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653	Genome-wide association study reveals that GhTRL1 and GhPIN8 affect cotton root development.	
652	Frozen in time: Rangewide genomic diversity, structure, and demographic history of relict American chestnut populations.	O

651 Genetic and ecological drivers of molt in a migratory bird.

650	Rare and common variant analyses of amyotrophic lateral sclerosis in the French-Canadian genome.	
649	Contrasting population differentiation in two sympatric Triplophysa loaches on the Qinghailibet Plateau. 13,	
648	Genomics-informed delineation of conservation units in a desert amphibian.	O
647	Selective and comparative genome architecture of Asian cultivated rice (Oryza sativa L.) attributed to domestication and modern breeding. 2022 ,	О
646	Whole-Genome Resequencing Reveals the Uniqueness of Subei Yak.	
645	A polygenic risk score predicts atrial fibrillation in cardiovascular disease.	О
644	Conservation Significance of the Rare and Endangered Tree Species, Trigonobalanus doichangensis (Fagaceae). 2022 , 14, 666	1
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642	Demographic modelling helps track the rapid and recent divergence of a conifer species pair from Central Mexico.	1
641	The genetic history of the Southern Arc: A bridge between West Asia and Europe. 2022, 377,	О
640	Simultaneous inference of parental admixture proportions and admixture times from unphased local ancestry calls. 2022 , 109, 1405-1420	o
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638	Whole Genome Sequencing and Morphological Trait-Based Evaluation of UPOV Option 2 for DUS Testing in Rice. 13,	
637	Diversification in ancient Lake Biwa: integrative taxonomy reveals overlooked species diversity of the Japanese freshwater snail genus Semisulcospira (Mollusca: Semisulcospiridae). 2022 , 1-37	0
636	A single introduction of wild rabbits triggered the biological invasion of Australia. 2022 , 119,	0
635	Tumor Infiltrating Lymphocytes in Multi-National Cohorts of Ductal Carcinoma In Situ (DCIS) of Breast. 2022 , 14, 3916	1
634	eQTLs play critical roles in regulating gene expression and identifying key regulators in rice.	O

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632	Rediscovery of a native freshwater shrimp, Neocaridina denticulata, and expansion of an invasive species in and around Lake Biwa, Japan: genetic and morphological approach.	
631	A gene-based capture assay for surveying patterns of genetic diversity and insecticide resistance in a worldwide group of invasive mosquitoes. 2022 , 16, e0010689	O
630	Imputed genomes and haplotype-based analyses of the Picts of early medieval Scotland reveal fine-scale relatedness between Iron Age, early medieval and the modern people of the UK.	
629	Genomic investigation of the Chinese alligator reveals wild-extinct genetic diversity and genomic consequences of their continuous decline.	0
628	Extent to which array genotyping and imputation with large reference panels approximate deep whole-genome sequencing. 2022 ,	О
627	Natural adaptation and human selection of northeast African sheep genomes. 2022, 114, 110448	О
626	Genomic, metabonomic and transcriptomic analyses of sweet osmanthus varieties provide insights into floral aroma formation. 2022 , 306, 111442	О
625	Heterosis and heterotic patterns of maize germplasm revealed by a multiple-hybrid population under well-watered and drought-stressed conditions. 2022 , 21, 2477-2491	0
624	Genetic Diversity and Population Structure of Locally Adapted Brazilian Horse Breeds Assessed Using Genome-wide Single Nucleotide Polymorphisms. 2022 , 105071	О
623	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. 2022 , 119,	1
622	Genome-Wide Population Structure Analysis and Genetic Diversity Detection of Four Chinese Indigenous Duck Breeds from Fujian Province. 2022 , 12, 2302	О
621	Genetic Diversity and Selection Signatures in Jianchang Black Goats Revealed by Whole-Genome Sequencing Data. 2022 , 12, 2365	О
620	Multi-omics study revealed the genetic basis of beer flavor quality in yeast. 2022 , 168, 113932	О
619	Associations between female birth sex and risk of chronic kidney disease development among people with HIV in the USA: A longitudinal, multicentre, cohort study. 2022 , 53, 101653	0
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616	Genetic Ancestry Inference for Pharmacogenomics. 2022 , 595-609	О

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613	Genomic Data Reveals Profound Genetic Structure and Multiple Glacial Refugia in Lonicera oblata (Caprifoliaceae), a Threatened Montane Shrub Endemic to North China. 13,	0
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610	Genomic Insights of Bruneian Malays.	Ο
609	Fine scale population structure of Acropora palmata and Acropora cervicornis in the Colombian Caribbean. 10, e13854	0
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607	Performance of the Use of Genetic Information to Assess the Risk of Colorectal Cancer in the Basque Population. 2022 , 14, 4193	Ο
606	Endophenotype effect sizes support variant pathogenicity in monogenic disease susceptibility genes. 2022 , 13,	Ο
605	HPV genotyping by L1 amplicon sequencing of archived invasive cervical cancer samples: a pilot study. 2022 , 17,	0
604	Evidence of prezygotic isolation, but not assortative mating, between locally adapted populations of Fundulus heteroclitus across a salinity gradient.	Ο
603	Leveraging genomic diversity for discovery in an electronic health record linked biobank: the UCLA ATLAS Community Health Initiative. 2022 , 14,	Ο
602	Assessing the risk stratification of breast cancer polygenic risk scores in two Brazilian samples.	O
601	Genome-wide association analysis of 101 accessions dissects the genetic basis of shell thickness for genetic improvement in Persian walnut (Juglans regia L.). 2022 , 22,	О
600	The Anglo-Saxon migration and the formation of the early English gene pool. 2022 , 610, 112-119	1
599	Genetic substructure of Guizhou Tai-Kadai-speaking people inferred from genome-wide single nucleotide polymorphisms data. 10,	0
598	Genome-Wide Population Structure and Selection Signatures of Yunling Goat Based on RAD-seq. 2022 , 12, 2401	Ο

597	The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. 2022 , 14, 774	0
596	Genome-wide SNPs confirm plumage polymorphism and hybridisation within a Cyornis flycatcher species complex.	o
595	Chromosome-scale genome assembly of a Japanese chili pepper landrace, Capsicum annuum 🌃 akanotsume 🛚	o
594	Cryptic species diversity in a widespread neotropical tree genus: the case of Cedrela odorata.	О
593	Genome-wide association study of traits in sacred lotus uncovers MITE-associated variants underlying stamen petaloid and petal number variations. 13,	1
592	Validating and automating learning of cardiometabolic polygenic risk scores from direct-to-consumer genetic and phenotypic data: implications for scaling precision health research. 2022 , 16,	О
591	Genetic Diversity and Selective Signature in Dabieshan Cattle Revealed by Whole-Genome Resequencing. 2022 , 11, 1327	1
590	Multi-omics provides new insights into the domestication and improvement of dark jute (Corchorus olitorius).	О
589	Identification of Signatures of Selection for Litter Size and Pubertal Initiation in Two Sheep Populations. 2022 , 12, 2520	О
588	Under-representation of Racial Groups in Genomics Studies of Gastroenteropancreatic Neuroendocrine Neoplasms.	О
587	Recombination rate variation shapes genomic variability of phylogeographic structure in a widespread North American songbird (Aves: Certhia americana).	О
586	Tracing Bai-Yue ancestry in aboriginal Li people on Hainan Island.	O
585	Demographic and selection histories of populations across the Sahel/Savannah belt.	3
584	Investigating community formation through dense spatial and temporal sampling of 5-6th century cemeteries in Pannonia.	О
583	Developing CIRdb as a catalog of natural genetic variation in the Canary Islanders. 2022, 12,	0
582	Integrating sex-bias into studies of archaic admixture on chromosome X.	О
581	Genomic evidence reveals intraspecific divergence of the hot-spring snake (Thermophis baileyi), an endangered reptile endemic to the Qinghai-Tibet plateau.	1
580	Favored single nucleotide variants identified using whole genome Re-sequencing of Austrian and Chinese cattle breeds. 13,	О

