.9	8
2886	Genome-scale sequencing and analysis of human, wolf, and bison DNA from 25,000-year-old sediment. <i>Current Biology</i> , 2021, 31, 3564-3574.e9.	1.8	34
2887	Global range expansion history of pepper (<i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
2888	Ancestral patterns of recessive dystrophic epidermolysis bullosa mutations in Hispanic populations suggest sephardic ancestry. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 3390-3400.	0.7	1
2889	Genomic analyses reveal distinct genetic architectures and selective pressures in Chinese donkeys. <i>Journal of Genetics and Genomics</i> , 2021, 48, 737-745.	1.7	16
2890	Population genetic structure of a major reef-building coral species <i>Acropora downingi</i> in northeastern Arabian Peninsula. <i>Coral Reefs</i> , 2022, 41, 743-752.	0.9	8
2891	Population genomics of <sc><i>Digitaria insularis</i></sc> from soybean areas in <sc>Brazil</sc>. <i>Pest Management Science</i> , 2021, 77, 5375-5381.	1.7	8
2892	Genome-wide association study of individual sugar content in fruit of Japanese pear (<i>Pyrus</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 378.	1.6	14
2893	Transposable elements and introgression introduce genetic variation in the invasive ant <i>Cardiocondyla obscurior</i>. <i>Molecular Ecology</i> , 2021, 30, 6211-6228.	2.0	20
2895	Admixture mapping reveals loci for carcass mass in red deer x sika hybrids in Kintyre, Scotland. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
2896	Identification of candidate genomic regions for chicken egg number traits based on genome-wide association study. <i>BMC Genomics</i> , 2021, 22, 610.	1.2	13
2897	Genomic sequencing confirms absence of introgression despite past hybridisation between a critically endangered bird and its common congener. <i>Global Ecology and Conservation</i> , 2021, 28, e01681.	1.0	9
2898	Within-population genotype “ Soil interactions drive phenotypic variation in a recovering fir forest from central Mexico. <i>Forest Ecology and Management</i> , 2021, 494, 119293.	1.4	3
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2904	Intraspecific variation in elemental accumulation and its association with salt tolerance in <i>Paspalum vaginatum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
2905	Population structure associated with bioregion and seasonal prey distribution for Indo-Pacific bottlenose dolphins (<i>Tursiops aduncus</i>) in South Africa. <i>Molecular Ecology</i> , 2021, 30, 4642-4659.	2.0	2
2906	Population Genetics of a Translocated Population of Mottled Ducks and Allies. <i>Journal of Wildlife Management</i> , 2021, 85, 1616-1627.	0.7	5
2907	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003354.	1.6	21
2909	Genetic susceptibility to multiple sclerosis in African Americans. <i>PLoS ONE</i> , 2021, 16, e0254945.	1.1	5
2910	Demographic History of the Brown Bear (<i>Ursus arctos</i>) on Hokkaido Island, Japan, Based on Whole-Genomic Sequence Analysis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
2911	Whole-Genome Sequencing of a 900-Year-Old Human Skeleton Supports Two Past Migration Events from the Russian Far East to Northern Japan. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
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2913	Genome-wide RAD-Seq analysis revealed subpopulation structures of the pecan (<i>Carya illinoensis</i>) germplasm collection and their relationship to geographical distribution patterns. <i>Acta Horticulturae</i> , 2021, , 177-184.	0.1	0
2914	Spatial Genetic Structure of <i>Prunus mongolica</i> in Arid Northwestern China Based on RAD Sequencing Data. <i>Diversity</i> , 2021, 13, 397.	0.7	3
2915	Genome-Wide Comparative Analysis of Genetic Diversity of Regular and Specialty Maize Inbred Lines Through Genotyping by Target Sequencing (GBTS). <i>Plant Molecular Biology Reporter</i> , 2022, 40, 221-231.	1.0	1
2916	Genetic diversity analysis of Korean peanut germplasm using 48K SNPs <i>~</i> Axiom_Arachis [™] Array and its application for cultivar differentiation. <i>Scientific Reports</i> , 2021, 11, 16630.	1.6	9
2917	Neuropsychiatric Genetics of Psychosis in the Mexican Population: A Genome-Wide Association Study Protocol for Schizophrenia, Schizoaffective, and Bipolar Disorder Patients and Controls. <i>Complex Psychiatry</i> , 2021, 7, 60-70.	1.3	6
2918	Building a Chinese pan-genome of 486 individuals. <i>Communications Biology</i> , 2021, 4, 1016.	2.0	13
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2921	Species divergence and repeated ancient hybridization in a Sulawesi lake system. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1767-1780.	0.8	13

