

# TASSEL-GBS: A High Capacity Genotyping by Sequencing

PLoS ONE

9, e90346

DOI: [10.1371/journal.pone.0090346](https://doi.org/10.1371/journal.pone.0090346)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448.	1.1	147
2	The Effects of Restrictionâ€Enzyme Choice on Properties of Genotypingâ€Byâ€Sequencing Libraries: A Study in Cassava ( <i>Manihot esculenta</i> ). Crop Science, 2014, 54, 2603-2608.	0.8	51
3	Duplicate and Conquer: Multiple Homologs of <i>PHOSPHORUS-STARVATION TOLERANCE1</i> Enhance Phosphorus Acquisition and Sorghum Performance on Low-Phosphorus Soils. Plant Physiology, 2014, 166, 659-677.	2.3	117
4	Limits on the reproducibility of marker associations with southern leaf blight resistance in the maize nested association mapping population. BMC Genomics, 2014, 15, 1068.	1.2	35
5	Flexible and scalable genotyping-by-sequencing strategies for population studies. BMC Genomics, 2014, 15, 979.	1.2	45
6	Characterization of a panel of Vietnamese rice varieties using DArT and SNP markers for association mapping purposes. BMC Plant Biology, 2014, 14, 371.	1.6	30
7	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. BMC Plant Biology, 2014, 14, 372.	1.6	85
8	Next generation sequencing technologies for next generation plant breeding. Frontiers in Plant Science, 2014, 5, 367.	1.7	69
9	High-Throughput SNP Genotyping to Accelerate Crop Improvement. Plant Breeding and Biotechnology, 2014, 2, 195-212.	0.3	330
10	Genomics to systems biology in animal and veterinary sciences: Progress, lessons and opportunities. Livestock Science, 2014, 166, 232-248.	0.6	69
11	SNP discovery in wild and domesticated populations of blue catfish, <i>Ictalurus furcatus</i> , using genotyping-by-sequencing and subsequent SNP validation. Molecular Ecology Resources, 2014, 14, 1261-1270.	2.2	28
12	Genome-Wide Association Study of Grain Polyphenol Concentrations in Global Sorghum [ <i>Sorghum bicolor</i> (L.) Moench] Germplasm. Journal of Agricultural and Food Chemistry, 2014, 62, 10916-10927.	2.4	133
13	High-Resolution Genetic Map for Understanding the Effect of Genome-Wide Recombination Rate on Nucleotide Diversity in Watermelon. G3: Genes, Genomes, Genetics, 2014, 4, 2219-2230.	0.8	34
14	Genetic structure of the four wild tomato species in the <i>Solanum peruvianum</i> s.l. species complex. Genome, 2014, 57, 169-180.	0.9	18
15	Multiparental Mapping of Plant Height and Flowering Time QTL in Partially Isogenic Sorghum Families. G3: Genes, Genomes, Genetics, 2014, 4, 1593-1602.	0.8	60
16	Novel Methods to Optimize Genotypic Imputation for Lowâ€Coverage, Nextâ€Generation Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023.	1.6	241
17	Phylogenomics of polyploid <i>Fothergilla</i> (Hamamelidaceae) by RADâ€tag based GBSâ€insights into species origin and effects of software pipelines. Journal of Systematics and Evolution, 2015, 53, 432-447.	1.6	39
18	Genomewide Association for Sugar Yield in Sweet Sorghum. Crop Science, 2015, 55, 2138-2148.	0.8	52

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19	The Genetic Makeup of a Global Barnyard Millet Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0067.	1.6	36
20	Tracking crop varieties using genotyping-by-sequencing markers: a case study using cassava ( <i>Manihot</i> ) Tj ETQq1 1 0.784314 rgBT /Over	2.7	89
21	A high-density genetic map for anchoring genome sequences and identifying QTLs associated with dwarf vine in pumpkin ( <i>Cucurbita maxima</i> Duch.). <i>BMC Genomics</i> , 2015, 16, 1101.	1.2	84
22	Mapping of the R <sub>Pc-1</sub> locus for <i>Phytophthora cactorum</i> resistance in <i>Fragaria vesca</i> . <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	15
23	Population genomics of pearl millet ( <i>Pennisetum glaucum</i> (L.) R. Br.): Comparative analysis of global accessions and Senegalese landraces. <i>BMC Genomics</i> , 2015, 16, 1048.	1.2	41
24	LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2383-2390.	0.8	407
25	High-Density Single Nucleotide Polymorphism Linkage Maps of Lowland Switchgrass using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0065.	1.6	8
26	Detection, Validation, and Application of Genotyping-by-Sequencing Based Single Nucleotide Polymorphisms in Upland Cotton. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.07.0034.	1.6	63
27	Population Genetics and Structure of a Global Foxtail Millet Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.07.0054.	1.6	28
28	Genotyping-by-Sequencing Enabled Mapping and Marker Development for the <i>BY-2</i> Potyvirus Resistance Allele in Common Bean. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0058.	1.6	51
29	Punctuated Distribution of Recombination Hotspots and Demarcation of Pericentromeric Regions in <i>Phaseolus vulgaris</i> L.. <i>PLoS ONE</i> , 2015, 10, e0116822.	1.1	52
30	Genotyping-By-Sequencing (GBS) Detects Genetic Structure and Confirms Behavioral QTL in Tame and Aggressive Foxes ( <i>Vulpes vulpes</i> ). <i>PLoS ONE</i> , 2015, 10, e0127013.	1.1	35
31	Construction of High Density Sweet Cherry ( <i>Prunus avium</i> L.) Linkage Maps Using Microsatellite Markers and SNPs Detected by Genotyping-by-Sequencing (GBS). <i>PLoS ONE</i> , 2015, 10, e0127750.	1.1	99
32	Identification of Genetic Variation between Obligate Plant Pathogens <i>Pseudoperonospora cubensis</i> and <i>P. humuli</i> Using RNA Sequencing and Genotyping-By-Sequencing. <i>PLoS ONE</i> , 2015, 10, e0143665.	1.1	29
33	Genome-Wide Association Mapping of <i>Aspergillus flavus</i> and Aflatoxin Accumulation Resistance in Maize. <i>Crop Science</i> , 2015, 55, 1857-1867.	0.8	43
34	Joint-multiple family linkage analysis predicts within-family variation better than single-family analysis of the maize nested association mapping population. <i>Heredity</i> , 2015, 114, 552-563.	1.2	74
35	QTL Analysis for Resistance to Blast Disease in U.S. Weedy Rice. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 834-844.	1.4	23
36	Whole Genome Sequencing of Fruit Tree Species. <i>Advances in Botanical Research</i> , 2015, , 1-37.	0.5	13

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37	A flexible multi-species genome-wide 60K SNP chip developed from pooled resequencing of 240 <i>Eucalyptus</i> tree genomes across 12 species. <i>New Phytologist</i> , 2015, 206, 1527-1540.	3.5	121
38	Single Nucleotide Polymorphism Identification in Polyploids: A Review, Example, and Recommendations. <i>Molecular Plant</i> , 2015, 8, 831-846.	3.9	159
39	Genomic Selection and Association Mapping in Rice ( <i>Oryza sativa</i> ): Effect of Trait Genetic Architecture, Training Population Composition, Marker Number and Statistical Model on Accuracy of Rice Genomic Selection in Elite, Tropical Rice Breeding Lines. <i>PLoS Genetics</i> , 2015, 11, e1004982.	1.5	425
40	Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1957-1968.	1.8	145
41	High-Throughput SNP Genotyping. , 2015, , 367-400.		3
42	Genome-environment associations in sorghum landraces predict adaptive traits. <i>Science Advances</i> , 2015, 1, e1400218.	4.7	257
43	Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , 2015, 114, 291-299.	1.2	187
44	Nucleotide diversity estimates of tomatillo ( <i>Physalis philadelphica</i> ) accessions including nine new inbred lines. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	11
45	Adaptive divergence in the monkey flower <i>Mimulus guttatus</i> is maintained by a chromosomal inversion. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1476-1486.	1.1	163
46	Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. <i>BMC Genomics</i> , 2015, 16, 248.	1.2	19
47	Genome-wide association study reveals a set of genes associated with resistance to the Mediterranean corn borer ( <i>Sesamia nonagrioides</i> L.) in a maize diversity panel. <i>BMC Plant Biology</i> , 2015, 15, 35.	1.6	73
48	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015, 6, 6914.	5.8	213
49	Recombination in diverse maize is stable, predictable, and associated with genetic load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3823-3828.	3.3	210
50	Relatedness predicts multiple measures of investment in cooperative nest construction in sociable weavers. <i>Behavioral Ecology and Sociobiology</i> , 2015, 69, 1835-1843.	0.6	5
51	SNP Discovery in Complex Allotetraploid Genomes ( <i>Gossypium</i> spp., Malvaceae) Using Genotyping by Sequencing. <i>Applications in Plant Sciences</i> , 2015, 3, 1400077.	0.8	16
52	Ensemble Learning of QTL Models Improves Prediction of Complex Traits. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2073-2084.	0.8	6
53	Next-generation sampling: Pairing genomics with herbarium specimens provides species-level signal in <i>Solidago</i> ( <i>Asteraceae</i> ). <i>Applications in Plant Sciences</i> , 2015, 3, 1500014.	0.8	62
54	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312.	1.2	67

