CITATION REPORT
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A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species

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326	Identification of late blight resistance quantitative trait loci in Solanum pimpinellifolium accession PI 270441.	
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255	Insight into resistance to Candidatus Liberibacter asiaticus, associated with Huanglongbing, in Oceanian citrus genotypes. 13,	0
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253	High genetic connectivity among large populations of Pteronotus gymnonotus in bat caves in Brazil and its implications for conservation. 10,	0
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251	An overview of salinity stress, mechanism of salinity tolerance and strategies for its management in cotton. 13,	2
250	Genetic diversity and structure in wild Robusta coffee (Coffea canephora A. Froehner) populations in Yangambi (DR Congo) and their relation with forest disturbance.	0
249	Progress in Marker-Assisted Selection to Genomics-Assisted Breeding in Tomato. 1-30	0
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238	Spatio-temporal modeling of high-throughput multi-spectral aerial images improves agronomic trait genomic prediction in hybrid maize.	0
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236	Identification and validation of a key genomic region on chromosome 6 for resistance to Fusarium stalk rot in tropical maize.	0
235	Genome-wide association analysis and validation with KASP markers for nut and shell traits in almond (Prunus dulcis [Mill.] D.A.Webb)..	0
234	Genetic dissection of fruit maturity date in apricot (P. armeniaca L.) through a Single Primer Enrichment Technology (SPET) approach. **2022**, 23,	0
233	Genotyping marker density and prediction models effects in long-term breeding schemes of cross-pollinated crops.	0
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231	Genomic prediction of drought tolerance during seedling stage in maize using low-cost molecular markers. **2022**, 218,	0
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228	Development of breeder chip for gene detection and molecular-assisted selection by target sequencing in wheat.	0
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224	Seascape genetics in a polychaete worm: Disentangling the roles of a biogeographic barrier and environmental factors.	0

223	Dissection of a grain yield QTL from wild emmer wheat reveals sub-intervals associated with culm length and kernel number. 13,	0
222	Phylogeography and genetic variation in Western Jacob's ladder (Polemonium occidentale) provide insights into the origin and conservation of rare species in the Great Lakes region.	0
221	A Common Resequencing-Based Genetic Marker Dataset for Global Maize Diversity.	0
220	Identifying Molecular Markers for Resistance to Septoria tritici Blotch in Bread Wheat.	0
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182	Multi-environment analysis enhances genomic prediction accuracy of agronomic traits in sesame.	0
181	Genetic Characterization of Downy Mildew Resistance from the Hop (Humulus lupulus) Line USDA 64035´M.	0
180	Developing best practices for genotyping-by-sequencing analysis using linkage maps as benchmarks.	0
179	Development of molecular inversion probes for soybean progeny genomic selection genotyping.	0
178	Phylogenomics and the flowering plant tree of life.	1
177	High-density linkage map constructed from a skim sequenced diploid potato population reveals transmission distortion and QTLs for tuber and pollen production.	0
176	Genomic differentiation among European perch in the western Baltic Sea reflects colonisation history and local adaptation.	0
175	Genomic selection performs as effectively as phenotypic selection for increasing seed yield in soybean.	0
174	Evaluating restriction enzyme selection for genome reduction in conservation genomics.	0
173	Genome-wide analysis-based single nucleotide polymorphism marker sets to identify diverse genotypes in cabbage cultivars (Brassica oleracea var. capitata). **2022**, 12,	0
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171	Population admixtures in medaka inferred by multiple arbitrary amplicon sequencing. **2022**, 12,	0
170	The Use of DArTseq Technology to Identify Markers Linked to Genes Responsible for Seed Germination and Seed Vigor in Maize. **2022**, 23, 14865	0