579	Genetic characterization of two North Italian villages: A story of isolation, ancient admixture, and genetic drift.	O
578	Ancient DNA Reveals China as a Historical Genetic Melting Pot in Tiger Evolution.	O
577	Genomic Testing in Localized Prostate Cancer Can Identify Subsets of African Americans With Aggressive Disease.	2
576	Genome Resequencing and Transcriptome Analysis Reveal the Genetic Diversity of Wolfiporia cocos Germplasm and Genes Related to High Yield. 2022 , 79,	O
575	Genome-wide species delimitation analyses of a silverside fish species complex in central Mexico indicate taxonomic over-splitting. 2022 , 22,	0
574	Testing the generalizability of ancestry-specific polygenic risk scores to predict prostate cancer in sub-Saharan Africa. 2022 , 23,	O
573	Analysis of genome and methylation changes in Chinese indigenous chickens over time provides insight into species conservation. 2022 , 5,	0
572	Whole-exome Sequencing of Nigerian Prostate Tumors from the Prostate Cancer Transatlantic Consortium (CaPTC) Reveals DNA Repair Genes Associated with African Ancestry. 2022 , 2, 1005-1016	1
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570	Ancestry-related distribution of Runs of homozygosity and functional variants in Qatari population. 2022 , 23,	О
569	Patterns of genetic variation and QTLs controlling grain traits in a collection of global wheat germplasm revealed by high-quality SNP markers. 2022 , 22,	0
568	Interspecific forced copulations generate most hybrids in broadly sympatric ducks. 2022 , 17, e0274059	О
567	Rapid intralacustrine evolution of an invasive pelagic three-spined stickleback (Gasterosteus aculeatus) ecotype in Lake Constance.	О
566	The genomic landscape of contemporary western Remote Oceanians. 2022,	O
565	Whole-genome resequencing reveals the origin of tea in Lincang. 13,	0
564	Dating the origin and spread of specialization on human hosts in Aedes aegypti mosquitoes.	O
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560	Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. 2022 , 54, 1553-1563	2
559	Hybrid-derived weedy rice maintains adaptive combinations of alleles associated with seed dormancy.	0
558	Genomic insights into rapid speciation within the world largest tree genus Syzygium. 2022, 13,	O
557	Biogeographic insights from a genomic survey of Salmo trouts from the Aralo-Caspian regions.	O
556	Genetic structure correlates with ethnolinguistic diversity in eastern and southern Africa. 2022 , 109, 1667-1679	O
555	Rapid, Reference-Free human genotype imputation with denoising autoencoders. 11,	О
554	The impact of using different ancestral reference populations in assessing crossbred population admixture and influence on performance. 13,	O
553	Ancient DNA from Tubo Kingdom-related tombs in northeastern Tibetan Plateau revealed their genetic affinity to both Tibeto-Burman and Altaic populations.	О
552	An oligogenic architecture underlying ecological and reproductive divergence in sympatric populations.	O
551	Genomic breed composition of pure registered Brazilian Gir. 2022 , 54,	О
550	High-quality Chromosome-scale Genomes Facilitate Effective Identification of Large Structural Variations in Hot and Sweet Peppers.	O
549	Localized variation in ancestral admixture identifies pilocytic astrocytoma risk loci among Latino children. 2022 , 18, e1010388	O
548	Chromosome-level genome assembly and resequencing of camphor tree (Cinnamomum camphora) provides insight into phylogeny and diversification of terpenoid and triglyceride biosynthesis of Cinnamomum.	O
547	Global genomic analysis reveals the genetic origin and secondary invasion of fall armyworm in the Eastern hemisphere.	0
546	Distinct selection signatures during domestication and improvement in crops: a tale of two genes in mungbean.	O
545	Influence of Pleistocene climate fluctuations on the demographic history and distribution of the critically endangered Chinese pangolin (Manis pentadactyla). 2022 , 7,	0
544	Teasing apart the joint effect of demography and natural selection in the birth of a contact zone.	O

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542	Pig Coat Color Manipulation by MC1R Gene Editing. 2022 , 23, 10356	1
541	Integration of multi-omics data reveals cis-regulatory variants that are associated with phenotypic differentiation of eastern from western pigs. 2022 , 54,	O
540	Selection and adaptive introgression guided the complex evolutionary history of European common bean.	O
539	Correlation research of susceptibility single nucleotide polymorphisms and the severity of clinical symptoms in attention deficit hyperactivity disorder. 13,	O
538	Population history and genome wide association studies of birth weight in a native high altitude Ladakhi population. 2022 , 17, e0269671	O
537	Construction of a SNP fingerprinting database and population genetic analysis of 329 cauliflower cultivars.	О
536	Saving the sea cucumbers: Using population genomic tools to inform fishery and conservation management of the Fijian sandfish Holothuria (Metriatyla) scabra. 2022 , 17, e0274245	O
535	Genetic diversity and population structure of wild and cultivated Crotalaria species based on genotyping-by-sequencing. 2022 , 17, e0272955	O
534	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. 2022 , 23,	O
533	Genetic diversity of wild rice accessions (Oryza rufipogon Griff.) in Guangdong and Hainan Provinces, China, and construction of a wild rice core collection. 13,	O
532	Genetic Ancestry Correlates with Somatic Differences in a Real-World Clinical Cancer Sequencing Cohort. OF1-OF14	O
531	Genome Reporting for Healthy Populations Pipeline for Genomic Screening from the GENCOV COVID-19 Study. 2022 , 2,	O
530	African AncestryAssociated Gene Expression Profiles in Triple-Negative Breast Cancer Underlie Altered Tumor Biology and Clinical Outcome in Women of African Descent. OF1-OF22	2
529	Horizontal transferred T-DNA and haplotype-based phylogenetic analysis uncovers the origin of sweetpotato.	O
528	Genomic Analysis of Two Phlebotomine Sand Fly Vectors of Leishmania from the New and Old World.	O
527	Applying genomic approaches to delineate conservation strategies using the freshwater mussel Margaritifera margaritifera in the Iberian Peninsula as a model. 2022 , 12,	О
526	Kleptoparasites of social spider colonies do not track hostsßubdivided population structure.	O

525	High genetic connectivity among large populations of Pteronotus gymnonotus in bat caves in Brazil and its implications for conservation. 10,	0
524	Association of Plasma and Cerebrospinal Fluid Alzheimer Disease Biomarkers With Race and the Role of Genetic Ancestry, Vascular Comorbidities, and Neighborhood Factors. 2022 , 5, e2235068	O
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522	ExPRSweb: An online repository with polygenic risk scores for common health-related exposures. 2022 , 109, 1742-1760	O
521	Linking pathogenthicrobiometost interactions to explain amphibian population dynamics.	0
520	Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. 2022 , 54, 1544-1552	2
519	Genomic divergence, local adaptation, and complex demographic history may inform management of a popular sportfish species complex. 2022 , 12,	0
518	Phylogenomic analysis of the bowfin (Amia calva) reveals unrecognized species diversity in a living fossil lineage. 2022 , 12,	2
517	Secondary contact rather than coexistence Erebia butterflies in the Alps.	O
516	The diverse genetic origins of a Classical period Greek army. 2022 , 119,	O
516 515	The diverse genetic origins of a Classical period Greek army. 2022 , 119, Species-informative SNP markers for characterising freshwater prawns of genus Macrobrachium in Cameroon. 2022 , 17, e0263540	0
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515 514	Species-informative SNP markers for characterising freshwater prawns of genus Macrobrachium in Cameroon. 2022, 17, e0263540 Convergence and molecular evolution of floral fragrance after independent transitions to self fertilization.	0
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515 514 513 512	Species-informative SNP markers for characterising freshwater prawns of genus Macrobrachium in Cameroon. 2022, 17, e0263540 Convergence and molecular evolution of floral fragrance after independent transitions to self fertilization. Genomic insight into genetic changes and shaping of major inbred rice cultivars in China. Time-ordering japonica / geng genomes analysis indicates the importance of large structural variants in rice breeding. The power of TOPMed imputation for the discovery of Latino enriched rare variants associated	O O 1
515 514 513 512 511	Species-informative SNP markers for characterising freshwater prawns of genus Macrobrachium in Cameroon. 2022, 17, e0263540 Convergence and molecular evolution of floral fragrance after independent transitions to self fertilization. Genomic insight into genetic changes and shaping of major inbred rice cultivars in China. Time-ordering japonica / geng genomes analysis indicates the importance of large structural variants in rice breeding. The power of TOPMed imputation for the discovery of Latino enriched rare variants associated with type 2 diabetes.	0 0 0

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506	Sequential hybridization may have facilitated ecological transitions in the Southwestern pinyon pine syngameon.	o
505	Comparative phylogeography of two commensal rat species (Rattus tanezumi and Rattus norvegicus) in China: Insights from mitochondrial DNA, microsatellite, and 2b-RAD data. 2022 , 12,	0
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503	Genomic signatures reveal selection in Lingxian white goose. 2022, 102269	0
502	Genome-Wide SNP Analysis Reveals the Genetic Diversity and Population Structure of the Domestic Reindeer Population (Rangifer tarandus) Inhabiting the Indigenous Tofalar Lands of Southern Siberia. 2022 , 14, 900	O
501	Geographical Patterns of Genetic Variation in Locoto Chile (Capsicum pubescens) in the Americas Inferred by Genome-Wide Data Analysis. 2022 , 11, 2911	O
500	Animal-SNPAtlas: a comprehensive SNP database for multiple animals.	O
499	Genomic Variation, Population Structure, and Gene Flow across Asian Pikas.	О
498	Integrative QTL mapping and selection signatures in Groningen White Headed cattle inferred from whole-genome sequences. 2022 , 17, e0276309	O
497	Genome-wide association study reveals novel QTLs and candidate genes for seed vigor in rice. 13,	О
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495	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. 2022 , 20,	1
494	Genomic Tools for the Characterization of Local Animal Genetic Resources: Application in Mascaruna Goat. 2022 , 12, 2840	О
493	Genetic dissection of fruit maturity date in apricot (P. armeniaca L.) through a Single Primer Enrichment Technology (SPET) approach. 2022 , 23,	O
492	An insight into the runs of homozygosity distribution and breed differentiation in Mangalitsa pigs. 13,	О
491	Human impact on the recent population history of the elusive European wildcat inferred from whole genome data. 2022 , 23,	0
490	Distribution characteristics of selenium, cadmium and arsenic in rice grains and their genetic dissection by genome-wide association study. 13,	1