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2923	Identification of putative key genes for thermal adaptation in the Japanese mantis shrimp (<i>Oratosquilla</i>). <i>Tj ETQq1 1 0.784314 rgBT /O</i> <i>Genomics and Proteomics</i> , 2021, 39, 100828.	0.4	1
2924	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <i>Plant Journal</i> , 2021, 108, 1174-1192.	2.8	16
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2927	Alignment-free methods for polyploid genomes: Quick and reliable genetic distance estimation. <i>Molecular Ecology Resources</i> , 2022, 22, 612-622.	2.2	5
2928	Population genomics of the critically endangered <i>kÄkÄpÄ</i> . <i>Cell Genomics</i> , 2021, 1, 100002.	3.0	106
2930	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. <i>Journal of Genetics and Genomics</i> , 2021, 48, 972-983.	1.7	2
2931	Ancestral Spectrum Analysis With Population-Specific Variants. <i>Frontiers in Genetics</i> , 2021, 12, 724638.	1.1	3
2932	High frequency of an otherwise rare phenotype in a small and isolated tiger population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
2933	Assessing the levels of intraspecific admixture and interspecific hybridization in Iberian wild goats (<i>Capra pyrenaica</i>). <i>Evolutionary Applications</i> , 2021, 14, 2618-2634.	1.5	6
2934	A genomic perspective on an old question: <i>Salmo</i> trouts or <i>Salmo trutta</i> (Teleostei: Salmonidae)? <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107204.	1.2	33
2936	Deciphering variation of 239 elite japonica rice genomes for whole genome sequences-enabled breeding. <i>Genomics</i> , 2021, 113, 3083-3091.	1.3	3
2937	Unveiling Comparative Genomic Trajectories of Selection and Key Candidate Genes in Egg-Type Russian White and Meat-Type White Cornish Chickens. <i>Biology</i> , 2021, 10, 876.	1.3	15
2938	Landscape genetics and the genetic legacy of Upper Paleolithic and Mesolithic hunter-gatherers in the modern Caucasus. <i>Scientific Reports</i> , 2021, 11, 17985.	1.6	2
2939	Recipient APOL1 risk alleles associate with death-censored renal allograft survival and rejection episodes. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	33
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2944	Genome of <i>Ganoderma</i> Species Provides Insights Into the Evolution, Conifers Substrate Utilization, and Terpene Synthesis for <i>Ganoderma tsugae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 724451.	1.5	13
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2954	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
2955	Cytonuclear discordance in the crowned-sparrows, <i>Zonotrichia atricapilla</i> and <i>Zonotrichia leucophrys</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107216.	1.2	7
2956	Pervasive admixture and the spread of a large-clipped form in a cichlid fish radiation. <i>Molecular Ecology</i> , 2021, 30, 5551-5571.	2.0	8
2957	The sardine run in southeastern Africa is a mass migration into an ecological trap. <i>Science Advances</i> , 2021, 7, eabf4514.	4.7	10
2958	The Impact of Ethnicity and Genetic Ancestry on Disease Prevalence and Risk in Colombia. <i>Frontiers in Genetics</i> , 2021, 12, 690366.	1.1	8
2959	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1631-1646.	2.6	12
2961	Rooting Out Genetic Structure of Invasive Wild Pigs in Texas. <i>Journal of Wildlife Management</i> , 2021, 85, 1563.	0.7	1
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2965	Projecting Ancient Ancestry in Modern-Day Arabians and Iranians: A Key Role of the Past Exposed Arabo-Persian Gulf on Human Migrations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
2966	Late Blight Resistance Evaluation and Genome-Wide Assessment of Genetic Diversity in Wild and Cultivated Potato Species. <i>Frontiers in Plant Science</i> , 2021, 12, 710468.	1.7	4
2968	Hidden Historical Habitat-Linked Population Divergence and Contemporary Gene Flow of a Deep-Sea Patellogastropod Limpet. <i>Molecular Biology and Evolution</i> , 2021, 38, 5640-5654.	3.5	12
2969	Corrigendum to: Range-wide population genetic analysis of Seaside Sparrows (<i>Amospiza maritima</i>) supports at least five distinct population segments that do not align with current subspecies descriptions. <i>Condor</i> , 0, , .	0.7	0
2970	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4016	Genetic analysis in African American children supports ancestry specific neuroblastoma susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, , cebp.EPI-21-0782-A.2021.	1.1	1
4017	Genomic evaluations for crossbred dairy cattle. <i>JDS Communications</i> , 2022, 3, 152-155.	0.5	0
4021	Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. <i>PLoS Genetics</i> , 2022, 18, e1010019.	1.5	4