169	Genetic diversity and structure of Bipolaris oryzae and Exserohilum rostratum populations causing brown spot of rice in Burkina Faso based on genotyping-by-sequencing. 13,	0
168	QTL Analysis and CAPS Marker Development Linked with Russet in Pear (Pyrus spp.). **2022**, 11, 3196	0
167	Quantitative trait locus mapping for important yield traits of a sorghum-sudangrass hybrid using a high-density single nucleotide polymorphism map. 13,	0
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164	3D-GBS: A universal genotyping-by-sequencing approach for genomic selection and other high-throughput low-cost applications in species with small to medium-sized genomes.	0
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162	Genetic Diversity and Population Structure of Chinese Chestnut (Castanea mollissima Blume) Cultivars Revealed by GBS Resequencing. **2022**, 11, 3524	0
161	Analysis of Genetic Diversity and Population Structure of Cowpea (Vigna unguiculata (L.) Walp) Genotypes Using Single Nucleotide Polymorphism Markers. **2022**, 11, 3480	1
160	Genome assembly and association tests identify interacting loci associated with vigor, precocity, and sex in interspecific pistachio rootstocks.	2
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155	High heterogeneity in genomic differentiation between phenotypically divergent songbirds: a test of mitonuclear co-introgression.	0
154	Characterization of Rsg3 , a novel greenbug resistance gene from the Chinese barley landrace PI 565676.	0
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151	Genetic basis of maize kernel protein content revealed by high-density bin mapping using recombinant inbred lines. 13,	0
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147	Multi-location trials and population-based genotyping reveal high diversity and adaptation to breeding environments in a large collection of red clover.	0
146	Selection of a CTAB protocol for high-quality DNA extraction in Oryza sativa L. validated for application in genotyping process based on Illumina sequencing.	0
145	Ancient vicariance is reinforced by adaptive divergence in the southern beech: Contributions from geogenomics.	0
144	Genetic analysis for detection of genes associated to drought tolerance in rice accessions belonging to north east India.	0
143	Predicting recombination frequency from map distance.	0
142	AgroGenome: Interactive Genomic-Based Web Server Developed Based on Data Collected for Accessions Stored in Polish Genebank. **2023**, 13, 193	0
141	Integrated Use of Molecular and Omics Approaches for Breeding High Yield and Stress Resistance Chili Peppers. **2023**, 279-335	0
140	A first look at sea-lavenders genomics can genome wide SNP information tip the scales of controversy in the Limonium vulgare species complex?. **2023**, 23,	0
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134	Genetic diversity and structure in wild Robusta coffee (Coffea canephora A. Froehner) populations in Yangambi (DR Congo) and their relation to forest disturbance.	0

133	Image-based assessment of plant disease progression identifies new genetic loci for resistance to Ralstonia solanacearum in tomato.	0
132	Contrasting Phylogeographic Patterns of Mitochondrial and Genome-Wide Variation in the Groundwater Amphipod Crangonyx islandicus That Survived the Ice Age in Iceland. **2023**, 15, 88	0
131	Construction of a genome-wide genetic linkage map and identification of quantitative trait loci for powdery mildew resistance in Gerbera daisy. 13,	0
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129	Biogeography of the Sunda Shelf revisited: Insights from Macaranga section Pruinosae (Euphorbiaceae). 10,	0
128	Outlier analyses and genome-wide association study identify glgC and ERD6-like 4 as candidate genes for foliar water-soluble carbohydrate accumulation in Trifolium repens. 13,	0
127	The influence of habitat characteristics on the occupancy and dispersal of two headwater fishes in a dendritic network. **2023**, 14,	0
126	Genotyping by sequencing and a newly developed mRNA-GBS approach to link population genetic and transcriptome analyses reveal pattern differences between sites and treatments in red clover (Trifolium pratense L.). 10,	0
125	Genetic diversity of North American popcorn germplasm and the effect of population structure on nicosulfuron response.	0
124	Genetic improvement of economic traits in Murrah buffalo using significant SNPs from genome wide association study.	0
123	Identification of Genomic Regions Associated with High Grain Zn Content in Polished Rice Using Genotyping-by-Sequencing (GBS). **2023**, 12, 144	0
122	Sweet Cherry Diversity and Relationships in Modern and Local Varieties Based on SNP Markers. **2023**, 12, 136	0
121	Population Genomics Study and Implications for the Conservation of Zabelia tyaihyonii Based on Genotyping-By-Sequencing. **2023**, 12, 171	0
120	Genome-wide assessment of population genetic and demographic history in Magnolia odoratissima based on SLAF-seq.	0
119	Population structure and genetic diversity of Triticum araraticum Jakubz. and Triticum timopheevii Zhuk..	0
118	Genetic approaches to exploit landraces for improvement of Triticum turgidum ssp. durum in the age of climate change. 14,	0
117	High-throughput sequencing confirms the boundary between traditionally considered species pairs in a group of lichenized fungi (Peltigeraceae, Pseudocyphellaria).	0
116	Genetic diversity and structure of the 4th cycle breeding population of Chinese fir (Cunninghamia lanceolata (lamb.) hook). 14,	0