489	Genetic Interrelation of the Chulym Turks with Khakass and Kets according to Autosomal SNP Data and Y-Chromosome Haplogroups. 2022 , 58, 1228-1234	1
488	Genetic admixture history and forensic characteristics of Tibeto-Burman-speaking Qiang people explored via the newly developed Y-STR panel and genome-wide SNP data. 10,	О
487	The Genomic Diversity of theEliurusgenus in northern Madagascar with a Putative New Species.	О
486	Genome-Wide Genetic Diversity and Population Structure of Local Sudanese Sheep Populations Revealed by Whole-Genome Sequencing. 2022 , 14, 895	O
485	The genome-wide allele and haplotype-sharing patterns suggested one unique Hmong-Mein-related lineage in Southwest China.	O
484	Microevolutionary mechanism of high-altitude adaptation in Tibetan chicken populations from an elevation gradient.	O
483	Polygenic heterogeneity in antidepressant treatment and placebo response. 2022 , 12,	0
482	Unsupervised Discovery of Ancestry Informative Markers and Genetic Admixture Proportions in Biobank-Scale Data Sets.	o
481	The power of geohistorical boundaries for modeling the genetic background of human populations: the case of the rural Catalan Pyrenees.	0
480	The Chromosome-level genome of Aesculus wilsonii provides new insights into terpenoid biosynthesis and Aesculus evolution. 13,	o
479	What lies behind a fruit crop variety name? A case study of the barn date palm from al-Dlobasis, Saudi Arabia.	0
478	Deep phylogeographic splits and limited mixing by sea surface currents govern genetic population structure in the mangrove genus Lumnitzera (Combretaceae) across the Indonesian Archipelago.	1
477	Genome-wide association study for systemic lupus erythematosus in an egyptian population. 13,	0
476	Contrasting levels of hybridization across the two contact zones between two hedgehog species revealed by genome-wide SNP data. 2022 , 129, 305-315	O
475	Genome sequencing reveals evidence of adaptive variation in the genus Zea.	1
474	Genetic architecture of behavioural resilience to ocean acidification.	O
473	Phylogeographic structure of Heteroplexis (Asteraceae), an endangered endemic genus in the limestone karst regions of southern China. 13,	О
472	Development and application of genetic ancestry reconstruction methods to study diversity of patient-derived models in the NCI PDXNet Consortium.	o

471	Genome-Wide Association Study of Growth Traits in a Four-Way Crossbred Pig Population. 2022 , 13, 1990	1
470	Whole-Genome Resequencing Highlights the Unique Characteristics of Kecai Yaks. 2022 , 12, 2682	1
469	Pan-mitogenomics reveals the genetic basis of cytonuclear conflicts in citrus hybridization, domestication, and diversification. 2022 , 119,	0
468	Population structure of threatened caribou in western Canada inferred from genome-wide SNP data.	O
467	Multiple migrations from East Asia led to linguistic transformation in NorthEast India and mainland Southeast Asia. 13,	0
466	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in Ganoderma.	O
465	A Prism Vote method for individualized risk prediction of traits in genotype data of Multi-population. 2022 , 18, e1010443	0
464	Evolutionary Responses of a Reef-building Coral to Climate Change at the End of the Last Glacial Maximum. 2022 , 39,	O
463	Forest cover and geographical distance influence fine-scale genetic structure of leaf-toed geckos in the tropical dry forests of western Mexico.	0
462	Counter the weaponization of genetics research by extremists. 2022 , 610, 444-447	O
461	Introgression of a Complex Genomic Structural Variation Causes Hybrid Male Sterility in GJ Rice (Oryza sativa L.) Subspecies. 2022 , 23, 12804	0
460	Identification of candidate genes related to highland adaptation from multiple Chinese local chicken breeds by whole genome sequencing analysis.	O
459	Assessing Genetic Diversity and Searching for Selection Signatures by Comparison between the Indigenous Livni and Duroc Breeds in Local Livestock of the Central Region of Russia. 2022 , 14, 859	0
458	Natural hybridisation reduces vulnerability to climate change.	O
457	Genetic architecture and selection of Anhui autochthonous pig population revealed by whole genome resequencing. 13,	0
456	Genetic Analyses of Response of Local Ghanaian Tanzanian Chicken Ecotypes to a Natural Challenge with Velogenic Newcastle Disease Virus. 2022 , 12, 2755	O
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454	Wolbachia wAlbB inhibit dengue and Zika infection in the mosquito Aedes aegypti with an Australian background. 2022 , 16, e0010786	O

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452	Traces of introgression from cAus into tropical Japonica observed in African upland rice varieties.	О
451	Historical dispersal and host-switching formed the evolutionary history of a globally distributed multi-host parasite - the Ligula intestinalisspecies complex.	0
450	Genetic introgression between different groups reveals the differential process of Asian cultivated rice. 2022 , 12,	O
449	Genomic insights into the genetic structure and population history of Mongolians in Liaoning Province. 13,	O
448	Genomic analyses reveal association of ASIP with a recurrently-evolving adaptive color pattern in frogs.	O
447	A within- and across-country assessment of the genomic diversity and autozygosity of South African and eSwatini Nguni cattle. 2022 , 54,	0
446	Severe inbreeding, increased mutation load and gene loss-of-function in the critically endangered Devils Hole pupfish. 2022 , 289,	2
445	Candidate gene discovery for salt tolerance in rice (Oryza sativa L.) at the germination stage based on genome-wide association study. 13,	0
444	Population genomic evidence of adaptive response during the invasion history of Plasmodium falciparumin the Americas.	O
443	How ancient forest fragmentation and riparian connectivity generate high levels of genetic diversity in a microendemic Malagasy tree.	0
442	Genome-wide association study reveals a GLYCOGEN SYNTHASE KINASE 3 gene regulating plant height in Brassica napus. 13,	1
441	Leaf physiology variations are modulated by natural variations that underlie stomatal morphology in Populus.	0
440	Selective sweeps on different pigmentation genes mediate convergent evolution of island melanism in two incipient bird species. 2022 , 18, e1010474	1
439	Genomic evidence for ancient human migration routes along South America's Atlantic coast. 2022 , 289,	0
438	Transcriptome-based analyses of adaptive divergence between two closely related spruce species on the Qinghai-Tibet Plateau and adjacent regions.	O
437	Genetic structure and demographic history of Northern Han people in Liaoning Province inferred from genome-wide array data. 10,	О
436	Genomic insights into local adaptation and future climate-induced vulnerability of a keystone forest tree in East Asia. 2022 , 13,	1

435	Biogeographical ancestry, variable selection, and PLS-DA method: a new panel to assess ancestry in forensic samples via MPS technology. 2023 , 62, 102806	1
434	Within-species plant phylogeny drives ectomycorrhizal fungal community composition in tree roots along a timberline. 2023 , 176, 108880	О
433	Teaching Computational Genomics and Bioinformatics on a High Performance Computing Cluster - A Primer.	О
432	Genomic trajectories of a near-extinction event in the Chatham Island black robin. 2022, 23,	О
431	Construction of an SNP fingerprinting database and population genetic analysis of 329 cauliflower cultivars. 2022 , 22,	0
430	Markhor-derived introgression of a genomic region encompassing PAPSS2 confers high-altitude adaptability in Tibetan goats.	О
429	Interspecific Gene Flow and Selective Sweeps in Picea wilsonii, P. neoveitchii and P. likiangensis. 2022 , 11, 2993	o
428	The genetic legacy of the Hunyadi descendants. 2022 , e11731	О
427	Balancing at the Borderline of a Breed: A Case Study of the Hungarian Short-Haired Vizsla Dog Breed, Definition of the Breed Profile Using Simple SNP-Based Methods. 2022 , 13, 2022	0
426	Identification of Genetic Variations and Candidate Genes Responsible for Stalk Sugar Content and Agronomic Traits in Fresh Corn via GWAS across Multiple Environments. 2022 , 23, 13490	О
425	A genome wide association study of chronic spontaneous urticaria risk and heterogeneity. 2022,	О
424	Selection signatures for fiber production in commercial species: A review.	О
423	Pantranscriptome combined with phenotypic quantification reveals germplasm kinship and regulation network of bract color variation in Bougainvillea. 13,	0
422	Combining phylogenomic and morphological data reveals new patterns of diversity in the national tree of Brasil, Paubrasilia echinata.	О
421	Watermelon domestication was shaped by stepwise selection and regulation of the metabolome.	О
420	Genome-wide association studies of five free amino acid levels in rice. 13,	О
419	Genetic Ancestry and Breast Cancer Subtypes in Hispanic/Latina Women. 2023, 79-88	O
418	A novel splice-affecting HNF1A variant with large population impact on diabetes in Greenland. 2022 , 100529	О

417	Genome-wide SNPs in the spiny lobster Panulirus homarus reveal a hybrid origin for its subspecies. 2022 , 23,	О
416	Population Diversity Analysis Provide Insights into Provenance Identification of Dendrobium catenatum. 2022 , 13, 2093	Ο
415	Whole-genome resequencing reveals complex effects of geographic-paleoclimatic interactions on diversification of Moustache toads in East Asia.	0
414	The oldest unvaccinated Covid-19 survivors in South America. 2022 , 19,	1
413	Genome screening, reporting, and genetic counseling for healthy populations.	0
412	Genome-wide SNPs reveal novel patterns of spatial genetic structure in Aedes albopictus (Diptera Culicidae) population in China. 10,	Ο
411	A genomic snapshot of demographic and cultural dynamism in Upper Mesopotamia during the Neolithic Transition. 2022 , 8,	Ο
410	Testing assertions of widespread introgressive hybridization in a clade of neotropical toads with low mate selectivity (Rhinella granulosa species group).	O
409	Exome Array Analysis of 9,721 ischemic stroke cases from the SiGN Consortium.	0
408	Conservation genomics of Agave tequilana Weber var. azul: low genetic differentiation and heterozygote excess in the tequila agave from Jalisco, Mexico. 10, e14398	Ο
407	Evolution of different rice ecotypes and genetic basis of flooding adaptability in Deepwater rice by GWAS. 2022 , 22,	0
406	Estimation of genetic variability and identification of regions under selection based on runs of homozygosity in Beijing-You Chickens. 2022 , 102342	O
405	Crimp: an efficient tool for summarizing multiple clusterings in population structure analysis and beyond.	0
404	Population Structure and Selection Signatures Underlying Domestication Inferred from Genome-Wide Copy Number Variations in Chinese Indigenous Pigs. 2022 , 13, 2026	1
403	Genomics reveals introgression and purging of deleterious mutations in the Arabian leopard (Panthera pardus nimr).	0
402	SLAF-Seq Technology-Based Genome-Wide Association and Population Structure Analyses of Ancient Camellia sinensis (L.) Kuntze in Sandu County, China. 2022 , 13, 1885	O
401	Genetic ancestry inference from cancer-derived molecular data across genomic and transcriptomic platforms.	0
400	Genomic architecture of autism from comprehensive whole-genome sequence annotation. 2022 , 185, 4409-4427.e18	1