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55	RIG: Recalibration and Interrelation of Genomic Sequence Data with the GATK. G3: Genes, Genomes, Genetics, 2015, 5, 655-665.	0.8	75
56	Marker-Based Estimates Reveal Significant Nonadditive Effects in Clonally Propagated Cassava ( <i>Manihot esculenta</i> ): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. G3: Genes, Genomes, Genetics, 2016, 6, 3497-3506.	0.8	34
57	Establishment and Optimization of Genomic Selection to Accelerate the Domestication and Improvement of Intermediate Wheatgrass. Plant Genome, 2016, 9, plantgenome2015.07.0059.	1.6	86
58	Genomic ancestry estimation quantifies use of wild species in grape breeding. BMC Genomics, 2016, 17, 478.	1.2	40
59	Genome-Wide SNP Calling from Genotyping by Sequencing (GBS) Data: A Comparison of Seven Pipelines and Two Sequencing Technologies. PLoS ONE, 2016, 11, e0161333.	1.1	109
60	Next Generation Mapping of Enological Traits in an F2 Interspecific Grapevine Hybrid Family. PLoS ONE, 2016, 11, e0149560.	1.1	40
61	Ascertainment bias from imputation methods evaluation in wheat. BMC Genomics, 2016, 17, 773.	1.2	5
62	Using Genome-Wide SNP Discovery and Genotyping to Reveal the Main Source of Population Differentiation in <i>Nothofagus dombeyi</i> (Mirb.) Oerst. in Chile. International Journal of Genomics, 2016, 2016, 1-10.	0.8	9
63	Identification of QTLs for yield-related traits in RILs derived from the cross between pLIA-1 carrying <i>Oryza longistaminata</i> chromosome segments and Norin 18 in rice. Breeding Science, 2016, 66, 720-733.	0.9	15
64	Genomic Selection in the Era of Next Generation Sequencing for Complex Traits in Plant Breeding. Frontiers in Genetics, 2016, 7, 221.	1.1	267
65	Using Genome-Wide SNPs to Detect Structure in High-Diversity and Low-Divergence Populations of Severely Impacted Eastern Tropical Pacific Spinner ( <i>Stenella longirostris</i> ) and Pantropical Spotted Dolphins ( <i>S. attenuata</i> ). Frontiers in Marine Science, 2016, 3, .	1.2	20
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67	GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data. PLoS Genetics, 2016, 12, e1005631.	1.5	30
68	A Genome-Wide Association Study on the Seedless Phenotype in Banana ( <i>Musa</i> spp.) Reveals the Potential of a Selected Panel to Detect Candidate Genes in a Vegetatively Propagated Crop. PLoS ONE, 2016, 11, e0154448.	1.1	61
69	Genetic Variation within Clonal Lineages of <i>Phytophthora infestans</i> Revealed through Genotyping-By-Sequencing, and Implications for Late Blight Epidemiology. PLoS ONE, 2016, 11, e0165690.	1.1	26
70	Genomics-assisted breeding in fruit trees. Breeding Science, 2016, 66, 100-115.	0.9	101
71	Association Mapping of Flowering Time QTLs and Insight into Their Contributions to Rapeseed Growth Habits. Frontiers in Plant Science, 2016, 7, 338.	1.7	77
72	Genotyping-by-Sequencing SNP Identification for Crops without a Reference Genome: Using Transcriptome Based Mapping as an Alternative Strategy. Frontiers in Plant Science, 2016, 7, 777.	1.7	21

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73	Combined Linkage and Association Mapping Reveals QTL and Candidate Genes for Plant and Ear Height in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 833.	1.7	117
74	Genome-Wide Association Study Identifies Loci for Salt Tolerance during Germination in Autotetraploid Alfalfa ( <i>Medicago sativa</i> L.) Using Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2016, 7, 956.	1.7	75
75	Genome-Wide Association and Prediction Reveals Genetic Architecture of Cassava Mosaic Disease Resistance and Prospects for Rapid Genetic Improvement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0118.	1.6	120
76	Eleven years of breeding efforts to combat cassava brown streak disease. <i>Breeding Science</i> , 2016, 66, 560-571.	0.9	75
77	Modeling Genotype × Environment Interaction for Genomic Selection with Unbalanced Data from a Wheat Breeding Program. <i>Crop Science</i> , 2016, 56, 2165-2179.	0.8	99
78	Quantifying variety-specific heat resistance and the potential for adaptation to climate change. <i>Global Change Biology</i> , 2016, 22, 2904-2912.	4.2	20
79	The population genomic basis of geographic differentiation in <i>North American common ragweed</i> ( <i>Ambrosia artemisiifolia</i> L.). <i>Ecology and Evolution</i> , 2016, 6, 3760-3771.	0.8	35
80	Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1775-1784.	1.8	9
81	GLPS: a toolkit for fast and accurate analyses of genotyping-by-sequencing data without a reference genome. <i>Molecular Ecology Resources</i> , 2016, 16, 979-990.	2.2	20
82	Using Genotyping by Sequencing to Map Two Novel Anthracnose Resistance Loci in <i>Sorghum bicolor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1935-1946.	0.8	29
83	A next-generation marker genotyping platform (AmpSeq) in heterozygous crops: a case study for marker-assisted selection in grapevine. <i>Horticulture Research</i> , 2016, 3, 16002.	2.9	90
84	Genome-wide Diversity and Association Mapping for Capsaicinoids and Fruit Weight in <i>Capsicum annum</i> L. <i>Scientific Reports</i> , 2016, 6, 38081.	1.6	60
85	Development of a High-Density Linkage Map and Tagging Leaf Spot Resistance in Pearl Millet Using Genotyping-by-Sequencing Markers. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0106.	1.6	20
86	Genome-Wide Association Studies of Grain Yield Components in Diverse Sorghum Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0091.	1.6	78
87	Genome-Wide Association for Plant Height and Flowering Time across 15 Tropical Maize Populations under Managed Drought Stress and Well-Watered Conditions in Sub-Saharan Africa. <i>Crop Science</i> , 2016, 56, 2365-2378.	0.8	88
88	Characterization of <i>Brassica napus</i> L. genotypes utilizing sequence-related amplified polymorphism and genotyping by sequencing in association with cluster analysis. <i>Molecular Breeding</i> , 2016, 36, 155.	1.0	4
89	Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2799-2808.	0.8	336
90	Genotyping-by-sequencing provides the discriminating power to investigate the subspecies of <i>Daucus carota</i> (Apiaceae). <i>BMC Evolutionary Biology</i> , 2016, 16, 234.	3.2	44

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91	High-throughput single nucleotide polymorphism (SNP) identification and mapping in the sesame ( <i>Sesamum indicum</i> L.) genome with genotyping by sequencing (GBS) analysis. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	29
92	Sequential Turnovers of Sex Chromosomes in African Clawed Frogs ( <i>Xenopus</i> ) Suggest Some Genomic Regions Are Good at Sex Determination. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3625-3633.	0.8	45
93	Population Dynamics Among six Major Groups of the <i>Oryza rufipogon</i> Species Complex, Wild Relative of Cultivated Asian Rice. <i>Rice</i> , 2016, 9, 56.	1.7	80
94	Using genotyping by sequencing (GBS) to identify loci in <i>Colocasia esculenta</i> linked to <i>Phytophthora colocasiae</i> resistance. <i>Acta Horticulturae</i> , 2016, , 131-138.	0.1	4
95	Characterization of genome-wide SNPs for the water flea <i>Daphnia pulicaria</i> generated by genotyping-by-sequencing (GBS). <i>Scientific Reports</i> , 2016, 6, 28569.	1.6	14
96	Development of a universal and simplified ddRAD library preparation approach for SNP discovery and genotyping in angiosperm plants. <i>Plant Methods</i> , 2016, 12, 39.	1.9	86
97	Marker imputation efficiency for genotyping-by-sequencing data in rice ( <i>Oryza sativa</i> ) and alfalfa ( <i>Medicago sativa</i> ). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	57
98	Population and Evolutionary Genomics of <i>Amblyomma americanum</i> , an Expanding Arthropod Disease Vector. <i>Genome Biology and Evolution</i> , 2016, 8, 1351-1360.	1.1	70
99	Association analysis for disease resistance to <i>Fusarium oxysporum</i> in cape gooseberry ( <i>Physalis</i> ). <i>Tj ETQqO O O rgBT /Qverlock 10 Tf 50 4</i>	1.2	41
100	Ecological population genomics in the marine environment. <i>Briefings in Functional Genomics</i> , 2016, 15, 342-351.	1.3	26
101	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. <i>Nature Genetics</i> , 2016, 48, 657-666.	9.4	432
102	Genomic variation among populations of threatened coral: <i>Acropora cervicornis</i> . <i>BMC Genomics</i> , 2016, 17, 286.	1.2	57
103	Bioinformatic analysis of genotype by sequencing (GBS) data with NGSEP. <i>BMC Genomics</i> , 2016, 17, 498.	1.2	49
104	Identification of major QTLs underlying tomato spotted wilt virus resistance in peanut cultivar Florida-EPTM 113. <i>BMC Genetics</i> , 2016, 17, 128.	2.7	31
105	A field ornithologist's guide to genomics: Practical considerations for ecology and conservation. <i>Auk</i> , 2016, 133, 626-648.	0.7	19
106	Genetic diversity analysis of <i>Gossypium arboreum</i> germplasm accessions using genotyping-by-sequencing. <i>Genetica</i> , 2016, 144, 535-545.	0.5	21
107	Genome-wide association mapping of provitamin A carotenoid content in cassava. <i>Euphytica</i> , 2016, 212, 97-110.	0.6	36
108	Single nucleotide polymorphism discovery via genotyping by sequencing to assess population genetic structure and recurrent polyploidization in <i>Andropogon gerardii</i> . <i>American Journal of Botany</i> , 2016, 103, 1314-1325.	0.8	20

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109	Genetic dissection of maize seedling root system architecture traits using an ultra-high density binmap and a recombinant inbred line population. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 266-279.	4.1	48
110	Toward the elucidation of cytoplasmic diversity in North American grape breeding programs. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	1
111	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. <i>Journal of Heredity</i> , 2016, 107, 481-495.	1.0	50
112	High-throughput and Cost-effective Chicken Genotyping Using Next-Generation Sequencing. <i>Scientific Reports</i> , 2016, 6, 26929.	1.6	55
113	Lessons from a Phenotyping Center Revealed by the Genome-Guided Mapping of Powdery Mildew Resistance Loci. <i>Phytopathology</i> , 2016, 106, 1159-1169.	1.1	27
114	Genome-wide SNP discovery and population structure analysis in pepper ( <i>Capsicum annuum</i> ) using genotyping by sequencing. <i>BMC Genomics</i> , 2016, 17, 943.	1.2	110
115	Genome-wide SNP discovery and genetic linkage map construction in sunflower ( <i>Helianthus annuus</i> L.) using a genotyping by sequencing (GBS) approach. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	27
116	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	2.0	16
117	Genomic Prediction of Single Crosses in the Early Stages of a Maize Hybrid Breeding Pipeline. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3443-3453.	0.8	107
118	Genetic Architecture of Domestication-Related Traits in Maize. <i>Genetics</i> , 2016, 204, 99-113.	1.2	39
119	Fast-Flowering Mini-Maize: Seed to Seed in 60 Days. <i>Genetics</i> , 2016, 204, 35-42.	1.2	25
120	An Overview of Genotyping by Sequencing in Crop Species and Its Application in Pepper. , 2016, , 101-116.		4
121	Rapid postglacial diversification and long-term stasis within the songbird genus <i>Junco</i> : phylogeographic and phylogenomic evidence. <i>Molecular Ecology</i> , 2016, 25, 6175-6195.	2.0	47
122	Recent demography drives changes in linked selection across the maize genome. <i>Nature Plants</i> , 2016, 2, 16084.	4.7	111
123	Genotyping-by-Sequencing Analysis for Determining Population Structure of Finger Millet Germplasm of Diverse Origins. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0058.	1.6	55
124	Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 857-863.	0.8	49
125	Genome-Wide Association Mapping of Fusarium Head Blight Resistance in Wheat using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2016, 9, plantgenome2015.04.0028.	1.6	161
126	QTL Mapping for Grain Yield, Flowering Time, and Stay-Green Traits in Sorghum with Genotyping-by-Sequencing Markers. <i>Crop Science</i> , 2016, 56, 1429-1442.	0.8	73