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114	Genetic linkage maps and QTLs associated with fruit skin color and acidity in apple (Malus □ domestica).	1
113	From Classical to Modern Computational Approaches to Identify Key Genetic Regulatory Components in Plant Biology. **2023**, 24, 2526	0
112	Identification of Commercial Cultivars in the Tabebuia Alliance Using Genotyping-by-Sequencing. **2023**, 14, 271	0
111	Circumpolar sampling reveals high genetic connectivity of Antarctic toothfish across their spatial distribution.	0
110	Use of genomics and phenomics in grain amaranths for diversity assessment and breeding in the Americas. **2023**, 95-114	0
109	Comparison of linear and semi-parametric models incorporating genomic, pedigree, and associated loci information for the prediction of resistance to stripe rust in an Austrian winter wheat breeding program. **2023**, 136, 1-12	0
108	Identification of genes for seed isoflavones based on bulk segregant analysis sequencing in soybean natural population. **2023**, 136, 1-12	1
107	DNA release from plant tissue using focused ultrasound extraction (FUSE).	0
106	Construction of a high-resolution genetic map and identification of single nucleotide polymorphism markers relevant to flower stalk height in onion. 14,	0
105	On the accuracy of threshold genomic prediction models for leaf miner and leaf rust resistance in arabica coffee. **2023**, 19,	0
104	Genome-wide diversity analysis suggests divergence among Upper Guinea and the Dahomey Gap populations of the Sisr□berry (Syn: miracle fruit) plant (Synsepalum dulcificum [Schumach. & Thonn.] Daniell) in West Africa.	0
103	Genome-wide association study of agronomical and root-related traits in spring barley collection grown under field conditions. 14,	0
102	White Lupin Drought Tolerance: Genetic Variation, Trait Genetic Architecture, and Genome-Enabled Prediction. **2023**, 24, 2351	1
101	Molecular Characterization and Mapping of Stress Resistance Genes Using SNP Platform in Legumes. **2023**, 149-188	0
100	Organellar DNA continues to provide a rich source of information in the genomics era.	0
99	Whole-exome sequencing of selected bread wheat recombinant inbred lines as a useful resource for allele mining and bulked segregant analysis. 13,	0
98	A neural network for phenotyping Fusarium -damaged kernels (FDKs) in wheat and its impact on genomic selection accuracy. **2023**, 6,	0

97 Genotyping by Sequencing (GBS) for Genome-Wide SNP Identification in Plants. **2023**, 1-8 o

96 A greenhouse-based high-throughput phenotyping platform for identification and genetic dissection of resistance to Aphanomyces root rot in field pea. **2023**, 6, o

95 Genomic Insights into the Origin of a Thermotolerant Tomato Line and Identification of Candidate Genes for Heat Stress. **2023**, 14, 535 o

94 Mapping quantitative trait loci for biomass yield and yield-related traits in lowland switchgrass (Panicum virgatum L.) multiple populations. o