399	The genomic footprint of social stratification in admixing American populations.	O
398	Cost-effectively dissecting the genetic architecture of complex wool traits in rabbits by low-coverage sequencing. 2022 , 54,	O
397	Contribution bias of parental genomes to the hybrid lineages of black Amur bream and topmouth culter revealed by low-coverage whole-genome sequencing. 2023 , 852, 147058	О
396	Genetic diversity of two native sheep breeds by genome-wide analysis of single nucleotide polymorphisms. 2023 , 17, 100690	O
395	Development of a low-density SNP genotyping panel by a novel technology mGPS and its application in germplasm identification of abalone. 2023 , 565, 739089	1
394	Species delimitation using genomic data to resolve taxonomic uncertainties in a speciation continuum of pelagic seabirds. 2023 , 179, 107671	O
393	Landscapes drive the dispersal of Monochamus alternatus, vector of the pinewood nematode, revealed by whole-genome resequencing. 2023 , 529, 120682	О
392	Origin of domesticated Qingtian paddy-field carp and its genetic differentiation from wild common carp populations. 2023 , 565, 739117	O
391	Protocol to analyze population structure and migration history based on human genome variation data. 2023 , 4, 101928	O
390	Associations of renal sinus fat with blood pressure and ectopic fat in a diverse cohort of adults. 2023 , 16, 200165	O
389	Genome-Wide Association Study of Abdominal Fat in Wenshang Barred Chicken Based on the Slaf-Seq Technology. 2022 , 24,	O
388	Allelic variations of <i>Vrn-1</i> and <i>Ppd-1</i> genes in Japanese wheat varieties reveal the genotype-environment interaction for heading time. 2022 , 72, 343-354	O
387	Baltic Migrants in the Middle Dnipro Region: A Comparative Study of the Late Viking Age Archaeological Complex of Ostriv, Ukraine. 2022 , 66, 221-265	1
386	Comparison of PIK3CA Mutation Prevalence in Breast Cancer Across Predicted Ancestry Populations. 2022 ,	O
385	Joint Analysis of Phenotypic and Genomic Diversity Sheds Light on the Evolution of Xenobiotic Metabolism in Humans. 2022 , 14,	O
384	Pistachio genomes provide insights into nut tree domestication and ZW sex chromosome evolution. 2022 , 100497	O
383	Genomic basis of the giga-chromosomes and giga-genome of tree peony Paeonia ostii. 2022, 13,	О
382	Reconstructing the formation of Hmong-Mien genetic fine-structure.	O

381	Genomic and machine learning-based screening of aquaculture associated introgression into at-risk wild North American Atlantic salmon (Salmo salar) populations.	1
380	Population genomics reveal distinct and diverging populations of An. minimus in Cambodia. 2022 , 5,	O
379	Allopatric origin, secondary contact and subsequent isolation of sympatric rockfishes (Sebastidae: Sebastes) in the north-western Pacific. 2023 , 138, 37-50	0
378	Unappreciated Subcontinental Admixture in Europeans and European Americans: Implications for Genetic Epidemiology Studies.	O
377	Analyzing the Korean reference genome with meta-imputation increased the imputation accuracy and spectrum of rare variants in the Korean population. 13,	0
376	The genomic analysis of current-day North African populations reveals the existence of trans-Saharan migrations with different origins and dates.	O
375	Identification of New Genes and Genetic Variant Loci Associated with Breast Muscle Development in the Mini-Cobb F2 Chicken Population Using a Genome-Wide Association Study. 2022 , 13, 2153	1
374	Multiple sources of genetic diversity contributed to the extensive ethnolinguistic diversity in Southwest China.	O
373	Genomic consequences of range expansion and colonisation in the reed warbler (Acrocephalus scirpaceus).	0
372	Integrating genome-wide association studies and population genomics analysis reveals the genetic architecture of growth and backfat traits in pigs. 13,	1
371	Rare copy number variants in males and females with childhood attention-deficit/hyperactivity disorder.	0
370	Characterization and genetic dissection of maize ear leaf midrib acquired by 3D digital technology.	O
369	Identification of Copy Number Variations in Four Horse Breed Populations in South Korea. 2022, 12, 3501	0
368	Population genetics analysis of Tolai hares (Lepus tolai) in Xinjiang, China using genome-wide SNPs from SLAF-seq and mitochondrial markers. 13,	O
367	As the Goose Flies: Migration Routes and Timing Influence Patterns of Genetic Diversity in a Circumpolar Migratory Herbivore. 2022 , 14, 1067	0
366	Identification of a regulatory pathway governing TRAF1 via an arthritis-associated non-coding variant.	O
365	The demographic history of house mice (Mus musculus domesticus) in eastern North America.	0
364	Duplicate Genes as Sources for Rapid Adaptive Evolution of Sperm Under Environmental Pollution in Tree Sparrow.	O

363	Genome-wide association study of salt tolerance at the germination stage in hemp. 2023, 219,	O
362	Association study of SNP locus for color related traits in herbaceous peony (Paeonia lactiflora Pall.) using SLAF-seq. 13,	O
361	Geographical classification of malaria parasites through applying machine learning to whole genome sequence data. 2022 , 12,	О
360	Cultural and demic co-diffusion of Tubo Empire on Tibetan Plateau. 2022 , 25, 105636	O
359	Resolving drug selection and migration in an inbred South American Plasmodium falciparum population with identity-by-descent analysis. 2022 , 18, e1010993	0
358	Uncovering the genomic basis of infection through co-genomic sequencing of hosts and parasites.	O
357	Challenges in selecting admixture models and marker sets to infer genetic ancestry in a Brazilian admixed population. 2022 , 12,	0
356	Genomic adaptation of Ethiopian indigenous cattle to high altitude. 13,	1
355	Evolution of weedy giant ragweed (Ambrosia trifida): Multiple origins and gene expression variability facilitates weediness. 2022 , 12,	0
354	Genomic differentiation with isolation by distance along a latitudinal gradient in the spotted-leg treefrog Polypedates megacephalus.	О
353	Genome-wide identification of SNPs associated with body weight in yak. 2022 , 23,	О
352	Whole-Genome Sequence Analysis Reveals the Origin of the Chakouyi Horse. 2022 , 13, 2411	O
351	Population genomics and subgenome evolution of the allotetraploid frog Xenopus laevis in southern Africa.	О
350	Joint Multi-Ancestry and Admixed GWAS Reveals the Complex Genetics behind Human Cranial Vault Shape.	O
349	Genetic Variation and Population Structure of Oryza sativa Accessions in the AfricaRice Collection and Development of the AfricaRice O. sativa Core Collection.	О
348	Interpreting mismatches between linguistic and genetic patterns among speakers of Tanimuka (Eastern Tukanoan) and Yukuna (Arawakan). 2023 , 13,	3
347	Estimating admixture pedigrees of recent hybrids without a contiguous reference genome.	О
346	Positive selection in the genomes of two Papua New Guinean populations at distinct altitude levels.	O

345	Recent speciation associated with range expansion and a shift to self-fertilization in North American Arabidopsis. 2022 , 13,	О
344	Historic DNA uncovers genetic effects of climate change and landscape alteration in two wild bee species.	O
343	The role of genomic signatures of directional selection and demographic history in the population structure of a marine teleost with high gene flow. 2022 , 12,	0
342	Selective sweeps linked to the colonization of novel habitats and climatic changes in a wild tomato species.	O
341	Genomic divergence between two sister Ostrya species through linked selection and recombination. 2022 , 12,	O
340	Effects of fruit dimorphism on genetic structure and gene flow in the coastal shrub Scaevola taccada.	O
339	Genome-wide data from medieval German Jews show that the Ashkenazi founder event pre-dated the 14th century. 2022 , 185, 4703-4716.e16	0
338	Estimates of genomic inbreeding and identification of candidate regions in Beijing-You chicken populations.	О
337	Spatiotemporal fluctuations of population structure in the Americas revealed by a meta-analysis of the first decade of archaeogenomes.	0
336	The evolutionary process of invasion in the fall armyworm (Spodoptera frugiperda). 2022 , 12,	О
335	Identification of the riceRcgene as a main regulator of seed survival under dry storage conditions.	0
334	Horizontally-transferred T-DNA and haplotype-based phylogenetic analysis uncovers the origin of sweetpotato.	О
333	Does selection occur at the intermediate zone of two insufficiently isolated populations? A whole-genome analysis along an altitudinal gradient.	0
332	Continent-wide phylogenomic framework reveals introgression as a driver of intra-specific diversity and enriched molecular pathways in caribou.	1
331	Stepping up to genome scan allows stock differentiation in the worldwide distributed blue shark Prionace glauca.	1
330	Association of genetic ancestry with HER2, GRB7 AND estrogen receptor expression among Colombian women with breast cancer. 12,	O
329	Extensive gene flow in secondary sympatry after allopatric speciation.	0
328	Whole-genome sequencing across 449 samples spanning 47 ethnolinguistic groups provides insights into genetic diversity in Nigeria.	0