4022	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
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#	ARTICLE	IF	CITATIONS
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4028	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
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4031	Genetic Connections and Convergent Evolution of Tropical Indigenous Peoples in Asia. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	2
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4037	Population genomics reveals that natural variation in <i>PRDM16</i> contributes to cold tolerance in domestic cattle. <i>Zoological Research</i> , 2022, 43, 275-284.	0.9	7
4038	Polymorphism of <i>HvDRO1</i> and <i>HvqSOR1</i> associated with root growth angle in barley accessions. <i>Plant Root</i> , 2022, 16, 1-10.	0.3	2
4040	Deep ancestry of collapsing networks of nomadic hunter-gatherers in Borneo. <i>Evolutionary Human Sciences</i> , 2022, 4, .	0.9	3
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4043	Revealing the Genetic Structure and Differentiation in Endangered <i>Pinus bungeana</i> by Genome-Wide SNP Markers. <i>Forests</i> , 2022, 13, 326.	0.9	5
4044	A major-effect genetic locus, <i>AprVII</i> , controlling resistance against both adapted and non-adapted aphid biotypes in pea. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1511-1528.	1.8	7
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#	ARTICLE	IF	CITATIONS
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4049	Drivers of phenotypic divergence in a Mesoamerican highland bird. <i>PeerJ</i> , 2022, 10, e12901.	0.9	2
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4051	Identification of Chilling Accumulation-Associated Genes for Litchi Flowering by Transcriptome-Based Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2022, 13, 819188.	1.7	1
4054	Genomic characterization of the world's longest selection experiment in mouse reveals the complexity of polygenic traits. <i>BMC Biology</i> , 2022, 20, 52.	1.7	4
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4059	Population genetics and microevolution of clinical <i>Candida glabrata</i> reveals recombinant sequence types and hyper-variation within mitochondrial genomes, virulence genes, and drug targets. <i>Genetics</i> , 2022, 221, .	1.2	11
4060	Population genomics of <i>Zea</i> species identifies selection signatures during maize domestication and adaptation. <i>BMC Plant Biology</i> , 2022, 22, 72.	1.6	9
4062	Genome Wide Association Study Identifies Candidate Genes Related to the Earlywood Tracheid Properties in <i>Picea crassifolia</i> Kom.. <i>Forests</i> , 2022, 13, 332.	0.9	2
4064	Genome variation in tick infestation and cryptic divergence in Tunisian indigenous sheep. <i>BMC Genomics</i> , 2022, 23, 167.	1.2	1
4065	Admixture in Africanized honey bees (<i>Apis mellifera</i>) from Panamá to San Diego, California (U.S.A.). <i>Ecology and Evolution</i> , 2022, 12, e8580.	0.8	7
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4072	Genomic Data Reveals Population Genetic and Demographic History of <i>Magnolia fistulosa</i> (Magnoliaceae), a Plant Species With Extremely Small Populations in Yunnan Province, China. <i>Frontiers in Plant Science</i> , 2022, 13, 811312.	1.7	12

#	ARTICLE	IF	CITATIONS
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4075	Red-Backed Shrike <i>Lanius collurio</i> Whole-Genome Sequencing Reveals Population Genetic Admixture. <i>Diversity</i> , 2022, 14, 216.	0.7	0
4077	Association Analysis between Genetic Variants of <i>elovl5a</i> and <i>elovl5b</i> and Poly-Unsaturated Fatty Acids in Common Carp (<i>Cyprinus carpio</i>). <i>Biology</i> , 2022, 11, 466.	1.3	3
4078	Genome-wide analysis suggests multiple domestication events of Chinese local pigs. <i>Animal Genetics</i> , 2022, 53, 293-306.	0.6	5
4079	SoySNP618K array: A high-resolution single nucleotide polymorphism platform as a valuable genomic resource for soybean genetics and breeding. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 632-648.	4.1	7
4080	Whole-genome analysis reveals the hybrid formation of Chinese indigenous DHB pig following human migration. <i>Evolutionary Applications</i> , 2022, 15, 501-514.	1.5	3
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4082	Population Structure, Genetic Diversity and Differentiation of <i>Triplophysa tenuis</i> in Xinjiang Tarim River. <i>Frontiers in Genetics</i> , 2022, 13, 860678.	1.1	2
4084	Extensive sampling of <i>Saccharomyces cerevisiae</i> in Taiwan reveals ecology and evolution of predomesticated lineages. <i>Genome Research</i> , 2022, , .	2.4	13