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128	Identification of SNPs associated with transgenic and sex phenotypes in coho salmon ( <i>Oncorhynchus tshawytscha</i> ) using genotyping-by-sequencing. <i>Journal of Heredity</i> , 2016, 107, 104-111.	0.4	1
129	Scab resistance in 'Genever' apple is conditioned by a resistance gene cluster with complex genetic control. <i>Molecular Plant Pathology</i> , 2016, 17, 159-172.	2.0	19
130	A multi-environment trials diallel analysis provides insights on the inheritance of fumonisin contamination resistance in tropical maize. <i>Euphytica</i> , 2016, 211, 277-285.	0.6	14
131	GBS-SNP-CROP: a reference-optional pipeline for SNP discovery and plant germplasm characterization using variable length, paired-end genotyping-by-sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 29.	1.2	109
132	Linkage mapping in prairie cordgrass ( <i>Spartina pectinata</i> Link) using genotyping-by-sequencing. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	10
133	Genome-wide identification of SNPs and copy number variation in common bean ( <i>Phaseolus vulgaris</i> L.) using genotyping-by-sequencing (GBS). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	87
134	Genome-wide association mapping of sexual incompatibility genes in cacao ( <i>Theobroma cacao</i> L.). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	22
135	Hybridization and introgression in two ecologically dissimilar <i>Fundulus</i> hybrid zones. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1051-1063.	1.1	17
136	Development and use of molecular markers: past and present. <i>Critical Reviews in Biotechnology</i> , 2016, 36, 290-302.	5.1	224
137	Quantitative trait loci mapping for <i>Gibberella</i> ear rot resistance and associated agronomic traits using genotyping-by-sequencing in maize. <i>Theoretical and Applied Genetics</i> , 2016, 129, 17-29.	1.8	40
138	Population genomics of Sociable Weavers <i>Philetairus socius</i> reveals considerable admixture among colonies. <i>Journal of Ornithology</i> , 2016, 157, 483-492.	0.5	4
139	Analytical workflow of double-digest restriction site-associated DNA sequencing based on empirical and <i>in silico</i> optimization in tomato. <i>DNA Research</i> , 2016, 23, 145-153.	1.5	113
140	Genetic dissection of maize plant architecture with an ultra-high density bin map based on recombinant inbred lines. <i>BMC Genomics</i> , 2016, 17, 178.	1.2	104
141	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016, 44, D1195-D1201.	6.5	170
142	Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. <i>Theoretical and Applied Genetics</i> , 2016, 129, 753-765.	1.8	94
143	Genomics of the hop pseudo-autosomal regions. <i>Euphytica</i> , 2016, 209, 171-179.	0.6	10
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147	Distant eQTLs and Non-coding Sequences Play Critical Roles in Regulating Gene Expression and Quantitative Trait Variation in Maize. <i>Molecular Plant</i> , 2017, 10, 414-426.	3.9	137
148	Genetic divergence in two tropical maize composites after four cycles of reciprocal recurrent selection. <i>Plant Breeding</i> , 2017, 136, 41-49.	1.0	12
149	Genetic dissection of powdery mildew resistance in interspecific half-sib grapevine families using SNP-based maps. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	82
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152	Genome-wide divergence, haplotype distribution and population demographic histories for <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> as revealed by genome-anchored SNPs. <i>Scientific Reports</i> , 2017, 7, 41285.	1.6	12
153	Genetic diversity of farmer-preferred cassava landraces in Tanzania based on morphological descriptors and single nucleotide polymorphisms. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 138-146.	0.4	4
154	Development of a maize 55K SNP array with improved genome coverage for molecular breeding. <i>Molecular Breeding</i> , 2017, 37, 20.	1.0	82
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156	QTL examination of a bi-parental mapping population segregating for "short-stature" in hop ( <i>Humulus lupululus</i> ). <i>Genetics</i> , 2017, 195, 1079-1086.	1.1	10
157	Genotyping-by-sequencing of waxy and glossy near-isogenic broccoli lines. <i>Euphytica</i> , 2017, 213, 1.	0.6	7
158	A small secreted protein in <i>Zymoseptoria tritici</i> is responsible for avirulence on wheat cultivars carrying the <i>Stb6</i> resistance gene. <i>New Phytologist</i> , 2017, 214, 619-631.	3.5	218
159	A study of allelic diversity underlying flowering-time adaptation in maize landraces. <i>Nature Genetics</i> , 2017, 49, 476-480.	9.4	254
160	Population genomics of an endemic Mediterranean fish: differentiation by fine scale dispersal and adaptation. <i>Scientific Reports</i> , 2017, 7, 43417.	1.6	83
161	Genome-wide association study for performance traits in chickens using genotype by sequencing approach. <i>Scientific Reports</i> , 2017, 7, 41748.	1.6	33
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164	Quantitative trait loci mapping of heat tolerance in broccoli ( <i>Brassica oleracea</i> var. <i>italica</i> ) using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , 2017, 130, 529-538.	1.8	39
165	Increased Power To Dissect Adaptive Traits in Global Sorghum Diversity Using a Nested Association Mapping Population. <i>Genetics</i> , 2017, 206, 573-585.	1.2	152
166	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. <i>BMC Genomics</i> , 2017, 18, 72.	1.2	91
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170	Genome-wide SNP discovery and QTL mapping for fruit quality traits in inbred backcross lines (IBLs) of <i>solanum pimpinellifolium</i> using genotyping by sequencing. <i>BMC Genomics</i> , 2017, 18, 1.	1.2	690
171	Population genomics of the raccoon dog ( <i>Nyctereutes procyonoides</i> ) in Denmark: insights into invasion history and population development. <i>Biological Invasions</i> , 2017, 19, 1637-1652.	1.2	13
172	Genomic diversity guides conservation strategies among rare terrestrial orchid species when taxonomy remains uncertain. <i>Annals of Botany</i> , 2017, 119, 1267-1277.	1.4	18
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174	Large-scale SNP discovery and construction of a high-density genetic map of <i>Colossoma macropomum</i> through genotyping-by-sequencing. <i>Scientific Reports</i> , 2017, 7, 46112.	1.6	32
175	Adapting Genotyping-by-Sequencing for Rice F2 Populations. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 881-893.	0.8	83
176	Genetic architecture of kernel composition in global sorghum germplasm. <i>BMC Genomics</i> , 2017, 18, 15.	1.2	67
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180	Genotyping-by-sequencing: a promising tool for plant genetics research and breeding. <i>Horticulture Environment and Biotechnology</i> , 2017, 58, 425-431.	0.7	81

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182	tGBS <sup>®</sup> genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017, 45, e178-e178.	6.5	115
183	A mixed model to multiple harvest-location trials applied to genomic prediction in <i>Coffea canephora</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	23
184	Karyotype Stability and Unbiased Fractionation in the Paleo-Allotetraploid <i>Cucurbita</i> Genomes. <i>Molecular Plant</i> , 2017, 10, 1293-1306.	3.9	263
185	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
186	The bottle gourd genome provides insights into Cucurbitaceae evolution and facilitates mapping of a <i>Papaya ring-spot virus</i> resistance locus. <i>Plant Journal</i> , 2017, 92, 963-975.	2.8	101
187	Genome-Wide Linkage-Disequilibrium Mapping to the Candidate Gene Level in Melon ( <i>Cucumis melo</i> ). <i>Scientific Reports</i> , 2017, 7, 9770.	1.6	62
188	Genomic signatures of local adaptation reveal source-sink dynamics in a high gene flow fish species. <i>Scientific Reports</i> , 2017, 7, 8618.	1.6	28
189	Constructing high-density genetic maps for polyploid sugarcane ( <i>Saccharum</i> spp.) and identifying quantitative trait loci controlling brown rust resistance. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	34
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191	Genome-Wide Analysis of Tar Spot Complex Resistance in Maize Using Genotyping-by-Sequencing SNPs and Whole-Genome Prediction. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0099.	1.6	69
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194	Genomic Prediction in a Large African Maize Population. <i>Crop Science</i> , 2017, 57, 2361-2371.	0.8	25
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207	Characterization of twenty <i>Camelina</i> spp. accessions using single nucleotide polymorphism genotyping. <i>Horticulture Environment and Biotechnology</i> , 2017, 58, 187-194.	0.7	4
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212	A GBS-SNP-based linkage map and quantitative trait loci (QTL) associated with resistance to <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> race 2 identified in <i>Citrullus lanatus</i> var. <i>citroides</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 319-330.	1.8	38
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219	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2062.	1.7	84
220	The Impact of Genotyping-by-Sequencing Pipelines on SNP Discovery and Identification of Markers Associated with <i>Verticillium</i> Wilt Resistance in Autotetraploid Alfalfa ( <i>Medicago sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 89.	1.7	23
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237	Optimized double-digest genotyping by sequencing (ddGBS) method with high-density SNP markers and high genotyping accuracy for chickens. <i>PLoS ONE</i> , 2017, 12, e0179073.	1.1	33
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242	Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize. <i>PLoS Genetics</i> , 2017, 13, e1007019.	1.5	136
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252	A Distinct Genetic Cluster in Cultivated Chickpea as Revealed by Genome-wide Marker Discovery and Genotyping. <i>Plant Genome</i> , 2017, 10, plantgenome2016.11.0115.	1.6	54