327	Population diversity analyses provide insights into key horticultural traits of Chinese native thymes.	1
326	Genetic dissection of yield-related traits in response to drought stress in common bean. 2022 ,	O
325	The development of a 30 K SNP genotyping tool targeting genomic regions of temperature and salinity adaptation in estuarine oyster. 2022 , 739168	1
324	Using the Software DeepWings' to Classify Honey Bees across Europe through Wing Geometric Morphometrics. 2022 , 13, 1132	1
323	Genomic innovation and regulatory rewiring during evolution of the cotton genus Gossypium. 2022 , 54, 1959-1971	1
322	The genomic analysis of a wide peach germplasm collection revealed genetic relationships between European landraces and American ferals and landraces. 2022 , 81-88	O
321	Spatial and temporal heterogeneity in human mobility patterns in Holocene Southwest Asia and the East Mediterranean. 2022 ,	О
320	Historical dispersal and host-switching formed the evolutionary history of a globally distributed multi-host parasite - the Ligula intestinalis species complex. 2022 , 107677	O
319	Genetic diversity in global populations of the critically endangered addax (Addax nasomaculatus) and its implications for conservation.	О
318	Genomic insights intoPlasmodium vivaxpopulation structure and diversity in central Africa.	O
317	Purging due to self-fertilization does not prevent accumulation of expansion load.	О
316	First genome-wide association study and genomic prediction for growth traits in spotted sea bass (Lateolabrax maculatus) using whole-genome resequencing. 2022 , 739194	O
315	Systematic revision of the Japanese freshwater snail. 2022 , 36, 1139-1177	О
314	Genetic admixture and language shift in the medieval Volga-Oka interfluve. 2022,	O
313	On the Inclusion of Adaptive Potential in Species Distribution Models: Towards a Genomic-Informed Approach to Forest Management and Conservation. 2023 , 10, 3	О
312	Genetic analysis for detection of genes associated to drought tolerance in rice accessions belonging to north east India.	O
311	Ancestral risk modification for multiple sclerosis susceptibility detected across the Major Histocompatibility Complex in a multi-ethnic population. 2022 , 17, e0279132	О
310	Genomic Consequences of and Demographic Response to Pervasive Hybridization over Time in Climate-sensitive Pikas.	О

309	African ancestry GWAS of dementia in a large military cohort identifies significant risk loci.	1
308	Chromosome-scale genome assembly of a Japanese chili pepper landrace, Capsicum annuum Takanotsume	O
307	Genomes of the cosmopolitan fruit pest Bactrocera dorsalis (Diptera: Tephritidae) reveal its global invasion history and thermal adaptation. 2022 ,	O
306	Genome-wide RAD sequencing data suggest predominant role of vicariance in Sino-Japanese disjunction of the monotypic genus Conandron (Gesneriaceae).	O
305	Common protein-coding variants influence the racing phenotype in galloping racehorse breeds. 2022 , 5,	O
304	Genome-Wide Association Studies of Salt Tolerance at the Seed Germination Stage and Yield-Related Traits in Brassica napus L 2022 , 23, 15892	O
303	Harshening stem cell research and precision medicine: The states of human pluripotent cells stem cell repository diversity, and racial and sex differences in transcriptomes. 10,	0
302	Identification of runs of homozygosity in Western honey bees (Apis mellifera) using whole-genome sequencing data. 2023 , 13,	O
301	Climate adaptation and vulnerability of foundation species in a global change hotspot.	0
300	Distinct traces of mixed ancestry in western commercial pig genomes following gene flow from Chinese indigenous breeds. 13,	O
299	Evidence for ancient introgression and gene flow in the genus Tamarix L. (Tamicaceae): a computational approach.	0
298	The power of geohistorical boundaries for modeling the genetic background of human populations: The case of the rural catalan Pyrenees. 13,	O
297	Analysis of genetic diversity and selection characteristics using the whole genome sequencing data of five buffaloes, including Xilin buffalo, in Guangxi, China. 13,	0
296	Characterization of Danube Swabian population samples on a high-resolution genome-wide basis. 2023 , 24,	O
295	Multi-omic association study identifies DNA methylation-mediated genotype and smoking exposure effects on lung function in children living in urban settings. 2023 , 19, e1010594	O
294	Performance evaluation of an in-house panel containing 59 autosomal InDels for forensic identification in Chinese Hui and Mongolian groups. 2023 , 115, 110552	O
293	Differentiated genomic footprints and connections inferred from 440 Hmong-Mien genomes suggest their isolation and long-distance migration.	O
292	Sweet Taste Receptor Gene and Caries Trajectory in the Life Course. 002203452211385	1

291	Whole-genome resequencing reveals genetic diversity and selection characteristics of dairy goat. 13,	O
290	Range-wide population genomics of the spongy moth, Lymantria dispar (Erebidae): Implications for biosurveillance, subspecies classification and phylogeography of a destructive moth.	1
289	Synchronous effective population size changes and genetic stability of forest trees through glacial cycles.	O
288	Genetic and ecological drivers of molt in a migratory bird. 2023 , 13,	0
287	Resequencing of 410 Sesame Accessions Identifies SINST1 as the Major Underlying Gene for Lignans Variation. 2023 , 24, 1055	1
286	The genetic history of Scandinavia from the Roman Iron Age to the present. 2023 , 186, 32-46.e19	Ο
285	Genome sequencing and resequencing identified three horizontal gene transfers and uncovered the genetic mechanism on the intraspecies adaptive evolution of Gastrodia elata Blume. 13,	0
284	Genomic diversity and relationship analyses of endangered German Black Pied cattle (DSN) to 68 other taurine breeds based on whole-genome sequencing. 13,	1
283	Bioregional boundaries and genomically-delineated stocks in snapper (Chrysophrys auratus) from southeastern Australia.	Ο
282	Detecting and Adjusting for Hidden Biases due to Phenotype Misclassification in Genome-Wide Association Studies.	Ο
281	Signatures of selection in indigenous Chinese cattle genomes reveal adaptive genes and genetic variations to cold climate.	Ο
280	Genetic Signature of Pinctada fucata Inferred from Population Genomics: Source Tracking of the Invasion in Mischief Reef of Nansha Islands. 2023 , 12, 97	Ο
279	Genomic vulnerability to climate change in Quercus acutissima , a dominant tree species in East Asian deciduous forests.	Ο
278	The genomic diversity of Taiwanese Austronesian groups: implications for the Ihto and Out of TaiwanImodels.	0
277	Integrating top-down and bottom-up approaches to understand the genetic architecture of speciation across a monkeyflower hybrid zone.	0
276	Genome-Wide Association Study of Rice Grain Shape and Chalkiness in a Worldwide Collection of Xian Accessions. 2023 , 12, 419	0
275	Detection of genomic regions that differentiate Bos indicus from Bos taurus ancestral breeds for milk yield in Indian crossbred cows. 13,	O
274	Unsupervised discovery of ancestry-informative markers and genetic admixture proportions in biobank-scale datasets. 2023 ,	Ο

273	Genomic evidence for three distinct species in the Erebia manto complex in Central Europe (Lepidoptera, Nymphalidae).	0
272	Spatial genetic structure of European wild boar, with inferences on late-Pleistocene and Holocene demographic history.	O
271	Complex multiple introductions drive fall armyworm invasions into Asia and Australia. 2023, 13,	0
270	Insight into forensic efficiency and genetic structure of the Guizhou Dong group via a 64-plex panel. 10,	O
269	Colonialism in South Africa leaves a lasting legacy of reduced genetic diversity in Cape buffalo.	0
268	Genetic diversity of North American popcorn germplasm and the effect of population structure on nicosulfuron response.	O
267	Multi-omic integration reveals cell-type-specific regulatory networks of insulin resistance in distinct ancestry populations. 2023 , 14, 41-57.e8	0
266	Common evolutionary trajectory of short life-cycle in Brassicaceae ruderal weeds. 2023, 14,	O
265	Genome-wide association study reveals novel loci and a candidate gene for resistance to frogeye leaf spot (Cercospora sojina) in soybean.	0
264	A comparison of 25 complete chloroplast genomes between sister mangrove species Kandelia obovata and Kandelia candel geographically separated by the South China Sea. 13,	O
263	Whole-genome resequencing reveals genetic differences and the genetic basis of parapodium number in Russian and Chinese Apostichopus japonicus. 2023 , 24,	0
262	Genetic diversity in early maturity Chinese and European elite soybeans: A comparative analysis. 2023 , 219,	O
261	Population-based genomic study of Plasmodium vivax malaria in seven Brazilian states and across South America. 2023 , 18, 100420	0
260	Genomic divergence and introgression among three Populus species. 2023 , 180, 107686	O
259	Genetic diversity analysis in dairy cows of Nariô, southwestern Colombia. 2022 , 43, 2563-2578	0
258	Sweet Cherry Diversity and Relationships in Modern and Local Varieties Based on SNP Markers. 2023 , 12, 136	O
257	Patterns of hybridization in a secondary contact zone between two passerine species, the common nightingale Luscinia megarhynchos and the thrush nightingale Luscinia luscinia.	0
256	Genetic diversity, population genetic structure and gene flow in the rare and endangered wild plant Cypripedium macranthos revealed by genotyping-by-sequencing.	O