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4086	Population genomic analysis reveals domestication of cultivated rye from weedy rye. <i>Molecular Plant</i> , 2022, 15, 552-561.	3.9	19
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4089	Norway spruce postglacial recolonization of Fennoscandia. <i>Nature Communications</i> , 2022, 13, 1333.	5.8	14
4090	Species Persistence with Hybridization in Toad-Headed Lizards Driven by Divergent Selection and Low Recombination. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
4091	Genome-Wide Association Study of Root-Lesion Nematodes <i>Pratylenchus</i> Species and Crown Rot <i>Fusarium culmorum</i> in Bread Wheat. <i>Life</i> , 2022, 12, 372.	1.1	6
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4093	Genomic consequences of domestication of the Siamese fighting fish. <i>Science Advances</i> , 2022, 8, eabm4950.	4.7	20
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#	ARTICLE	IF	CITATIONS
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4098	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	6.0	110
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4102	Genomic signatures for latitudinal selection in the tropical eel <i>Anguilla marmorata</i> . <i>Journal of Evolutionary Biology</i> , 2022, 35, 763-771.	0.8	1
4103	Whole-genome sequencing revealed genetic diversity and selection of Guangxi indigenous chickens. <i>PLoS ONE</i> , 2022, 17, e0250392.	1.1	7
4104	Integration of GWAS and transcriptome analyses to identify SNPs and candidate genes for aluminum tolerance in rapeseed (<i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2022, 22, 130.	1.6	10
4105	Genome-Wide Association Analyses Reveal Candidate Genes Controlling Harvest Index and Related Agronomic Traits in <i>Brassica napus</i> L.. <i>Agronomy</i> , 2022, 12, 814.	1.3	2
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4108	Riverscape Genomics Clarifies Neutral and Adaptive Evolution in an Amazonian Characin Fish (<i>Triportheus albus</i>). <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	2
4110	Polygenic risk for prostate cancer: Decreasing relative risk with age but little impact on absolute risk. <i>American Journal of Human Genetics</i> , 2022, 109, 900-908.	2.6	10
4111	Faster haplodiploid evolution under divergence with gene flow: Simulations and empirical data from pine-feeding hymenopterans. <i>Molecular Ecology</i> , 2022, 31, 2348-2366.	2.0	9
4113	Genome-Wide Association Study Reveals the Genetic Basis of Five Quality Traits in Chinese Wheat. <i>Frontiers in Plant Science</i> , 2022, 13, 835306.	1.7	8
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#	ARTICLE	IF	CITATIONS
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4121	Genome sequence and population genomics provide insights into chromosomal evolution and phytochemical innovation of <i>Hippophae rhamnoides</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1257-1273.	4.1	17
4122	Population structure, patterns of natal dispersal and demographic history in a declining aerial insectivore, the purple martin <i>Progne subis</i> . <i>Journal of Avian Biology</i> , 2022, 2022, .	0.6	1
4123	Genetic diversity and signatures of selection for heat tolerance and immune response in Iranian native chickens. <i>BMC Genomics</i> , 2022, 23, 224.	1.2	10
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4126	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. <i>Genome Biology</i> , 2022, 23, 75.	3.8	15
4127	Neutral and outlier single nucleotide polymorphisms disentangle the evolutionary history of a coastal Solanaceae species. <i>Molecular Ecology</i> , 2022, 31, 2847-2864.	2.0	3
4128	Genome Wide Scan to Identify Potential Genomic Regions Associated With Milk Protein and Minerals in Vrindavani Cattle. <i>Frontiers in Veterinary Science</i> , 2022, 9, 760364.	0.9	3
4129	METRO: Multi-ancestry transcriptome-wide association studies for powerful gene-trait association detection. <i>American Journal of Human Genetics</i> , 2022, 109, 783-801.	2.6	12
4130	Fixation of hybrid sterility genes and favorable alleles of key yield-related genes with dominance contribute to the high yield of the Yongyou series of intersubspecific hybrid rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 448-457.	1.7	2
4131	The genomic formation of Tanka people, an isolated "gypsies in water" in the coastal region of Southeast China. <i>American Journal of Biological Anthropology</i> , 2022, 178, 154-170.	0.6	4
4132	Genomic landscape of Epstein-Barr virus in familial nasopharyngeal carcinoma. <i>Journal of General Virology</i> , 2022, 103, .	1.3	1