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254	Genetic analysis and QTL mapping of the seed hardness trait in a black common bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl... 1.0 44	1.0	44
255	Improving accuracies of genomic predictions for drought tolerance in maize by joint modeling of additive and dominance effects in multi-environment trials. <i>Heredity</i> , 2018, 121, 24-37.	1.2	68
256	A comparison between genotyping-by-sequencing and array-based scoring of SNPs for genomic prediction accuracy in winter wheat. <i>Plant Science</i> , 2018, 270, 123-130.	1.7	67
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259	Analysis of genetic relatedness among Indian cattle ( <i>Bos indicus</i> ) using genotyping-by-sequencing markers. <i>Animal Genetics</i> , 2018, 49, 242-245.	0.6	24
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266	Construction of a genome-anchored, high-density genetic map for melon ( <i>Cucumis melo</i> L.) and identification of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> race 1 resistance QTL. <i>Theoretical and Applied Genetics</i> , 2018, 131, 829-837.	1.8	26
267	Identification of drought responsive QTLs during vegetative growth stage of rice using a saturated GBS-based SNP linkage map. <i>Euphytica</i> , 2018, 214, 1.	0.6	30
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272	Predictive ability of genomic selection models in a multi-population perennial ryegrass training set using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , 2018, 131, 703-720.	1.8	65
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275	Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in <i>Coffea arabica</i> L. <i>Scientific Reports</i> , 2018, 8, 465.	1.6	53
276	Genome-wide association study in Asia-adapted tropical maize reveals novel and explored genomic regions for sorghum downy mildew resistance. <i>Scientific Reports</i> , 2018, 8, 366.	1.6	39
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278	Genomic prediction of the general combining ability of maize lines ( <i>Zea mays</i> L.) and the performance of their single crosses. <i>Plant Breeding</i> , 2018, 137, 379-387.	1.0	14
279	Genome-wide association analysis of nutritional composition-related traits and iron bioavailability in cooked dry beans ( <i>Phaseolus vulgaris</i> L.). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	55
280	Which species, how many, and from where: Integrating habitat suitability, population genomics, and abundance estimates into species reintroduction planning. <i>Global Change Biology</i> , 2018, 24, 3729-3748.	4.2	30
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282	Genetic Loci Controlling Carotenoid Biosynthesis in Diverse Tropical Maize Lines. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1049-1065.	0.8	26
283	Genome-wide association mapping of fruit-quality traits using genotyping-by-sequencing approach in citrus landraces, modern cultivars, and breeding lines in Japan. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	27
284	High-throughput sequencing data clarify evolutionary relationships among North American <i>Vitis</i> species and improve identification in USDA <i>Vitis</i> germplasm collections. <i>American Journal of Botany</i> , 2018, 105, 215-226.	0.8	45
285	Genetic structure, diversity, and hybridization in populations of the rare arctic relict <i>Euphrasia hudsoniana</i> (Orobanchaceae) and its invasive congener <i>Euphrasia stricta</i> . <i>Conservation Genetics</i> , 2018, 19, 43-55.	0.8	6
286	SNP genotyping and parameter estimation in polyploids using low-coverage sequencing data. <i>Bioinformatics</i> , 2018, 34, 407-415.	1.8	78
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290	Breeding for Biomass Yield in Switchgrass Using Surrogate Measures of Yield. <i>Bioenergy Research</i> , 2018, 11, 1-12.	2.2	15
291	Unlocking the diversity of genebanks: whole-genome marker analysis of Swiss bread wheat and spelt. <i>Theoretical and Applied Genetics</i> , 2018, 131, 407-416.	1.8	47
292	Efficiency of multi-trait, indirect, and trait-assisted genomic selection for improvement of biomass sorghum. <i>Theoretical and Applied Genetics</i> , 2018, 131, 747-755.	1.8	139
293	Combination of Acylglucose QTL reveals additive and epistatic genetic interactions and impacts insect oviposition and virus infection. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	31
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295	SNP marker panels for parentage assignment and traceability in the Florida bass ( <i>Micropterus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	1.7	30
296	Evaluation of a QTL Mapping Population Composed of Hard Red Spring and Winter Wheat Alleles Using Various Marker Platforms. <i>Crop Science</i> , 2018, 58, 701-712.	0.8	9
297	Genotyping-by-sequencing for genomic selection of perennial ryegrass ( <i>Lolium perenne</i> ). <i>Acta Horticulturae</i> , 2018, , 9-16.	0.1	0
298	Development and Evolution of an Intermediate Wheatgrass Domestication Program. <i>Sustainability</i> , 2018, 10, 1499.	1.6	89
299	gmRAD: an integrated SNP calling pipeline for genetic mapping with RADseq across a hybrid population. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	4
300	A fully automated pipeline for quantitative genotype calling from next generation sequencing data in autopolyploids. <i>BMC Bioinformatics</i> , 2018, 19, 398.	1.2	62
301	Characterizing Palestinian snake melon ( <i>Cucumis melo</i> var. <i>flexuosus</i> ) germplasm diversity and structure using SNP and DArTseq markers. <i>BMC Plant Biology</i> , 2018, 18, 246.	1.6	19
302	Linkage and association analysis of dihydrochalcones phloridzin, sieboldin, and trilobatin in <i>Malus</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	14
303	Genotyping Polyploids from Messy Sequencing Data. <i>Genetics</i> , 2018, 210, 789-807.	1.2	157
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305	SNPiversity: a web-based tool for visualizing diversity. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	9
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308	An Automated Image Analysis Pipeline Enables Genetic Studies of Shoot and Root Morphology in Carrot ( <i>Daucus carota</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1703.	1.7	29
309	Evaluation of the genetic architecture of tofu traits in soybean towards genomics-assisted breeding. <i>Plant Breeding</i> , 2018, 137, 873-882.	1.0	6
310	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. <i>Plant Genome</i> , 2018, 11, 170076.	1.6	26
311	Construction of a highly saturated linkage map in Japanese plum ( <i>Prunus salicina</i> L.) using GBS for SNP marker calling. <i>PLoS ONE</i> , 2018, 13, e0208032.	1.1	20
312	Does the Genomic Landscape of Species Divergence in Phaseolus Beans Coerce Parallel Signatures of Adaptation and Domestication?. <i>Frontiers in Plant Science</i> , 2018, 9, 1816.	1.7	56
313	Breeding-assisted genomics: Applying meta-GWAS for milling and baking quality in CIMMYT wheat breeding program. <i>PLoS ONE</i> , 2018, 13, e0204757.	1.1	50
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315	Prospects and Challenges of Applied Genomic Selection—A New Paradigm in Breeding for Grain Yield in Bread Wheat. <i>Plant Genome</i> , 2018, 11, 180017.	1.6	65
316	Genome-Wide Association and Metabolic Pathway Analysis of Corn Earworm Resistance in Maize. <i>Plant Genome</i> , 2018, 11, 170069.	1.6	20
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318	Surveying the genome and constructing a high-density genetic map of napiergrass ( <i>Cenchrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 26	1.6	32
319	Resource allocation optimization with multi-trait genomic prediction for bread wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.8	86
320	Genetic Analysis of <i>Gossypium</i> Fiber Quality Traits in Reciprocal Advanced Backcross Populations. <i>Plant Genome</i> , 2018, 11, 170057.	1.6	15
321	Ancestral Hybridization Yields Evolutionary Distinct Hybrids Lineages and Species Boundaries in Crocodiles, Posing Unique Conservation Conundrums. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	33
322	Population genomics of <i>Fundulus grandis</i> exposed to oil from Deepwater Horizon. <i>Journal of Experimental Marine Biology and Ecology</i> , 2018, 509, 82-90.	0.7	3
323	Genotyping-by-sequencing highlights patterns of genetic structure and domestication in artichoke and cardoon. <i>PLoS ONE</i> , 2018, 13, e0205988.	1.1	43
324	Seed Transmission of <i>Epichloa</i> Endophytes in <i>Lolium perenne</i> Is Heavily Influenced by Host Genetics. <i>Frontiers in Plant Science</i> , 2018, 9, 1580.	1.7	51

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326	Genome-Wide Association Study Reveals Novel Genomic Regions Associated with 10 Grain Minerals in Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3237.	1.8	72
327	Tolerance to <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> in a kiwifruit breeding parent is conferred by multiple loci. <i>Acta Horticulturae</i> , 2018, , 67-70.	0.1	4
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329	Assembling the genome of the African wild rice <i>Oryza longistaminata</i> by exploiting synteny in closely related <i>Oryza</i> species. <i>Communications Biology</i> , 2018, 1, 162.	2.0	39
330	Rapid establishment of a flowering cline in <i>Medicago polymorpha</i> after invasion of North America. <i>Molecular Ecology</i> , 2018, 27, 4758-4774.	2.0	17
331	Genome-wide association study reveals favorable alleles associated with common bunt resistance in synthetic hexaploid wheat. <i>Euphytica</i> , 2018, 214, 1.	0.6	23
332	GBS-derived SNP catalogue unveiled wide genetic variability and geographical relationships of Italian olive cultivars. <i>Scientific Reports</i> , 2018, 8, 15877.	1.6	84
333	Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3903-3913.	0.8	23
334	Molecular dissection of sugar related traits and it's attributes in <i>Saccharum</i> spp. hybrids. <i>Euphytica</i> , 2018, 214, 1.	0.6	4
335	Mapping and KASP marker development for wheat curl mite resistance in TAM 112 wheat using linkage and association analysis. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	30
336	Association mapping by aerial drone reveals 213 genetic associations for <i>Sorghum bicolor</i> biomass traits under drought. <i>BMC Genomics</i> , 2018, 19, 679.	1.2	37
337	Analysis of evolution and genetic diversity of sweetpotato and its related different polyploidy wild species <i>I. trifida</i> using RAD-seq. <i>BMC Plant Biology</i> , 2018, 18, 181.	1.6	27
338	The State of Omics Research for Farmed Penaeids: Advances in Research and Impediments to Industry Utilization. <i>Frontiers in Genetics</i> , 2018, 9, 282.	1.1	22
339	Genetic and Molecular Regulation of Seed Storage Proteins (SSPs) to Improve Protein Nutritional Value of Oilseed Rape ( <i>Brassica napus</i> L.) Seeds. <i>Frontiers in Plant Science</i> , 2018, 9, 890.	1.7	38
340	Genomic Signatures of Adaptation to a Precipitation Gradient in Nigerian Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3269-3281.	0.8	23
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342	Genome-Wide Association Study of Resistance to Ear Rot by <i>Fusarium verticillioides</i> in a Tropical Field Maize and Popcorn Core Collection. <i>Crop Science</i> , 2018, 58, 564-578.	0.8	32