255	Long-term Small Population Size, Deleterious Variation, and Altitude Adaptation in the Ethiopian Wolf, a Severely Endangered Canid. 2023 , 40,	O
254	Genome-wide assessment of population genetic and demographic history in Magnolia odoratissima based on SLAF-seq.	O
253	Sympatric or micro-allopatric speciation in a glacial lake? Genomic islands support neither.	О
252	Phylogeography of the closely related Littorina (Neritrema) species in the North-East Atlantic. 2022 , 19, 404-424	O
251	Genetic Diversity and Population Structure of Traditional Chinese Herb Radix bupleuri Resources Using Genome-Wide SNPs through Genotyping-by-Sequencing. 2022 , 58, 1485-1492	0
250	Ancient DNA from Protohistoric Period Cambodia indicates that South Asians admixed with local populations as early as 1stBrd centuries CE. 2022 , 12,	o
249	Genome-wide association analysis of chilling-tolerant germination in a new maize association mapping panel.	0
248	Exome Array Analysis of 9721 Ischemic Stroke Cases from the SiGN Consortium. 2023 , 14, 61	О
247	Population Genomic Evidence for the Diversification of Bellamya aeruginosa in Different River Systems in China. 2023 , 12, 29	O
246	412. Genetic diversity of the Cameroon Blackbelly sheep, an indigenous sheep from West Africa. 2022 ,	О
245	193. Genetic architecture of a composite beef cattle population. 2022 ,	O
244	729. Genetic characterization and connectedness of dairy goats in Canada, France, Italy and Switzerland. 2022 ,	О
243	213. Following the hidden footsteps of past human migrations via the goat genome. 2022 ,	0
242	173. Evaluating the use of genotype information for the prediction of breed composition in purebred and crossbred cattle. 2022 ,	О
241	192. Genetic diversity and population structure of Slovenian local breed Drefiica goat. 2022 ,	0
240	Variance component estimates, phenotypic characterization, and genetic evaluation of bovine congestive heart failure in commercial feeder cattle.	O
239	Population structure and genetic diversity of Triticum araraticum Jakubz. and Triticum timopheevii Zhuk	0
238	Population Genomic Analysis of Diploid-Autopolyploid Species. 2023 , 297-324	О

237	Combined linkage mapping and association analysis uncovers candidate genes for 25 leaf-related traits across three environments in maize. 2023 , 136, 1-14	О
236	First GWAS on Alzheimer Disease in Argentina and Chile populations.	0
235	Evolutionarily recent retrotransposons contribute to schizophrenia.	О
234	Emergence of Antifungal Resistant Subclades in the Global Predominant Phylogenetic Population of Candida albicans.	O
233	Evolution of two gene networks underlying adaptation to drought stress in the wild tomatoSolanum chilense.	0
232	Genetic diversity and structure of the 4th cycle breeding population of Chinese fir (Cunninghamia lanceolata (lamb.) hook). 14,	О
231	Genome-wide allele and haplotype-sharing patterns suggested one unique HmongMein-related lineage and biological adaptation history in Southwest China. 2023 , 17,	О
230	Bioinformatic tools for interrogating DNA recovered from human skeletal remains. 2023 , 433-458	O
229	Genome-wide association study reveals novel genetic loci involved in anaerobic germination tolerance in Indica rice. 2023 , 43,	О
228	Whole exome sequencing and replication for breast cancer among Hispanic/Latino women identifiesFANCMas a susceptibility gene for estrogen-receptor-negative breast cancer.	O
227	Establishment of Tibetan-Sheep-Specific SNP Genetic Markers. 2023 , 13, 322	0
226	Chromosome-level wild Hevea brasiliensis genome provides new tools for genomic-assisted breeding and valuable loci to elevate rubber yield.	1
225	Natural hybridization reduces vulnerability to climate change.	О
224	Multiple transitions between realms shape relict lineages of Proteus cave salamanders.	O
223	Genomic signatures of past megafrugivore-mediated dispersal in Malagasy palms.	О
222	Staying in situ or shifting range under ongoing climate change: A case of an endemic herb in the Himalaya-Hengduan Mountains across elevational gradients.	O
221	Evidence for Ecotone Speciation Across an African Rainforest-Savanna Gradient.	О
220	Genomic insight into the influence of selection, crossbreeding, and geography on population structure in poultry. 2023 , 55,	O

219	The computational implementation of a platform of relative identity-by-descent scores algorithm for introgressive mapping. 13,	O
218	Genomic vulnerability to climate change and mutation load are affected by past declines in effective population size in two sedentary arctic bird species.	О
217	Whole genome re-sequencing uncovers significant population structure and low genetic diversity in the endangered clouded apollo (Parnasssius mnemosyne) in Sweden.	O
216	Whole-genome resequencing reveals recent divergence of geographic populations of the dung beetle Phelotrupes auratus with color variation. 2023 , 13,	О
215	Resolving the haplotypes of arbuscular mycorrhizal fungi highlights the role of two nuclear populations in host interactions.	0
214	Duck pan-genome reveals two transposon-derived structural variations caused bodyweight enlarging and white plumage phenotype formation during evolution.	О
213	Genetic determinants and absence of breast cancer in Xavante Indians in Sangradouro Reserve, Brazil. 2023 , 13,	О
212	The worldwide invasion history of a pest ambrosia beetle inferred using population genomics.	О
211	Single nucleotide polymorphisms (SNPs): Ancestry-, phenotype-, and identity-informative SNPs. 2023 , 247-270	O
210	Genomic Insights into the Population History of the Resande or Swedish Travelers. 2023, 15,	О
209	Exploring the Italian equine gene pool via high-throughput genotyping. 14,	О
208	Admixture-introduced complex landscape of genetic diversity contributed to the extensive Southwestern Chinese ethnolinguistic diversity.	О
207	Prevalent introgression underlies convergent evolution in the diversification of Pungitius sticklebacks.	О
206	Genome-wide association study reveals genetic loci and candidate genes for meat quality traits in a four-way crossbred pig population. 14,	О
205	Evidence of prezygotic isolation, but not assortative mating, between locally adapted populations of Fundulus heteroclitus across a salinity gradient. 2023 , 36, 687-697	O
204	Allelic variation of TaWD40-4B.1 contributes to drought tolerance by modulating catalase activity in wheat. 2023 , 14,	1
203	Structure and origin of Tuvan gene pool according to autosome SNP and Y-chromosome haplogroups. 2023 , 27, 36-45	1
202	Biobank-scale methods and projections for sparse polygenic prediction from machine learning.	О

201	Genome-Wide Association Study of Submergence Tolerance in Rice (Oryza sativa L.). 2023, 11, 25-33	O
200	Genome-wide association studies reveal novel loci controlling tuber flesh color and oxidative browning inDioscorea alata.	O
199	Genomic divergence between two sister Medicago species triggered by the quaternary climatic oscillations on the Qinghaillibet plateau and northern China.	O
198	Genetic and ecophysiological evidence that hybridization facilitated lineage diversification in yellow Camellia (Theaceae) species: a case study of natural hybridization between C. micrantha and C. flavida. 2023 , 23,	O
197	History cooling events contributed to the endangered status of Pseudotsuga brevifolia endemic to limestone habitats. 2023 , 42, e02414	O
196	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. 2023 , 14,	O
195	Phylogenomics reveal extensive phylogenetic discordance due to incomplete lineage sorting following the rapid radiation of alpine butterflies (Papilionidae: Parnassius).	O
194	Hunter-gatherer admixture facilitated natural selection in Neolithic European farmers. 2023, 33, 1365-137	′1.e3 ⊙
193	The genome sequence and demographic history of Przewalskia tangutica (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau.	O
192	Whole-Genome Resequencing Reveals the Genetic Diversity and Selection Signatures of the Brassica juncea from the Yunnan duizhou Plateau. 2023 , 13, 1053	O
191	The hybridization origin of the Chinese endemic herb genus Notopterygium (Apiaceae): Evidence from population genomics and ecological niche analysis. 2023 , 182, 107736	O
190	Genome-wide association study of alkylresorcinols content in 161 wheat cultivars. 2023, 111, 103679	O
189	Diversification and introgression in four chromosomal taxa of the Pearson horseshoe bat (Rhinolophus pearsoni) group. 2023 , 183, 107784	O
188	Pharmacotherapy exposure as a marker of disease complexity in bipolar disorder: Associations with clinical & amp; genetic risk factors. 2023 , 323, 115174	O
187	Insight into the genetic basis of ammonia tolerance in razor clam Sinonovacula constricta by genome-wide association study. 2023 , 569, 739351	O
186	Comparative evaluation of the MAPlex, Precision ID Ancestry Panel, and VISAGE Basic Tool for biogeographical ancestry inference. 2023 , 64, 102850	O
185	Deep genome-wide divergences among species in White Cloud Mountain minnow Tanichthys albonubes (Cypriniformes: Tanichthyidae) complex: Conservation and species management implications. 2023 , 182, 107734	0
184	Impact of tooth mineral tissues genes on dental caries: A birth-cohort study. 2023 , 133, 104505	O