4133	Mechanisms of pre-attachment Striga resistance in sorghum through genome-wide association studies. <i>Molecular Genetics and Genomics</i> , 2022, 297, 751-762.	1.0	12
4134	A neurodegenerative disease landscape of rare mutations in Colombia due to founder effects. <i>Genome Medicine</i> , 2022, 14, 27.	3.6	16
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#	ARTICLE	IF	CITATIONS
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4139	Global population genomic signature of <i>Spodoptera frugiperda</i> (fall armyworm) supports complex introduction events across the Old World. <i>Communications Biology</i> , 2022, 5, 297.	2.0	34
4140	AFA: Ancestry-specific allele frequency estimation in admixed populations: The Hispanic Community Health Study/Study of Latinos. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100096.	1.0	2
4141	Association of Transthyretin Val122Ile Variant With Incident Heart Failure Among Black Individuals. <i>JAMA - Journal of the American Medical Association</i> , 2022, 327, 1368.	3.8	19
4142	Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. <i>Plant Journal</i> , 2022, 110, 1498-1515.	2.8	21
4143	Single nucleotide polymorphisms (SNPs) and indels identified from whole-genome re-sequencing of four Chinese donkey breeds. <i>Animal Biotechnology</i> , 2022, , 1-12.	0.7	0
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4145	NAToRA, a relatedness-pruning method to minimize the loss of dataset size in genetic and omics analyses. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1821-1828.	1.9	6
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4147	New York's Polyethnic-1000: a regional initiative to understand how diverse ancestries influence the risk, progression, and treatment of cancers. <i>Trends in Cancer</i> , 2022, 8, 269-272.	3.8	3
4148	Bronze and Iron Age population movements underlie Xinjiang population history. <i>Science</i> , 2022, 376, 62-69.	6.0	27
4149	A generalist's specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118879119.	3.3	5
4150	Role of Sexual Reproduction in the Evolution of the Wheat Stripe Rust Fungus Races in China. <i>Phytopathology</i> , 2022, 112, 1063-1071.	1.1	2
4151	Hard vs. soft selective sweeps during domestication and improvement in soybean. <i>Molecular Ecology</i> , 2022, , .	2.0	4
4153	Genetic diversity and population structure of the swimming crab (<i>Portunus trituberculatus</i>) in China seas determined by genotyping-by-sequencing (GBS). <i>Aquaculture</i> , 2022, 555, 738233.	1.7	12
4154	Multidisciplinary investigation reveals an individual of West African origin buried in a Portuguese Mesolithic shell midden four centuries ago. <i>Journal of Archaeological Science: Reports</i> , 2022, 42, 103370.	0.2	3
4155	A whole genome sequencing study of moderate to severe asthma identifies a lung function locus associated with asthma risk. <i>Scientific Reports</i> , 2022, 12, 5574.	1.6	9
4157	Inferring population structure in biobank-scale genomic data. <i>American Journal of Human Genetics</i> , 2022, 109, 727-737.	2.6	16

#	ARTICLE	IF	CITATIONS
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4162	Genome-wide identification, expression analysis and evolutionary relationships of the IQ67-domain gene family in common wheat (<i>Triticum aestivum</i> L.) and its progenitors. <i>BMC Genomics</i> , 2022, 23, 264.	1.2	1
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4165	The Genetic Structure and East-West Population Admixture in Northwest China Inferred From Genome-Wide Array Genotyping. <i>Frontiers in Genetics</i> , 2021, 12, 795570.	1.1	8
4166	Ancient Demographics Determine the Effectiveness of Genetic Purging in Endangered Lizards. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	22
4167	Genomic Insights Into the Genetic Structure and Natural Selection of Mongolians. <i>Frontiers in Genetics</i> , 2021, 12, 735786.	1.1	5
4169	Fish out of water: Genomic insights into persistence of rainbowfish populations in the desert. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 171-183.	1.1	10
4172	Genomics Confirm an Alarming Status of the Genetic Diversity of Belgian Red and Belgian White Red Cattle. <i>Animals</i> , 2021, 11, 3574.	1.0	3
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4174	The Genetic Landscape of Fiber Flax. <i>Frontiers in Plant Science</i> , 2021, 12, 764612.	1.7	11
4175	Fine-scale population structure and demographic history of British Pakistanis. <i>Nature Communications</i> , 2021, 12, 7189.	5.8	21
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4177	Male-biased migration from East Africa introduced pastoralism into southern Africa. <i>BMC Biology</i> , 2021, 19, 259.	1.7	4