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344	High-resolution genetic linkage map of European pear ( <i>Pyrus communis</i> ) and QTL fine-mapping of vegetative budbreak time. <i>BMC Plant Biology</i> , 2018, 18, 175.	1.6	26
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347	Underutilised and Neglected Crops: Next Generation Sequencing Approaches for Crop Improvement and Better Food Security. , 2018, , 287-380.		3
348	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2735-2747.	0.8	74
349	Molecular characterization of genetic basis of <i>Sugarcane Yellow Leaf Virus</i> (<sc>SCYLV</sc>) resistance in <i>Saccharum</i> spp. hybrid. <i>Plant Breeding</i> , 2018, 137, 598-604.	1.0	21
350	Genome-Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. <i>Crop Science</i> , 2018, 58, 1907-1918.	0.8	28
351	Morphometrics Reveals Complex and Heritable Apple Leaf Shapes. <i>Frontiers in Plant Science</i> , 2017, 8, 2185.	1.7	46
352	Genetic Architecture of Capitate Glandular Trichome Density in Florets of Domesticated Sunflower ( <i>Helianthus annuus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 2227.	1.7	7
353	Population Genetic Structure in Glyphosate-Resistant and -Susceptible Palmer Amaranth ( <i>Amaranthus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	31
354	Genotyping by Sequencing and Genome-Environment Associations in Wild Common Bean Predict Widespread Divergent Adaptation to Drought. <i>Frontiers in Plant Science</i> , 2018, 9, 128.	1.7	129
355	Identification of Genomic Regions Controlling Leaf Scald Resistance in Sugarcane Using a Bi-parental Mapping Population and Selective Genotyping by Sequencing. <i>Frontiers in Plant Science</i> , 2018, 9, 877.	1.7	21
356	QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2018, 19, 441.	1.8	37
357	UGbS-Flex, a novel bioinformatics pipeline for imputation-free SNP discovery in polyploids without a reference genome: finger millet as a case study. <i>BMC Plant Biology</i> , 2018, 18, 117.	1.6	54
358	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree ( <i>Hevea brasiliensis</i> ). <i>Frontiers in Plant Science</i> , 2018, 9, 815.	1.7	20
359	Adaptive introgression and maintenance of a trispecies hybrid complex in range-edge populations of <i>Populus</i> . <i>Molecular Ecology</i> , 2018, 27, 4820-4838.	2.0	56
360	Single nucleotide polymorphism (SNP) diversity in an olive germplasm collection. <i>Acta Horticulturae</i> , 2018, , 27-32.	0.1	14

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362	GBS Mapping and Analysis of Genes Conserved between <i>Gossypium tomentosum</i> and <i>Gossypium hirsutum</i> Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC2F2 Generation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1614.	1.8	39
363	Genomic prediction accuracy for switchgrass traits related to bioenergy within differentiated populations. <i>BMC Plant Biology</i> , 2018, 18, 142.	1.6	13
364	Combining High-Throughput Phenotyping and Genomic Information to Increase Prediction and Selection Accuracy in Wheat Breeding. <i>Plant Genome</i> , 2018, 11, 170043.	1.6	175
365	Bioinformatics Approaches for Genomics and Post Genomics Applications of Anticancer Plants. , 2018, , 283-317.		3
366	Characterization of a large sex determination region in <i>Salix purpurea</i> L. (Salicaceae). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1437-1452.	1.0	61
367	Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2319-2332.	0.8	30
368	Genotyping by sequencing reveals contrasting patterns of population structure, ecologically mediated divergence, and long-distance dispersal in North American palms. <i>Ecology and Evolution</i> , 2018, 8, 5873-5890.	0.8	17
369	Mapping a male-fertility restoration locus for the A4 cytoplasmic-genic male-sterility system in pearl millet using a genotyping-by-sequencing-based linkage map. <i>BMC Plant Biology</i> , 2018, 18, 65.	1.6	10
370	Genotypic and phenotypic evaluation of off-type grasses in hybrid Bermudagrass [ <i>Cynodon dactylon</i> (L.) Pers. x <i>C. transvaalensis</i> Burt-Davy] putting greens using genotyping-by-sequencing and morphological characterization. <i>Hereditas</i> , 2018, 155, 8.	0.5	8
371	Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. <i>Molecular Breeding</i> , 2018, 38, 66.	1.0	29
372	The Guiana cacao genetic group ( <i>Theobroma cacao</i> L.): a new core collection in French Guiana. <i>Botany Letters</i> , 2018, 165, 248-254.	0.7	5
373	Association mapping of days to flowering in common bean ( <i>Phaseolus vulgaris</i> L.) revealed by DArT markers. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	17
374	Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. <i>BMC Genomics</i> , 2018, 19, 591.	1.2	76
375	Genome-wide association study of <i>Gossypium arboreum</i> resistance to reniform nematode. <i>BMC Genetics</i> , 2018, 19, 52.	2.7	7
376	Tolerance to mild salinity stress in japonica rice: A genome-wide association mapping study highlights calcium signaling and metabolism genes. <i>PLoS ONE</i> , 2018, 13, e0190964.	1.1	57
377	Identification of Loci Controlling Timing of Stem Elongation in Red Clover Using GBS of Pooled Phenotypic Extremes. , 2018, , 109-112.		0
378	Population Structure of Red Clover Ecotypes Collected from Europe and Asia. , 2018, , 20-26.		0

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380	SNP markers tightly linked to root knot nematode resistance in grapevine ( <i>Vitis cinerea</i> ) identified by a genotyping-by-sequencing approach followed by Sequenom MassARRAY validation. <i>PLoS ONE</i> , 2018, 13, e0193121.	1.1	17
381	Genome-wide genotyping of a novel Mexican Chile Pepper collection illuminates the history of landrace differentiation after <i>Capsicum annuum</i> L. domestication. <i>Evolutionary Applications</i> , 2019, 12, 78-92.	1.5	21
382	Molecular diagnosis for a <i>Tamarix</i> species from two reclaimed lands along the Yellow Sea in Korea inferred from genome wide SNP markers. <i>Journal of Systematics and Evolution</i> , 2019, 57, 247-255.	1.6	7
383	Accurate genomic prediction of <i>Coffea canephora</i> in multiple environments using whole-genome statistical models. <i>Heredity</i> , 2019, 122, 261-275.	1.2	36
384	Water Deficit-Responsive QTLs for Cell Wall Degradability and Composition in Maize at Silage Stage. <i>Frontiers in Plant Science</i> , 2019, 10, 488.	1.7	17
385	Genetic diversity and population structure analysis of synthetic and bread wheat accessions in Western Siberia. <i>Journal of Applied Genetics</i> , 2019, 60, 283-289.	1.0	17
386	Genome-wide association study for leaf area, rachis length and total dry weight in oil palm ( <i>Elaeis guineensis</i> ) using genotyping by sequencing. <i>PLoS ONE</i> , 2019, 14, e0220626.	1.1	13
387	Adaptive phenotypic divergence in an annual grass differs across biotic contexts*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2230-2246.	1.1	22
388	Advanced software programs for the analysis of genetic diversity in livestock genomics: a mini review. <i>Biological Rhythm Research</i> , 2019, , 1-11.	0.4	6
389	Developmental Pleiotropy Shaped the Roots of the Domesticated Common Bean ( <i>Phaseolus</i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2230-2246.	2.3	32
390	Genome-wide Association Study of Popping Expansion in Tropical Popcorn and Field Corn Germplasm. <i>Crop Science</i> , 2019, 59, 2007-2019.	0.8	23
391	High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. <i>Scientia Horticulturae</i> , 2019, 257, 108734.	1.7	30
392	Sex-specific markers for waterhemp ( <i>Amaranthus tuberculatus</i> ) and Palmer amaranth ( <i>Amaranthus palmeri</i> ). <i>Weed Science</i> , 2019, 67, 412-418.	0.8	25
393	Genotyping-by-sequencing and SNP-arrays are complementary for detecting quantitative trait loci by tagging different haplotypes in association studies. <i>BMC Plant Biology</i> , 2019, 19, 318.	1.6	45
394	Genome-wide SNP-based diversity analysis and association mapping in linseed ( <i>Linum usitatissimum</i> L.). <i>Euphytica</i> , 2019, 215, 1.	0.6	16
395	Rapid, complete reproductive isolation in two closely related <i>Zosterops</i> White-eye bird species despite broadly overlapping ranges*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1647-1662.	1.1	27
396	QTL Analysis of Resistance to High-Intensity UV-B Irradiation in Soybean ( <i>Glycine max</i> [L.] Merr.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 3287.	1.8	9