183	A genome-wide scan to identify signatures of selection in Lueyang black -bone chicken. 2023 , 102721	O
182	Preliminary Investigation of Essentially Derived Variety of Tea Tree and Development of SNP Markers. 2023 , 12, 1643	O
181	Geography and past climate changes have shaped the evolution of a widespread lizard in arid Central Asia. 2023 , 184, 107781	0
180	Role of SNPs located in the exon 9 of ATAPA1 gene on goose egg production. 2023 , 102, 102488	O
179	Population genomics of Corsican wildcats: Paving the way toward a new subspecies within the Felis silvestris spp. complex?. 2023 , 32, 1908-1924	О
178	Genomic diversity and differentiation between island and mainland populations of white-tailed eagles (Haliaeetus albicilla). 2023 , 32, 1925-1942	Ο
177	Genomic evidence for adaptation to tuberculosis in the Andes before European contact. 2023 , 26, 106034	O
176	Extensive hybridisation between multiple differently adapted species may aid persistence in a changing climate.	O
175	New insights from GWAS on BMI-related growth traits in a longitudinal cohort of admixed children with Native American and European ancestry. 2023 , 26, 106091	О
174	Deciphering complex reticulate evolution of AsianBuddleja(Scrophulariaceae): insights into the taxonomy and speciation of polyploid taxa in the Sino-Himalayan region.	O
173	The Michigan Genomics Initiative: A biobank linking genotypes and electronic clinical records in Michigan Medicine patients. 2023 , 3, 100257	О
172	Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal ancestry proportions. 2023 , 110, 359-367	1
171	Identification of QTNs, QTN-by-environment interactions, and their candidate genes for grain size traits in main crop and ratoon rice. 14,	О
170	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (Juglans nigra). 2023 , 10,	O
169	X-Chromosome Association Study in Latin American Cohorts Identifies New Loci in Parkinson Disease.	О
168	Genomic regions underlying positive selection in local, Alpine cattle breeds.	O
167	Opening the Black Box of Imputation Software to Study the Impact of Reference Panel Composition on Performance. 2023 , 14, 410	О
166	Variability and genetic merits of white Guinea yam landraces in Nigeria. 14,	O

165	Genotyping of DNA pools identifies untapped landraces and genomic regions to develop next-generation varieties.	O
164	Range-wide whole-genome resequencing of the brown bear reveals drivers of intraspecies divergence. 2023 , 6,	O
163	Genetic and self-perceived ancestries in Argentina: Beyond the three-hybrid model. 2023, 181, 85-95	0
162	Discovering novel clues of natural selection on four worldwide goat breeds. 2023, 13,	O
161	Genomic signatures of bottleneck and founder effects in dingoes.	O
160	Genome wide association analysis for grain micronutrients and anti-nutritional traits in mungbean [Vigna radiata (L.) R. Wilczek] using SNP markers. 10,	O
159	A complex genomic architecture underlies reproductive isolation in a North American oriole hybrid zone. 2023 , 6,	O
158	204. Assessing existing admixture in indigenous veld ecotypes and non-descript goat populations of Southern Africa. 2022 ,	O
157	575. Exploiting genomics to infer population structure and genetic variability in wild and farmed seabream and seabass. 2022 ,	O
156	707. Genetic diversity and population structure of dairy goat populations in Kenya. 2022 ,	O
155	189. Exploring genetic diversity and selection signatures in indigenous African cattle breeds. 2022 ,	0
154	243. Genetic diversity and inbreeding in US Jersey population and germplasm collection. 2022 ,	O
153	587. Genetic architecture of body weight and carcass traits in Ghanaian local chickens. 2022 ,	0
152	Whole-genome re-sequencing, diversity analysis, and stress-resistance analysis of 77 grape rootstock genotypes. 14,	O
151	Retrospective analysis of Plasmodium vivax genomes from a pre-elimination China inland population in the 2010s. 14,	O
150	418. Genetic structure and diversity of Jersey dairy cattle in Rwanda. 2022 ,	O
149	Genome and haplotype provide insights into the population differentiation and breeding improvement of Gossypium barbadense. 2023 ,	0
148	Insights into the differentiation and adaptation within Circaeasteraceae from Circaeaster agrestis genome sequencing and resequencing. 2023 , 26, 106159	O

147	Genetic polymorphism (rs6587666) in FLG protects from eczema in admixed Brazilian children population with high African ancestry. 2023 , 9, e13659	O
146	Insight into the Complex Genetic Relationship of Chinese Fir (Cunninghamia lanceolata (Lamb.) Hook.) Advanced Parent Trees Based on SSR and SNP Datasets. 2023 , 14, 347	O
145	Human Populations Drigins and Movement. 2023 , 629-645	O
144	Genomic decoding of breeding history to guide breeding-by-design in rice. 2023 , 10,	O
143	Origins, timing and introgression of domestic geese revealed by whole genome data. 2023, 14,	O
142	Genomic, genetic and phylogenetic evidence for a new falcon species using chromosome-level genome assembly of the gyrfalcon and population genomics.	O
141	Analysis of Genetic Ancestry from NGS Data Using EthSEQ. 2023 , 3,	О
140	Selection Maintains the Phenotypic Divergence of Cave and Surface Fish.	O
139	Genome assembly, resequencing and genome-wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry.	О
138	Genetic diversity variation during the natural regeneration of Vatica guangxiensis, an endangered tree species with extremely small populations. 2023 , 42, e02400	O
137	Genome-wide assessment of genetic diversity and association mapping for salt tolerance traits in okra (Abelmoschus esculentus L. Moench) using genotyping-by-sequencing. 2023 , 313, 111922	0
136	Genomic analysis reveals a KIT -related chromosomal translocation associated with the white coat phenotype in yak. 2023 , 140, 330-342	O
135	An improved reference genome for Trifolium subterraneum L. provides insight into molecular diversity and intra-specific phylogeny. 14,	O
134	The population genomic analyses of chloroplast genomes shed new insights on the complicated ploidy and evolutionary history in Fragaria. 13,	O
133	Genome wide variation in the Angolan Namib desert reveals unique Pre-Bantu ancestry.	0
132	The idiosyncratic genome of Korean long-tailed chicken as a valuable genetic resource. 2023 , 26, 106236	O
131	Evolution of horn length and lifting strength in the Japanese rhinoceros beetleTrypoxylus dichotomus.	O
130	Species boundaries and conservation implications of Cinnamomum japonicum , an endangered plant in China.	O

129	Genomic analysis, trajectory tracking, and field surveys reveal sources and long-distance dispersal routes of wheat stripe rust pathogen in China. 2023 , 100563	0
128	Genome-wide association study reveals markers and candidate genes associated with growth in the rice flower carp, an economic fish species of integrated rice-fish culture in China. 10,	O
127	Thermal heterogeneity is an important factor for maintaining the genetic differentiation pattern of the pelagic barnacle Lepas anatifera in the northwest Pacific. 2023 , 13,	0
126	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. 2023 , 100562	O
125	Socio-cultural practices affect sexual dimorphism in stature in Early Neolithic Europe.	O
124	Genomics reveals the role of admixture in the evolution of structure among sperm whale populations within the Mediterranean Sea.	O
123	Long divergent haplotypes introgressed from wild sheep are associated with distinct morphological and adaptive characteristics in domestic sheep. 2023 , 19, e1010615	O
122	Contrasting Patterns of Single Nucleotide Polymorphisms and Structural Variation Across Multiple Invasions. 2023 , 40,	O
121	The genetic and evolutionary basis of gene expression variation in East Africans. 2023, 24,	O
120	Selective footprints and genes relevant to cold adaptation and other phenotypic traits are unscrambled in the genomes of divergently selected chicken breeds. 2023 , 14,	O
119	Environmental drivers behind the genetic differentiation in mountain chickadees (Poecile gambeli).	O
118	Conservation implications of elucidating the Korean wolf taxonomic ambiguity through whole-genome sequencing.	O
117	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (Salvelinus alpinus) populations of anadromous and landlocked origin from Scandinavia.	O
116	Whole-genome sequencing of ethnolinguistic diverse northwestern Chinese Hexi Corridor people from the 10K_CPGDP project suggested the differentiated East-West genetic admixture along the Silk Road and their biological adaptations.	O
115	Evolutionary origin and establishment of a dioecious diploid-tetraploid complex.	O
114	Traces of Introgression from cAus into Tropical Japonica Observed in African Upland Rice Varieties. 2023 , 16,	O
113	An oligogenic architecture underlying ecological and reproductive divergence in sympatric populations. 12,	О
112	First in family Rhabdiasidae: the reference-guided genome assembly of an invasive parasite, the cane toad lungworm (Rhabdias pseudosphaerocephala).	O

111	Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. 2023 , 186, 923-939.e14	1
110	Equine exploitation at Pompeii (AD 79). 2023 , 48, 103902	O
109	Dual domestications and origin of traits in grapevine evolution. 2023 , 379, 892-901	1
108	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. 2023 , 40,	О
107	Population Structure Analysis and Genome-Wide Association Study of Tea (Camellia sinensis (L.) Kuntze) Germplasm in Qiannan, China, Based on SLAF-Seq Technology. 2022 , 91, 791-809	0
106	Chromosome-level reference genome of Tetrastigma hemsleyanum (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids.	О
105	Long-term population decline of a genetically homogeneous continental-wide top Arctic predator.	О
104	Geography, environment, and colonization history interact with morph type to shape genomic variation in an Arctic fish.	О
103	Identification of Selection Signatures and Loci Associated with Important Economic Traits in Yunan Black and Huainan Pigs. 2023 , 14, 655	О
102	A key gene for the climatic adaptation of Apis cerana populations in China according to selective sweep analysis. 2023 , 24,	О
101	Three sequential sex chromosome lautosome fusions inHeliconiusbutterflies.	О
100	Indigenous people from Amazon show genetic signatures of pathogen-driven selection. 2023, 9,	О
99	Demographic Modeling of Admixed Latin American Populations from Whole Genomes.	О
98	Identification of the rice Rc gene as a main regulator of seed survival under dry storage conditions.	О
97	Relationship of the gene pool of the Khants with the peoples of Western Siberia, Cis-Urals and the Altai-Sayan Region according to the data on the polymorphism of autosomic locus and the Y-chromosome. 2023 , 27, 46-54	О
96	Dating the origin and spread of specialization on human hosts in Aedes aegypti mosquitoes. 12,	О
95	Genetic Diversity of Global Faba Bean Germplasm Resources Based on the 130K TNGS Genotyping Platform. 2023 , 13, 811	O
94	Genetic diversity and population structure of a Peruvian cattle herd using SNP data. 14,	О