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4179	Assessment of cold stress tolerance in maize through quantitative trait locus, genome-wide association study and transcriptome analysis. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12525.	0.5	3

#	ARTICLE	IF	CITATIONS
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4183	The genetic scenario of Mercheros: an under-represented group within the Iberian Peninsula. <i>BMC Genomics</i> , 2021, 22, 897.	1.2	1
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4187	Genome-Wide Association Analysis of Salt-Tolerant Traits in Terrestrial Cotton at Seedling Stage. <i>Plants</i> , 2022, 11, 97.	1.6	11
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4193	The pink salmon genome: Uncovering the genomic consequences of a two-year life cycle. <i>PLoS ONE</i> , 2021, 16, e0255752.	1.1	14
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#	ARTICLE	IF	CITATIONS
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4672	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	6.0	77
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4710	Landscape genetics reveals contrasting patterns of connectivity in two newt species (<i>Lissotriton</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.0	3
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4714	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei (<i>Rubus</i>) Tj ETQq0,0,0 rgBT /Overlock 1	3.0	3
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#	ARTICLE	IF	CITATIONS
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4733	Dynamics of Methylation of CpG Sites Associated With Systemic Lupus Erythematosus Subtypes in a Longitudinal Cohort. <i>Arthritis and Rheumatology</i> , 2022, 74, 1676-1686.	2.9	5
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4737	Genetic Diversity and Genetic Differentiation of Populations of Golden-Backed Carp (<i>Cyprinus carpio</i>) Tj ETQq0 0 0 JgBT /Overlock 10 Tf	1.8	3
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4777	Genome-wide <i>scn</i> SNPs of vegetable leafminer, <i>Liriomyza sativae</i> : Insights into the recent Australian invasion. <i>Evolutionary Applications</i> , 2022, 15, 1129-1140.	1.5	1
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4779	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1286-1297.	2.6	30
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4781	Genome-wide association analysis of nine reproduction and morphological traits in three goat breeds from Southern China. <i>Animal Bioscience</i> , 2023, 36, 191-199.	0.8	7
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#	ARTICLE	IF	CITATIONS
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4787	Molecular and archaeological evidence on the geographical origin of domestication for <i>Camelina sativa</i> . <i>American Journal of Botany</i> , 2022, 109, 1177-1190.	0.8	10
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#	ARTICLE	IF	CITATIONS
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4823	Whole-genome resequencing reveals molecular imprints of anthropogenic and natural selection in wild and domesticated sheep. <i>Zoological Research</i> , 2022, 43, 695-705.	0.9	6
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4876	A Late Pleistocene human genome from Southwest China. <i>Current Biology</i> , 2022, 32, 3095-3109.e5.	1.8	6
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4941	Fine-mapping and association analysis of candidate genes for papilla number in sea cucumber, <i>Apostichopus japonicus</i> . <i>Marine Life Science and Technology</i> , 2022, 4, 343-355.	1.8	2
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4945	Inference of population structure and admixture proportion from Y chromosomal data of Chinese population. <i>Electrophoresis</i> , 0, , .	1.3	0
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#	ARTICLE	IF	CITATIONS
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4961	Complex population history affects admixture analyses in nine-spined sticklebacks. <i>Molecular Ecology</i> , 2022, 31, 5386-5401.	2.0	14
4962	Cryptic genetic divergence of the red dwarf rasbora, <i>Microrasbora rubescens</i> , in and around Inle Lake: implications for the origin of endemism in the ancient lake in Myanmar. <i>Journal of Fish Biology</i> , 2022, 101, 1235-1247.	0.7	3
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4964	Genome-wide association study reveals that GhTRL1 and GhPIN8 affect cotton root development. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3161-3176.	1.8	3
4965	Frozen in time: Rangewide genomic diversity, structure, and demographic history of relict American chestnut populations. <i>Molecular Ecology</i> , 2022, 31, 4640-4655.	2.0	9