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397	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. <i>Euphytica</i> , 2019, 215, 138.	0.6	29
398	QTL Mapping of Fusarium Head Blight Resistance in Winter Wheat Cultivars "Art"™ and "Everest"™. <i>Crop Science</i> , 2019, 59, 911-924.	0.8	8
399	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. <i>Molecular Ecology</i> , 2019, 28, 3544-3560.	2.0	32
400	Cold stress tolerance of soybeans during flowering: QTL mapping and efficient selection strategies under controlled conditions. <i>Plant Breeding</i> , 2019, 138, 708-720.	1.0	11
401	Genetic dissection of developmental responses of agro-morphological traits under different doses of nutrient fertilizers using high-density SNP markers. <i>PLoS ONE</i> , 2019, 14, e0220066.	1.1	10
402	<i>Diatraea saccharalis</i> history of colonization in the Americas. The case for human-mediated dispersal. <i>PLoS ONE</i> , 2019, 14, e0220031.	1.1	17
403	Genome-Wide Association Study for Multiple Biotic Stress Resistance in Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3667.	1.8	31
404	A High-Density Linkage Map of the Forage Grass <i>Eragrostis curvula</i> and Localization of the Diplospory Locus. <i>Frontiers in Plant Science</i> , 2019, 10, 918.	1.7	12
405	Genomic prediction offers the most effective marker assisted breeding approach for ability to prevent arsenic accumulation in rice grains. <i>PLoS ONE</i> , 2019, 14, e0217516.	1.1	31
406	Genome Wide Associations of Growth, Phenology, and Plasticity Traits in Willow [ <i>Salix viminalis</i> (L.)]. <i>Frontiers in Plant Science</i> , 2019, 10, 753.	1.7	16
407	Genomic Prediction of Pumpkin Hybrid Performance. <i>Plant Genome</i> , 2019, 12, 180082.	1.6	13
408	Thermal plasticity of the circadian clock is under nuclear and cytoplasmic control in wild barley. <i>Plant, Cell and Environment</i> , 2019, 42, 3105-3120.	2.8	12
409	Single-plant GWAS coupled with bulk segregant analysis allows rapid identification and corroboration of plant-height candidate SNPs. <i>BMC Plant Biology</i> , 2019, 19, 412.	1.6	21
410	Genetic diversity and population structure of the Mediterranean sesame core collection with use of genome-wide SNPs developed by double digest RAD-Seq. <i>PLoS ONE</i> , 2019, 14, e0223757.	1.1	28
411	Genetic and Phenotypic Diversity of the Sunflower Collection of the Pustovoit All-Russia Research Institute of Oil Crops (VNIIMK). <i>Helia</i> , 2019, 42, 45-60.	0.0	3
412	The lonome of a Genetically Diverse Set of Wild Soybean Accessions. <i>Crop Science</i> , 2019, 59, 1983-1991.	0.8	3
413	Extensive phenotypic diversity in the cultivated Florist"™s <i>Gloxinia</i> , <i>Sinningia speciosa</i> (Lodd.) Hiern, is derived from the domestication of a single founder population. <i>Plants People Planet</i> , 2019, 1, 363-374.	1.6	4
414	Genotyping by Sequencing of Cultivated Lentil ( <i>Lens culinaris</i> Medik.) Highlights Population Structure in the Mediterranean Gene Pool Associated With Geographic Patterns and Phenotypic Variables. <i>Frontiers in Genetics</i> , 2019, 10, 872.	1.1	35



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416	Genomics of Plant Disease Resistance in Legumes. <i>Frontiers in Plant Science</i> , 2019, 10, 1345.	1.7	27
417	GWAS Discovery Of Candidate Genes for Yield-Related Traits in Peanut and Support from Earlier QTL Mapping Studies. <i>Genes</i> , 2019, 10, 803.	1.0	25
418	Genomic characterization of the Native Seeds/SEARCH common bean ( <i>Phaseolus vulgaris</i> L.) collection and its seed coat patterns. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1469-1482.	0.8	22
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542	High-density SNP-based genetic diversity and heterotic patterns of tropical maize breeding lines. <i>Crop Science</i> , 2020, 60, 779-787.	0.8	9
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544	QTL mapping of resistance to <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> race 2 and Papaya ringspot virus in <i>Citrullus amarus</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 677-687.	1.8	18
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558	Phenotypic and genetic variation in phosphorus-deficiency-tolerance traits in Chinese wheat landraces. <i>BMC Plant Biology</i> , 2020, 20, 330.	1.6	19



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701	Deciphering the Genetic Diversity of Landraces With High-Throughput SNP Genotyping of DNA Bulks: Methodology and Application to the Maize 50k Array. <i>Frontiers in Plant Science</i> , 2020, 11, 568699.	1.7	9
702	RAD-R scripts: R pipeline for RAD-seq from FASTQ files to linkage maps construction and run R/QTL, operating only at copying and pasting scripts into R console. <i>Breeding Science</i> , 2021, 71, 426-434.	0.9	6



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704	Major locus for spontaneous haploid genome doubling detected by a caseâ€“control GWAS in exotic maize germplasm. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1423-1434.	1.8	9
705	Assessment of genetic diversity and agronomic traits of durum wheat germplasm under drought environment of the northern Great Plains. <i>Crop Science</i> , 2021, 61, 1194-1206.	0.8	7
706	Current status and impending progress for cassava structural genomics. <i>Plant Molecular Biology</i> , 2022, 109, 177-191.	2.0	11
707	Population structure, genetic diversity and genomic selection signatures among a Brazilian common bean germplasm. <i>Scientific Reports</i> , 2021, 11, 2964.	1.6	46
708	A referenceâ€“free approach to analyse RADseq data using standard next generation sequencing toolkits. <i>Molecular Ecology Resources</i> , 2021, 21, 1085-1097.	2.2	12
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710	Analysis of the Genome D Polymorphism of Synthetic Wheat Obtained on the Basis of <i>Ae. tauschii</i> L. <i>Russian Journal of Genetics</i> , 2021, 57, 188-195.	0.2	2
711	Analysis of the primary sources of quantitative adult plant resistance to stripe rust in U.S. soft red winter wheat germplasm. <i>Plant Genome</i> , 2021, 14, e20082.	1.6	1
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713	Construction of a High-Density Genetic Map of <i>Acca sellowiana</i> (Berg.) Burret, an Outcrossing Species, Based on Two Connected Mapping Populations. <i>Frontiers in Plant Science</i> , 2021, 12, 626811.	1.7	3
714	Genomic Resource Development for <i>Hydrangea</i> ( <i>Hydrangea macrophylla</i> (Thunb.) Ser.)â€“A Transcriptome Assembly and a High-Density Genetic Linkage Map. <i>Horticulturae</i> , 2021, 7, 25.	1.2	6
715	Comprehensive genotyping of a Brazilian cassava ( <i>Manihot esculenta</i> Crantz) germplasm bank: insights into diversification and domestication. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1343-1362.	1.8	15
716	Unraveling the Sclerotinia Basal Stalk Rot Resistance Derived From Wild <i>Helianthus argophyllus</i> Using a High-Density Single Nucleotide Polymorphism Linkage Map. <i>Frontiers in Plant Science</i> , 2020, 11, 617920.	1.7	8
718	Adaptive Divergence under Gene Flow along an Environmental Gradient in Two Coexisting Stickleback Species. <i>Genes</i> , 2021, 12, 435.	1.0	5
719	Population genomic and historical analysis suggests a global invasion by bridgehead processes in <i>Mimulus guttatus</i> . <i>Communications Biology</i> , 2021, 4, 327.	2.0	24
720	Genetic characterization of a <i>Sorghum bicolor</i> multiparent mapping population emphasizing carbon-partitioning dynamics. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	23
721	Genome-wide association analysis for arabinoxylan content in common wheat ( <i>T. Aestivum</i> L.) flour. <i>Journal of Cereal Science</i> , 2021, 98, 103166.	1.8	14

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723	The History of Lentil ( <i>Lens culinaris</i> subsp. <i>culinaris</i> ) Domestication and Spread as Revealed by Genotyping-by-Sequencing of Wild and Landrace Accessions. <i>Frontiers in Plant Science</i> , 2021, 12, 628439.	1.7	25
724	K-seq, an affordable, reliable, and open Klenow NGS-based genotyping technology. <i>Plant Methods</i> , 2021, 17, 30.	1.9	4
725	Biogeography of Neotropical mastiff bats: A case of multiple dispersals between the Caribbean and mainland. <i>Journal of Biogeography</i> , 2021, 48, 1353-1365.	1.4	1
726	Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. <i>Communications Biology</i> , 2021, 4, 375.	2.0	11
727	QTL Analysis of Adult Plant Resistance to Stripe Rust in a Winter Wheat Recombinant Inbred Population. <i>Plants</i> , 2021, 10, 572.	1.6	8
728	Sperm Methylome Profiling Can Discern Fertility Levels in the Porcine Biomedical Model. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2679.	1.8	15
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731	Elucidating the genetics of grain yield and stress-resilience in bread wheat using a large-scale genome-wide association mapping study with 55,568 lines. <i>Scientific Reports</i> , 2021, 11, 5254.	1.6	11
732	Genetic structure of wild and farmed Nile tilapia ( <i>Oreochromis niloticus</i> ) populations in Benin based on genome wide SNP technology. <i>Aquaculture</i> , 2021, 535, 736432.	1.7	9
733	Optimizing imputation of marker data from genotyping-by-sequencing (GBS) for genomic selection in non-model species: Rubber tree ( <i>Hevea brasiliensis</i> ) as a case study. <i>Genomics</i> , 2021, 113, 655-668.	1.3	7
734	Genotyping-by-Sequencing in <i>Vigna unguiculata</i> Landraces and Its Utility for Assessing Taxonomic Relationships. <i>Plants</i> , 2021, 10, 509.	1.6	10
735	Low impact of different SNP panels from two building-loci pipelines on RAD-Seq population genomic metrics: case study on five diverse aquatic species. <i>BMC Genomics</i> , 2021, 22, 150.	1.2	7
736	Identification of resistance loci against new pathotypes of <i>Plasmodiophora brassicae</i> in <i>Brassica napus</i> based on genome-wide association mapping. <i>Scientific Reports</i> , 2021, 11, 6599.	1.6	14
737	Genome wide association mapping for heat tolerance in sub-tropical maize. <i>BMC Genomics</i> , 2021, 22, 154.	1.2	28
738	High-throughput NGS-based genotyping and phenotyping: Role in genomics-assisted breeding for soybean improvement. , 2021, 3, e81.		13
739	An integrative analysis of yield stability for a GWAS in a small soybean breeding population. <i>Crop Science</i> , 2021, 61, 1903-1914.	0.8	9

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742	ngsComposer: an automated pipeline for empirically based NGS data quality filtering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
743	Genetic components of consumer liking based on visual appearance of leaf types in Brassica vegetables. <i>Euphytica</i> , 2021, 217, 1.	0.6	0
744	High-density mapping for gray leaf spot resistance using two related tropical maize recombinant inbred line populations. <i>Molecular Biology Reports</i> , 2021, 48, 3379-3392.	1.0	5
745	Genetic diversity structure of western-type carrots. <i>BMC Plant Biology</i> , 2021, 21, 200.	1.6	8
746	Genetic variation and population structure in China summer maize germplasm. <i>Scientific Reports</i> , 2021, 11, 8012.	1.6	16
748	QTL Mapping of Cucurbit yellow stunting disorder virus Resistance in Melon Accession PI 313970. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2021, 56, 424-430.	0.5	6
749	Segregation Distortion for Male Parents in High Density Genetic Maps from Reciprocal Crosses between Two Self-Incompatible Cultivars Confirms a Gametophytic System for Self-Incompatibility in Citrus. <i>Agriculture (Switzerland)</i> , 2021, 11, 379.	1.4	12
751	<i>Brassica rapa</i> Domestication: Untangling Wild and Feral Forms and Convergence of Crop Morphotypes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3358-3372.	3.5	30
752	A genomics resource for genetics, physiology, and breeding of West African sorghum. <i>Plant Genome</i> , 2021, 14, e20075.	1.6	14
753	Characterizing the oligogenic architecture of plant growth phenotypes informs genomic selection approaches in a common wheat population. <i>BMC Genomics</i> , 2021, 22, 402.	1.2	12
755	Growth-defense trade-offs masked in unadmixed populations are revealed by hybridization. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 1450-1465.	1.1	3
756	Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
757	Co-located quantitative trait loci mediate resistance to <i>Agrobacterium tumefaciens</i> , <i>Phytophthora cinnamomi</i> , and <i>P. pini</i> in <i>Juglans microcarpa</i> × <i>J. regia</i> hybrids. <i>Horticulture Research</i> , 2021, 8, 111.	2.9	4
758	Genetic variation in a radish ( <i>Raphanus sativus</i> L.) geodiversity collection. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 163-171.	0.8	5
760	Single nucleotide polymorphisms reveal genetic diversity in New Mexican chile peppers ( <i>Capsicum</i> spp.). <i>BMC Genomics</i> , 2021, 22, 356.	1.2	14
761	Cryptic introgressions contribute to transgressive segregation for early blight resistance in tomato. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2561-2575.	1.8	6