93	Population whole-genome resequencing reveals the phylogenetic relationships and population structure of four Hunan typical tea landraces. 2023 , 3, 0-0	O
92	Associations of atrial natriuretic peptide with measures of insulin and adipose depots. 2023, 11,	O
91	Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. 2023 , 100574	О
90	A spatial approach to jointly estimate Wright neighborhood size and long-term effective population size.	O
89	Geographic-genomic and geographic-phenotypic differentiation of the Aquilegia viridiflora complex.	О
88	Deciphering the genetic basis of resistance to soybean cyst nematode combining IBD and association mapping. 2023 , 136,	O
87	Two major chromosome evolution events with unrivaled conserved gene content in pomegranate. 14,	O
86	Population Structure, Genetic Diversity and Candidate Genes for the Adaptation to Environmental Stress in Picea koraiensis. 2023 , 12, 1266	O
85	Multi-ancestry genome-wide association analyses improve resolution of genes and pathways influencing lung function and chronic obstructive pulmonary disease risk. 2023 , 55, 410-422	О
84	Genetic Diversity and Population Structure in Solanum nigrum Based on Single-Nucleotide Polymorphism (SNP) Markers. 2023 , 13, 832	O
83	Inferring biological kinship in ancient datasets: comparing the response of ancient DNA-specific software packages to low coverage data. 2023 , 24,	О
82	Molecular signature of domestication in the arboviral vectorAedes aegypti.	O
81	Polygenic prediction of bipolar disorder in a Latin American sample.	O
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79	Deleterious mutation load in the admixed mice population. 11,	0
78	Population genomics unravels the Holocene history of bread wheat and its relatives. 2023, 9, 403-419	O
77	Hybrid zone or hybrid lineage: a genomic reevaluation of Sibley⊠ classic species conundrum inPipilotowhees. 2023 , 77, 852-869	1
76	The multifaceted genomic history of Ashaninka from Amazonian Peru. 2023 ,	O

75	Human genetic history on the Tibetan Plateau in the past 5100 years. 2023 , 9,	О
74	Exploring the sorghum race level diversity utilizing 272 sorghum accessions genomic resources. 14,	O
73	The genomic characteristics affect phenotypic diversity from the perspective of genetic improvement of economic traits. 2023 , 26, 106426	О
72	Genome-wide phylogeography reveals cryptic speciation in the circumglobal planktonic calcifier Limacina bulimoides.	O
71	A web tool for the global identification of pig breeds. 2023 , 55,	О
70	Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland.	O
69	Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. 2023 , 12, 476	O
68	Genomic analyses of hair from Ludwig van Beethoven. 2023,	O
67	Current allele distribution of the human longevity gene APOE in Europe can mainly be explained by ancient admixture.	O
66	Genome-wide mapping of signatures of selection using a high-density array identified candidate genes for growth traits and local adaptation in chickens. 2023 , 55,	O
65	A diverse panel of 755 bread wheat accessions harbors untapped genetic diversity in landraces and reveals novel genetic regions conferring powdery mildew resistance.	1
64	Detection of Genetic Differences between Holstein and Iranian North-West Indigenous Hybrid Cattles using Genomic Data. 2022 , 13, 175-186	O
63	Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus. 2023 , 6,	О
62	Understanding Complex Trait Susceptibilities and Ethnical Diversity in a Sample of 4,145 Russians Through Analysis of Clinical and Genetic Data.	O
61	Comprehensive genomic analyses of Vigna unguiculata provide insights into population differentiation and the genetic basis of key agricultural traits.	О
60	A 37 K SNP array for the management and conservation of Golden Eagles (Aquila chrysaetos).	O
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58	The Bayesian lens and Bayesian blinkers. 2023 , 381,	1

57	Discovery of SNP Molecular Markers and Candidate Genes Associated with Sacbrood Virus Resistance in Apis cerana cerana Larvae by Whole-Genome Resequencing. 2023 , 24, 6238	Ο
56	The bHLH transcription factor gene, OsbHLH38 , plays a key role in controlling rice salt tolerance.	О
55	Entwined African and Asian genetic roots of medieval peoples of the Swahili coast. 2023, 615, 866-873	О
54	Comprehensive evaluations of individual discrimination, kinship analysis, genetic relationship exploration and biogeographic origin prediction in Chinese Dongxiang group by a 60-plex DIP panel. 2023 , 160,	О
53	Replicate contact zones suggest a limited role of plumage in reproductive isolation among subspecies of the variable seedeater (Sporophila corvina).	O
52	Population structure and selective signature of sheep around Tarim Basin. 11,	O
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50	Population Structure and Selection Signatures of Domestication in Geese. 2023 , 12, 532	О
49	Implications of past and present genetic connectivity for management of the saltwater crocodile (Crocodylus porosus).	O
48	A comprehensive analysis of the genetic diversity and environmental adaptability in worldwide Merino and Merino-derived sheep breeds. 2023 , 55,	O
47	Population Structure and Genetic Diversity in the Natural Distribution of Neolamarckia cadamba in China. 2023 , 14, 855	О
46	Ongoing introgression of a secondary sexual plumage trait in a stable avian hybrid zone.	О
45	A look under the hood of genomic-estimated breed compositions for brangus cattle: What have we learned?. 14,	O
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43	Runs of homozygosity and cross-generational inbreeding of Iranian fat-tailed sheep.	О
42	Insight into the evolutionary and domesticated history of the most widely cultivated mushroom Agaricus bisporus via mitogenome sequences of 361 global strains. 2023 , 24,	О
41	Assessing the current genetic status of Lubei white goat based on the whole-genome data.	О
40	The Identification of a Yield-Related Gene Controlling Multiple Traits Using GWAS in Sorghum (Sorghum bicolor L.). 2023 , 12, 1557	О

39	High-density SNP markers reveals the population structure of two local chicken genetic resources. 2023 , 102692	О
38	Genomic adaptation to extreme climate conditions in beef cattle as a consequence of cross-breeding program. 2023 , 24,	O
37	Unraveling the Genetic Population Structure of Mongolian Indigenous Cattle Breeds Using Whole Genome Sequencing Data. 2023 , 36-42	О
36	Echoes from the last Green Sahara: whole genome analysis of Fulani, a key population to unveil the genetic evolutionary history of Africa.	O
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33	The origin of a mountain biota: hyper-aridity shaped reptile diversity in an Arabian biodiversity hotspot.	0
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31	Genomic analysis of two phlebotomine sand fly vectors of leishmania from the new and old World. 2023 , 17, e0010862	O
30	Genome-wide association screening and MassARRAY for detection of high-temperature resistance-related SNPs and genes in a hybrid abalone (Haliotis discus hannai ?TH. fulgens ?) based on super genotyping-by-sequencing. 2023 , 573, 739576	O
29	Detection and distribution of two dominant alleles associated with the sweet kernel phenotype in almond cultivated germplasm. 14,	O
28	Comparative population genomics provide new insight into the evolutionary history and adaptive potential of World Ocean krill.	О
27	Evaluating the potential impact of selection for the A2 milk allele on inbreeding and performance in Australian Holstein cattle. 4,	0
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25	Population genomics of fall armyworm by genotyping-by-sequencing: Implications for pest management. 2023 , 18, e0284587	0
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23	Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. 2023 , 21,	0
22	Dissecting genetic basis of grain color and pre-harvest sprouting resistance by association analysis in common wheat. 2023 ,	O

21	Population dynamics and drug resistance mutations in Plasmodium falciparum on the Bijag® Archipelago, Guinea-Bissau. 2023 , 13,	0
20	Population Genetic Analysis of Six Chinese Indigenous Pig Meta-Populations Based on Geographically Isolated Regions. 2023 , 13, 1396	O
19	Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. 2023, 136,	О
18	Development of a microhaplotype panel to inform management of gray wolves.	O
17	Forensic biogeographical ancestry inference: recent insights and current trends.	O
16	An integrative framework and recommendations for the study of DNA methylation in the context of race and ethnicity. 2023 , 3,	o
15	Genome-wide association study reveals genomic loci influencing agronomic traits in Ethiopian sorghum (Sorghum bicolor (L.) Moench) landraces. 2023 , 43,	0
14	Use of Molecular Technologies in Plant Breeding. 2022 , 157-203	О
13	The evolutionary patterns, expression profiles, and genetic diversity of expanded genes in barley. 14,	0
12	A metabolic perspective of selection for fruit quality related to apple domestication and improvement. 2023 , 24,	o
11	Movement and Genomic Methods Reveal Mechanisms Promoting Connectivity in a Declining Shorebird: The Lesser Yellowlegs. 2023 , 15, 595	0
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