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4970	Selective and comparative genome architecture of Asian cultivated rice (<i>Oryza sativa</i> L.) attributed to domestication and modern breeding. <i>Journal of Advanced Research</i> , 2022, 42, 1-16.	4.4	8
4972	A polygenic risk score predicts atrial fibrillation in cardiovascular disease. <i>European Heart Journal</i> , 2023, 44, 221-231.	1.0	21
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4974	Perspectives in plant evolutionary genetics: A field guide in 15 "easy steps" to modern tools in evolutionary genetics and genomics. <i>Botanical Sciences</i> , 0, 100, .	0.3	2
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4978	Whole-genome resequencing of Chinese pangolins reveals a population structure and provides insights into their conservation. <i>Communications Biology</i> , 2022, 5, .	2.0	11
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4983	<sc>eQTLs</sc> play critical roles in regulating gene expression and identifying key regulators in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 2357-2371.	4.1	9
4984	Unique genetic signature and selection footprints in Dutch population of German Longhaired Pointer dogs. <i>Animal Genetics</i> , 0, , .	0.6	1
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4990	Natural adaptation and human selection of northeast African sheep genomes. <i>Genomics</i> , 2022, 114, 110448.	1.3	6
4991	Genomic, metabonomic and transcriptomic analyses of sweet osmanthus varieties provide insights into floral aroma formation. <i>Scientia Horticulturae</i> , 2022, 306, 111442.	1.7	7
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5005	Phylogeography and taxonomy of <i>Coleonyx elegans</i> Gray 1845 (Squamata: Eublepharidae) in Mesoamerica: The Isthmus of Tehuantepec as an environmental barrier. <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107632.	1.2	6
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5009	Characterization of genetic predisposition to molecular subtypes of breast cancer in Brazilian patients. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
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5027	Multiomics provides new insights into the domestication and improvement of dark jute (<i>T. tetragynum</i>). <i>Overlook 10</i> 11 50 102 T	2.8	1
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#	ARTICLE	IF	CITATIONS
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5031	Tracing Bai-Yue Ancestry in Aboriginal Li People on Hainan Island. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
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5038	Genetic characterization of two North Italian villages: A story of isolation, ancient admixture, and genetic drift. <i>American Journal of Biological Anthropology</i> , 0, , .	0.6	0
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5057	Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. <i>Nature Genetics</i> , 2022, 54, 1553-1563.	9.4	46
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5068	Localized variation in ancestral admixture identifies pilocytic astrocytoma risk loci among Latino children. <i>PLoS Genetics</i> , 2022, 18, e1010388.	1.5	2
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5078	Correlation research of susceptibility single nucleotide polymorphisms and the severity of clinical symptoms in attention deficit hyperactivity disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	1
5079	Population history and genome wide association studies of birth weight in a native high altitude Ladakhi population. <i>PLoS ONE</i> , 2022, 17, e0269671.	1.1	3
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5093	Association of Plasma and Cerebrospinal Fluid Alzheimer Disease Biomarkers With Race and the Role of Genetic Ancestry, Vascular Comorbidities, and Neighborhood Factors. <i>JAMA Network Open</i> , 2022, 5, e2235068.	2.8	13
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5099	A machine learning approach for missing persons cases with high genotyping errors. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
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5105	Genomic insight into genetic changes and shaping of major inbred rice cultivars in China. <i>New Phytologist</i> , 0, , .	3.5	1
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5110	Étude paléogéographique des migrations humaines autour de la mer Caspienne au cours de la Préhistoire. <i>Bulletins Et Memoires De La Societe D'Anthropologie De Paris</i> , 2022, 34, .	0.0	0
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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