93 White Lupin Adaptation to Moderately Calcareous Soils: Phenotypic Variation and Genome-Enabled Prediction. **2023**, 12, 1139 o

92 Genome-wide association study for the extractable phenolic profile and coat color of common bean seeds (Phaseolus vulgaris L.). **2023**, 23, o

91 Genome-wide association study of leaf-related traits in tea plant in Guizhou based on genotyping-by-sequencing. **2023**, 23, o

90 Geography and past climate changes have shaped the evolution of a widespread lizard in arid Central Asia. **2023**, 184, 107781 o

89 Analysis of genetic diversity and agronomic variation in banana sub-populations for genomic selection under drought stress in southern Benin. **2023**, 859, 147210 o

88 Marker-assisted selection in a Pacific oyster population for an antiviral QTL conferring increased survival to OsHV-1 mortality events in Tomales Bay. **2023**, 567, 739291 o

87 A common resequencing-based genetic marker data set for global maize diversity. **2023**, 113, 1109-1121 o

86 Genetic diversity and local adaption of alfalfa populations (Medicago sativa L.) under long-term grazing. **2023**, 13, o

85 An Improved Method for Efficient DNA Extraction from Grapevine. o

84 Efficiency of genotyping by sequencing in inferring genomic relatedness and molecular insights into fat tail selection in Tunisian sheep. o

83 Designs to Improve Capability of Neural Networks to Make Structural Predictions. o

82 3D-GBS: a universal genotyping-by-sequencing approach for genomic selection and other high-throughput low-cost applications in species with small to medium-sized genomes. **2023**, 19, o

81 Improving selection efficiency inC. americana □C. avellanainterspecific hybrids through the development of an indel-based genetic map. o

80 A highly multiplexed assay to monitor pathogenicity, fungicide resistance and gene flow in the fungal wheat pathogen Zymoseptoria tritici. **2023**, 18, e0281181 o

79	Genome-wide association analysis and validation with KASP markers for nut and shell traits in almond (Prunus dulcis [Mill.] D.A.Webb). **2023**, 19,	0
78	Genome wide association analysis for grain micronutrients and anti-nutritional traits in mungbean [Vigna radiata (L.) R. Wilczek] using SNP markers. 10,	0
77	764. Recent advances in genomics of equine health, welfare and performance. **2022**,	0
76	Development of breeder chip for gene detection and molecular-assisted selection by target sequencing in wheat. **2023**, 43,	0
75	Double Digest Restriction-Site Associated DNA Sequencing (ddRADseq) Technology. **2023**, 37-57	0
74	Polyploid SNP Genotyping Using the MassARRAY System. **2023**, 93-113	0
73	Innovative Advances in Plant Genotyping. **2023**, 451-465	0
72	Disentangling Crocus Series Verni and Its Polyploids. **2023**, 12, 303	1
71	Genetic diversity variation during the natural regeneration of Vatica guangxiensis, an endangered tree species with extremely small populations. **2023**, 42, e02400	0
70	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
69	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,	0
68	Genomic insights into the NPGS intermediate wheatgrass germplasm collection.	0
67	Sparse multi-trait genomic prediction under balanced incomplete block design.	0
66	Phylogeography and population structure of the global, wide host-range hybrid pathogen Phytophthora cambivora. **2023**, 14,	0
65	Inter- and intra-island speciation and their morphological and ecological correlates inAeonium(Crassulaceae), a species-rich Macaronesian radiation.	0
64	Exploring genomic regions involved in bread wheat resistance to leaf rust at seedling/adult stages by using GWAS analysis. **2023**, 24,	0
63	Population genomics reveals differences in genetic structure between two endemic arboreal rodent species in threatened cloud forest habitat. **2023**, 68, 223-235	0
62	Multi-location trials and population-based genotyping reveal high diversity and adaptation to breeding environments in a large collection of red clover. 14,	0