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764	Characterization and Mapping of Spot Blotch in <i>Triticum durum</i> — <i>Aegilops speltoides</i> Introgression Lines Using SNP Markers. <i>Frontiers in Plant Science</i> , 2021, 12, 650400.	1.7	6
765	QTL mapping of resistance to <i>Pseudoperonospora cubensis</i> clade 1, mating type A2, in <i>Cucumis melo</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2577-2586.	1.8	6
766	Genome-wide association mapping of the “super-soft” kernel texture in white winter wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2547-2559.	1.8	12
767	Genetic Architecture of Maize Rind Strength Revealed by the Analysis of Divergently Selected Populations. <i>Plant and Cell Physiology</i> , 2021, 62, 1199-1214.	1.5	14
769	The Genetic Base for Peanut Height-Related Traits Revealed by a Meta-Analysis. <i>Plants</i> , 2021, 10, 1058.	1.6	7
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771	Skim sequencing: an advanced NGS technology for crop improvement. <i>Journal of Genetics</i> , 2021, 100, 1.	0.4	10
772	A High-Density SNP Genetic Map Construction Using ddRAD-Seq and Mapping of Capsule Shattering Trait in Sesame. <i>Frontiers in Plant Science</i> , 2021, 12, 679659.	1.7	10
773	Marker-assisted development and evaluation of monogenic lines of rice cv. Kaohsiung 145 carrying blast resistance genes. <i>Plant Disease</i> , 2021, , PDIS01210142RE.	0.7	3
774	The Assessment of Agrobiological and Disease Resistance Traits of Grapevine Hybrid Populations ( <i>Vitis</i> ) Tj ETQq1 1 0.784314 rgBT /Over 1215.	1.6	10
775	Exploring genotype × environment interaction in sweet sorghum under tropical environments. <i>Agronomy Journal</i> , 2021, 113, 3005-3018.	0.9	6
776	High resolution mapping and candidate gene identification of downy mildew race 16 resistance in spinach. <i>BMC Genomics</i> , 2021, 22, 478.	1.2	14
777	Genomic Prediction of Yield Traits in Single-Cross Hybrid Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 692870.	1.1	7
778	Development of an Aus-Derived Nested Association Mapping (Aus-NAM) Population in Rice. <i>Plants</i> , 2021, 10, 1255.	1.6	23
779	The pan-genome of the cultivated soybean (PanSoy) reveals an extraordinarily conserved gene content. <i>Plant Biotechnology Journal</i> , 2021, 19, 1852-1862.	4.1	41
780	Development of genome-wide single nucleotide polymorphism markers for variety identification of F1 hybrids in cucumber ( <i>Cucumis sativus</i> L.). <i>Scientia Horticulturae</i> , 2021, 285, 110173.	1.7	4

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782	Single Nucleotide Polymorphism Discovery and Genetic Differentiation Analysis of Geese Bred in Poland, Using Genotyping-by-Sequencing (GBS). <i>Genes</i> , 2021, 12, 1074.	1.0	8
784	Annual and perennial <i>Medicago</i> show signatures of parallel adaptation to climate and soil in highly conserved genes. <i>Molecular Ecology</i> , 2021, 30, 4448-4465.	2.0	9
785	Association mapping of sponge cake volume in U.S. Pacific Northwest elite soft white wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 427 Td (bonasus)	1.8	3
786	Genetic variability and nitrogen response indices in common bean ( <i>Phaseolus vulgaris</i> ) cultivars under contrasting nitrogen environments. <i>Plant Breeding</i> , 2021, 140, 907.	1.0	3
787	Genetic diversity and GWAS of agronomic traits using an ICARDA lentil ( <i>Lens culinaris</i> Medik.) Reference Plus collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 279-288.	0.4	12
788	Genome-Wide Association Study of Nitrogen Use Efficiency and Agronomic Traits in Upland Rice. <i>Rice Science</i> , 2021, 28, 379-390.	1.7	14
789	Does rice breeding affect the ability of plants to interact with earthworms in nutrient-depleted Ferralsols?. <i>Applied Soil Ecology</i> , 2021, 163, 103958.	2.1	4
790	In Search of Species-Specific SNPs in a Non-Model Animal (European Bison ( <i>Bison</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td (bonasus) Genotyping-by-Sequencing (GBS) Data. <i>Animals</i> , 2021, 11, 2226.	1.0	2
791	Robust and efficient software for reference-free genomic diversity analysis of genotyping-by-sequencing data on diploid and polyploid species. <i>Molecular Ecology Resources</i> , 2022, 22, 439-454.	2.2	6
792	Morphometric relationships and their contribution to biomass and cannabinoid yield in hybrids of hemp ( <i>Cannabis sativa</i> ). <i>Journal of Experimental Botany</i> , 2021, 72, 7694-7709.	2.4	18
794	Genomic Prediction of Resistance to Tar Spot Complex of Maize in Multiple Populations Using Genotyping-by-Sequencing SNPs. <i>Frontiers in Plant Science</i> , 2021, 12, 672525.	1.7	6
795	Multi-trait genomic-enabled prediction enhances accuracy in multi-year wheat breeding trials. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
796	Mapping and identification of genetic loci affecting earliness of bolting and flowering in lettuce. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3319-3337.	1.8	12
797	Strong isolation by distance among local populations of an endangered butterfly species ( <i>Euphydryas aurinia</i> ). <i>Ecology and Evolution</i> , 2021, 11, 12790-12800.	0.8	6
798	Deep scoping: a breeding strategy to preserve, reintroduce and exploit genetic variation. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3845-3861.	1.8	6
799	Association mapping and pathway analysis of ear rot disease caused by <i>Aspergillus flavus</i> in a panel of tropical maize germplasm. <i>Crop Science</i> , 2021, 61, 4128-4138.	0.8	3
800	Identification of Candidate Genes Regulating the Seed Coat Color Trait in Sesame ( <i>Sesamum indicum</i> L.) Using an Integrated Approach of QTL Mapping and Transcriptome Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 700469.	1.1	8