61	Convergence or redundancy: alternative views about the evolutionary genomics of character displacement.	0
60	Genetic variation for plant growth traits in a common wheat population is dominated by known variants and novel QTL.	0
59	Heritability and gene functions associated with sclerotia formation of Rhizoctonia solani AG-7 using whole genome sequencing and genome-wide association study. **2023**, 9,	0
58	Genes and genetic mechanisms contributing to fall armyworm resistance in maize.	0
57	Genomic and evolutionary relationships among wild and cultivated blueberry species. **2023**, 23,	0
56	Smooth Descent: A ploidy-aware algorithm to improve linkage mapping in the presence of genotyping errors. 14,	0
55	Genetic clustering, and diversity of African panel of released common bean genotypes and breeding lines.	0
54	Turning Garlic into a Modern Crop: State of the Art and Perspectives. **2023**, 12, 1212	0
53	Pipeline to Design Inbred Lines and F1 Hybrids of Leaf Chicory (Radicchio) Using Male Sterility and Genotyping-by-Sequencing. **2023**, 12, 1242	0
52	Genome-Wide Association Studies (GWAS) for Agronomic Traits in Maize. **2023**, 83-98	0
51	Characterization of adaptation mechanisms in sorghum using a multi-reference back-cross nested association mapping design and envirotyping.	0
50	Genetic structure and local adaptation of Neptunea cumingii crosse populations in China based on GBS technology. 11,	0
49	Multi-environment analysis enhances genomic prediction accuracy of agronomic traits in sesame. 14,	0
48	Genome Wide Assosiation Study (GWAS) in some Chamomile Genotypes (Matricaria chamomilla L.) using Morphological, Phenological Traits. **2022**, 14, 46-55	0
47	Novel QTL for chilling tolerance at germination and early seedling stages in sorghum. 14,	0
46	Consolidating 23 years of historical data from an irrigated subtropical rice breeding program in Uruguay.	0
45	A genetic linkage map and improved genome assembly of the termite symbiont Termitomyces cryptogamus. **2023**, 24,	0
44	Geographic variability of hybridization between red-breasted and red-naped sapsuckers. **2023**, 77, 580-592	0

43	Trait Mapping of Phenolic Acids in an Interspecific (Vaccinium corymbosum var. caesariense ×V. darrowii) Diploid Blueberry Population. **2023**, 12, 1346	0
42	Identification of Causal Gene-Specific SNP Markers for the Development of Gynoecious Hybrids in Cucumber (Cucumis sativa L.) Using the PathoLogic Algorithm. **2023**, 9, 389	0
41	Assessment of the Genetic Diversity and Population Structure of the Peruvian Andean Legume, Tarwi (Lupinus mutabilis), with High Quality SNPs. **2023**, 15, 437	0
40	Resistance in pea (Pisum sativum) genetic resources to the pea aphid, Acyrthosiphon pisum.	0
39	Rice3K56 is a high-quality SNP array for genome-based genetic studies and breeding in rice (Oryza sativa L.). **2023**,	0
38	Genetic diversity assessment and genome-wide association study reveal candidate genes associated with component traits in sweet potato (Ipomoea batatas (L.) Lam).	0
37	Genetic dissection of complex traits in citrus: additive and non-additive genetic variances, inbreeding depression, and single-chromosome heritability. **2023**, 315, 111985	0
36	Genomic-assisted breeding for climate-smart coffee.	0
35	Integration of GWAS, linkage analysis and transcriptome analysis to reveal the genetic basis of flowering time-related traits in maize. 14,	0
34	The Use of DArTseq Technology to Identify Markers Related to the Heterosis Effects in Selected Traits in Maize. **2023**, 45, 2644-2660	0
33	Genomic clustering by geography not species in taxonomically complex British and Irish eyebrights (Euphrasia).	0
32	Imputation of Missing Genotypes with Intelegent K-Nearest Neighbore Algorithm. **2022**, 13, 130-138	0
31	Genome-Wide Association Study for Root Morphology and Phosphorus Acquisition Efficiency in Diverse Maize Panels. **2023**, 24, 6233	0
30	Population Genomics of Eucalypts. **2023**,	0
29	Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome. **2023**, 6,	0
28	The role of geography, ecology, and hybridisation in the evolutionary history of Canary Island Descurainia.	0
27	Identification and validation of QTLs for tuber quality related traits in yam Dioscorea alata. **2023**, 381-388	0
26	Applying molecular and genetic methods to trees and their fungal communities. **2023**, 107, 2783-2830	0