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802	<i>Rsg1.a3</i> : A new allele conferring unique resistance to greenbug Biotype H at the <i>Rsg1</i> locus in <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> . Crop Science, 2021, 61, 3578-3585.	0.8	7
803	Genomic Assessment of Global Population Structure in a Highly Migratory and Habitat Versatile Apex Predator, the Tiger Shark ( <i>Galeocerdo cuvier</i> ). Journal of Heredity, 2021, 112, 497-507.	1.0	10
804	The Genetic Diversity and Population Structure of Different Geographical Populations of Bottle Gourd ( <i>Lagenaria siceraria</i> ) Accessions Based on Genotyping-by-Sequencing. Agronomy, 2021, 11, 1677.	1.3	9
805	Mapping of a novel major effect Hessian fly field partial-resistance locus in southern soft red winter wheat line LA03136E71. Theoretical and Applied Genetics, 2021, 134, 3911-3923.	1.8	2
807	Genomic sequencing confirms absence of introgression despite past hybridisation between a critically endangered bird and its common congener. Global Ecology and Conservation, 2021, 28, e01681.	1.0	9
808	GBS-SNP and SSR based genetic mapping and QTL analysis for drought tolerance in upland cotton. Physiology and Molecular Biology of Plants, 2021, 27, 1731-1745.	1.4	11
810	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. Plant Physiology, 2021, 187, 2544-2562.	2.3	23
811	Genome-Wide Comparative Analysis of Genetic Diversity of Regular and Specialty Maize Inbred Lines Through Genotyping by Target Sequencing (GBTS). Plant Molecular Biology Reporter, 2022, 40, 221-231.	1.0	1
812	Development of high-resolution multiple-SNP arrays for genetic analyses and molecular breeding through genotyping by target sequencing and liquid chip. Plant Communications, 2021, 2, 100230.	3.6	38
813	Genome-wide approaches for the identification of markers and genes associated with sugarcane yellow leaf virus resistance. Scientific Reports, 2021, 11, 15730.	1.6	21
815	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	11
816	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
817	Germplasm evaluation for crop improvement: Analysis of grain quality and cadmium accumulation in barley. Journal of Cereal Science, 2021, 101, 103297.	1.8	4
818	The <i>Melampsora americana</i> population on <i>Salix purpurea</i> in the Great Lakes region is highly diverse with a contributory influence of clonality. Phytopathology, 2021, .	1.1	2
820	DNA Variation in a Diversity Panel of Tomato Genetic Resources. Journal of the American Society for Horticultural Science, 2021, 146, 339-345.	0.5	0
822	Genetic Analysis of Mitochondrial Sorting from the MSC3 Mosaic Mutant of Cucumber. Journal of the American Society for Horticultural Science, 2021, 146, 346-350.	0.5	0
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824	Genetic characterization of melon accessions in the U.S. National Plant Germplasm System and construction of a melon core collection. <i>Molecular Horticulture</i> , 2021, 1, .	2.3	12
825	<i>Beta vulgaris</i> ssp. <i>vulgaris</i> chromosome 8 shows significant association with geosmin concentration in table beet. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
826	Broad Resistance to Post-Harvest Fruit Rot in USVL Watermelon Germplasm Lines to isolates of <i>Phytophthora capsici</i> from across USA. <i>Plant Disease</i> , 2021, , .	0.7	4
827	Genomic Insights into the Historical Population Dynamics and Spatial Differentiation of an Endangered Island Endemic Palm, <i>Brahea edulis</i> . <i>International Journal of Plant Sciences</i> , 2021, 182, 695-711.	0.6	1
828	Construction of high-density SNP genetic maps and QTL mapping for dwarf-related traits in Litchi <i>chinensis</i> Sonn. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2900-2913.	1.7	5
829	Genomic consequences of apple improvement. <i>Horticulture Research</i> , 2021, 8, 9.	2.9	53
830	Developing SNPs and Strategies for Genomic Analysis in Alfalfa. <i>Compendium of Plant Genomes</i> , 2021, , 159-175.	0.3	0
831	Optimization of training sets for genomic prediction of early-stage single crosses in maize. <i>Theoretical and Applied Genetics</i> , 2021, 134, 687-699.	1.8	13
832	QTL Mapping of Traits Associated with Dual Resistance to the African Stem Borer ( <i>Busseola fusca</i> ) and Spotted Stem Borer ( <i>Chilo partellus</i> ) in Sorghum ( <i>Sorghum bicolor</i> ). <i>International Journal of Genomics</i> , 2021, 2021, 1-17.	0.8	3
833	Management tools for genetic diversity in an isolated population of the honeybee ( <i>Apis mellifera</i> ) in New Zealand. <i>Animal Production Science</i> , 2021, , .	0.6	1
834	QTL Mapping Using High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1284, 257-285.	0.4	24
835	Genomic Approaches for Climate Resilience Breeding in Oats. , 2020, , 133-169.		9
836	Harnessing Maize Biodiversity. <i>Compendium of Plant Genomes</i> , 2018, , 335-366.	0.3	7
837	Rapid, Affordable, and Scalable Genotyping for Germplasm Exploration in Maize. <i>Compendium of Plant Genomes</i> , 2018, , 31-46.	0.3	6
838	Genetic architecture of photosynthesis energy partitioning as revealed by a genome-wide association approach. <i>Photosynthesis Research</i> , 2021, 150, 97-115.	1.6	8
839	Candidate genetic determinants of intraspecific variation in pea aphid susceptibility to RNA interference. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 123, 103408.	1.2	18
840	Deriving genotypes from RAD-seq short-read data using Stacks. <i>Nature Protocols</i> , 2017, 12, 2640-2659.	5.5	335
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843	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	3.1	31
889	DNA sequence-based mapping and comparative genomics of the <i>St</i> genome of <i>Pseudoroegneria spicata</i> (Pursh) Á. L. Á. versus wheat ( <i>Triticum aestivum</i> L.) and barley ( <i>Hordeum</i> ) Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50 65	1.1	10
890	Molecular confirmation of varietal status in bottle gourd ( <i>Lagenaria siceraria</i> ) using genotyping-by-sequencing. <i>Genome</i> , 2020, 63, 535-545.	0.9	3
891	A frog with three sex chromosomes that co-mingle together in nature: <i>Xenopus tropicalis</i> has a degenerate W and a Y that evolved from a Z chromosome. <i>PLoS Genetics</i> , 2020, 16, e1009121.	1.5	21
892	Gene regulatory effects of a large chromosomal inversion in highland maize. <i>PLoS Genetics</i> , 2020, 16, e1009213.	1.5	46
893	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. <i>PLoS ONE</i> , 2015, 10, e0121624.	1.1	69
894	Classification and Characterization of Species within the Genus <i>Lens</i> Using Genotyping-by-Sequencing (GBS). <i>PLoS ONE</i> , 2015, 10, e0122025.	1.1	135
895	Validation of Genotyping-By-Sequencing Analysis in Populations of Tetraploid Alfalfa by 454 Sequencing. <i>PLoS ONE</i> , 2015, 10, e0131918.	1.1	22
896	Genomic Resources for Water Yam ( <i>Dioscorea alata</i> L.): Analyses of EST-Sequences, De Novo Sequencing and GBS Libraries. <i>PLoS ONE</i> , 2015, 10, e0134031.	1.1	29
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898	Genotyping by Sequencing for SNP-Based Linkage Map Construction and QTL Analysis of Chilling Requirement and Bloom Date in Peach [ <i>Prunus persica</i> (L.) Batsch]. <i>PLoS ONE</i> , 2015, 10, e0139406.	1.1	115
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927	Grass pea natural variation reveals oligogenic resistance to <i>Fusarium oxysporum</i> f. sp. <i>pisi</i> . <i>Plant Genome</i> , 2021, 14, e20154.	1.6	5
928	Surveying Grassland Islands: the genetics and performance of Appalachian switchgrass ( <i>Panicum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	0
929	Subsampling and DNA pooling can increase gains through genomic selection in switchgrass. <i>Plant Genome</i> , 2021, 14, e20149.	1.6	3
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950	Applications of Genomics in Weed Science. , 2017, , 185-217.		0
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1004	Population demographic history and population structure for Pakistani Nili-Ravi breeding bulls based on SNP genotyping to identify genomic regions associated with male effects for milk yield and body weight. <i>PLoS ONE</i> , 2020, 15, e0242500.	1.1	2
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1009	Genetic diversity of Norway spruce ecotypes assessed by GBS-derived SNPs. <i>Scientific Reports</i> , 2021, 11, 23119.	1.6	12
1010	Reproductive barriers in cassava: Factors and implications for genetic improvement. <i>PLoS ONE</i> , 2021, 16, e0260576.	1.1	8
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1012	Accelerating wheat breeding for end-use quality through association mapping and multivariate genomic prediction. <i>Plant Genome</i> , 2021, 14, e20164.	1.6	12
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1024	The World Vegetable Center <i>Amaranthus</i> germplasm collection: Core collection development and evaluation of agronomic and nutritional traits. <i>Crop Science</i> , 2022, 62, 1173-1187.	0.8	12
1025	The Diversity of <i>Passalora fulva</i> Isolates Collected from Tomato Plants in U.S. High Tunnels. <i>Phytopathology</i> , 2022, 112, 1350-1360.	1.1	3
1026	Insights into opium poppy ( <i>Papaver</i> spp.) genetic diversity from genotyping-by-sequencing analysis. <i>Scientific Reports</i> , 2022, 12, 111.	1.6	16
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1031	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	5.8	31
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1038	Genetic Diversity on a Rare Terrestrial Orchid, <i>Habenaria linearifolia</i> in South Korea: Implications for Conservation Offered by Genome-Wide Single Nucleotide Polymorphisms. <i>Frontiers in Plant Science</i> , 2022, 13, 772621.	1.7	1
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1041	Assessment of Phenotypic and Genotypic Diversity in Elite Temperate and Tropical Sweet Sorghum Cultivars. <i>Sugar Tech</i> , 0, , 1.	0.9	0
1042	Genome wide association study identifies SNPs associated with northern corn leaf blight caused by <i>Exserohilum turcicum</i> in tropical maize germplasm ( <i>Zea mays</i> L.). <i>Euphytica</i> , 2022, 218, 1.	0.6	3
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1047	Applied phenomics and genomics for improving barley yellow dwarf resistance in winter wheat. G3: <i>Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
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1052	Whole-genome sequence and methylome profiling of the almond [ <i>Prunus dulcis</i> (Mill.) D.A. Webb] cultivar 'Nonpareil'™. G3: <i>Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	14
1053	Genetic differentiation of grain, fodder and pod vegetable type cowpeas ( <i>Vigna unguiculata</i> L.) identified through single nucleotide polymorphisms from genotyping-by-sequencing. <i>Molecular Horticulture</i> , 2022, 2, .	2.3	5
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1301	Early stages of speciation with gene flow in the Amazilia Hummingbird ( <i>Amazilia amazilia</i> ) subspecies complex of Western South America. <i>Ecology and Evolution</i> , 2022, 12, e8895.	0.8	1
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1303	Dissecting the Genetic Architecture of Carbon Partitioning in Sorghum Using Multiscale Phenotypes. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
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1315	Genome properties of key oil palm ( <i>Elaeis guineensis</i> Jacq.) breeding populations. <i>Journal of Applied Genetics</i> , 0, , .	1.0	0
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1319	Identification and validation of candidate genes for high calcium content in finger millet [ <i>Eleusine coracana</i> (L.) Gaertn.] through genome-wide association study. <i>Journal of Cereal Science</i> , 2022, 107, 103517.	1.8	11

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1321	Genome-Wide Association Mapping Identifies Key Genomic Regions for Grain Zinc and Iron Biofortification in Bread Wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1322	Partial Least Squares Enhances Genomic Prediction of New Environments. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	12
1323	Identification of Genetic Diversity, Pyrroclidine-Producing Strains and Transmission Modes of Endophytic <i>Sarocladium zeae</i> Fungi from Zea Crops. <i>Microorganisms</i> , 2022, 10, 1415.	1.6	3
1324	Development and Validation of Diagnostic KASP Markers for Brown Planthopper Resistance in Rice. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
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1328	COMPILE: a GWAS computational pipeline for gene discovery in complex genomes. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
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1330	Profiling of Fusarium head blight resistance QTL haplotypes through molecular markers, genotyping-by-sequencing, and machine learning. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3177-3194.	1.8	6
1331	Quantitative Trait Loci Mapping Analysis for Cold Tolerance Under Cold Stress and Brassinosteroid-Combined Cold Treatment at Germination and Bud Burst Stages in Rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
1332	A joint learning approach for genomic prediction in polyploid grasses. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
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1335	Genotyping by Sequencing Advancements in Barley. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1337	Descriptive Genomic Analysis and Sequence Genotyping of the Two Papaya Species ( <i>Vasconcellea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	2
1338	Autopolyploid inheritance and a heterozygous reciprocal translocation shape chromosome genetic behavior in tetraploid blueberry ( <i>Vaccinium corymbosum</i> ). <i>New Phytologist</i> , 2023, 237, 1024-1039.	3.5	9



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1340	A genome-wide association study investigating fumonisin contamination in a panel of tropical maize elite lines. <i>Euphytica</i> , 2022, 218, .	0.6	3
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1351	Selection and Validation of 48 KASP Markers for Variety Identification and Breeding Guidance in Conventional and Hybrid Rice ( <i>Oryza sativa</i> L.). <i>Rice</i> , 2022, 15, .	1.7	6
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