25	Replicate contact zones suggest a limited role of plumage in reproductive isolation among subspecies of the variable seedeater (Sporophila corvina).	0
24	GBScleanR: robust genotyping error correction using a hidden Markov model with error pattern recognition.	0
23	RNA-seq analysis revealed considerable genetic diversity and enabled the development of specific KASP markers for Psathyrostachys huashanica. 14,	0
22	Genetic diversity of the threatened <i>Saussurea dorogostaiskii</i> (Asteraceae) in the Khuvsgul region of Mongolia. **2023**, 53, 14-24	0
21	Elucidating the process of SNPs identification in non-reference genome crops. 1-9	0
20	Genotyping by Sequencing for SNP-Based Linkage Analysis and the Development of KASPar Markers for Male Sterility and Polyembryony in Citrus. **2023**, 12, 1567	0
19	Genomic Relationships of Glycine remota, a Recently Discovered Perennial Relative of Soybean, within Glycine. **2023**, 48, 78-87	0
18	Geographically consistent hybridization dynamics between the Black-crested and Tufted Titmouse with evidence of hybrid zone expansion.	0
17	Genome-wide association study of grain iron and zinc concentration in common bean (Phaseolus vulgaris).	0
16	Meiotic Behaviors of Allotetraploid Citrus Drive the Interspecific Recombination Landscape, the Genetic Structures, and Traits Inheritance in Tetrazyg Progenies Aiming to Select New Rootstocks. **2023**, 12, 1630	0
15	Genomic and population characterization of a diversity panel of dwarf and giant coconut accessions from the International Coconut Genebank for Latin America and Caribbean.	0
14	Haplotyping interspecific hybrids by dual alignment to both parental genomes.	0
13	Detection and distribution of two dominant alleles associated with the sweet kernel phenotype in almond cultivated germplasm. 14,	0
12	Phylogenomic investigation of safflower (Carthamus tinctorius) and related species using genotyping-by-sequencing (GBS). **2023**, 13,	0
11	Genomic-regions associated with cold stress tolerance in Asia-adapted tropical maize germplasm. **2023**, 13,	0
10	Introgression of Heterotic Genomic Segments from Brassica carinata into Brassica juncea for Enhancing Productivity. **2023**, 12, 1677	0
9	Large-Scale Phenotyping and Genotyping: State of the Art and Emerging Challenges. **2023**, 103-139	0
8	Genome-environment associations along elevation gradients in two snowbed species of the North-Eastern Calcareous Alps. **2023**, 23,	0

7	Identification of qBK2.1, a novel QTL controlling rice resistance against Fusarium fujikuroi. **2023**, 64,	0
6	Genome-wide association study reveals genomic loci influencing agronomic traits in Ethiopian sorghum (Sorghum bicolor (L.) Moench) landraces. **2023**, 43,	0
5	Exploring the impact of read clustering thresholds on RADseq-based systematics: an empirical example from European amphibians..	0
4	A novel SNP panel developed for targeted genotyping-by-sequencing (GBS) reveals genetic diversity and population structure of Musa spp. germplasm collection.	0
3	A New Assessment of Robust Capuchin Monkey (Sapajus) Evolutionary History Using Genome-Wide SNP Marker Data and a Bayesian Approach to Species Delimitation. **2023**, 14, 970	0
2	Genetic structure of an endangered species Ormosia henryi in southern China, and implications for conservation. **2023**, 23,	0
1	Two simple methods to improve the accuracy of the genomic selection methodology. **2023**, 24,	0